

83	10.8	63.5	24	22	AAA89163	Canine dystrophin
84	10.6	62.4	20	20	AAx29338	JNK2-specific prob
85	10.6	62.4	20	21	AA62881	JNK antisense olig
86	10.6	62.4	20	22	AAD14816	Human glycogen syn
87	10.6	62.4	20	24	ABL45103	Human chromosome 1
88	10.6	62.4	22	17	AA127173	PLU1S exon 2 sense
89	10.6	62.4	22	17	AA127930	PLU1S gene exon 2
90	10.6	62.4	24	19	AAV07067	Primer p3 for A. f
91	10.6	62.4	24	24	AB189774	Capture oligonucle
92	10.6	62.4	24	24	AB189775	Capture oligonucle
93	10.6	62.4	25	20	AA03487	Fragment #9 of Chl
94	10.6	61.2	15	22	AA651333	IGF-1 oligonucleot
95	10.4	61.2	18	21	AA651337	IGF-1 oligonucleot
96	10.4	61.2	15	22	AA651337	Panaeus monodon mi
97	10.4	61.2	18	22	AA651752	B. napus KCS assoc
98	10.4	61.2	19	22	AA652722	Human DNA polymera
99	10.4	61.2	20	18	AA796810	Human IgG-gamma1 c
100	10.4	61.2	20	19	AAV48007	Human B7-1 target
101	10.4	61.2	20	19	AA794145	Primer Z610315 for
102	10.4	61.2	20	21	AA293619	Antisense oligonuc
103	10.4	61.2	20	22	AA545617	Human PAMP-1 antis
104	10.4	61.2	20	22	AAH75353	Human uridine kina
105	10.4	61.2	20	22	AAH27664	Human bcl-x antis
106	10.4	61.2	20	22	AA695123	hba gene PCR prim
107	10.4	61.2	20	22	AA632849	Human B7-1 mRNA an
108	10.4	61.2	20	22	AA632950	Human B7-1 antis
109	10.4	61.2	20	22	AA633168	Human B7-1 antis
110	10.4	61.2	20	24	ABN93590	Fungi PCR primer S
111	10.4	61.2	20	24	AA596601	Telomerase reverse
112	10.4	61.2	20	24	ABK2187	Penicillium specie
113	10.4	61.2	21	19	AA226277	Human polymorphic
114	10.4	61.2	21	24	ABK1331	Arabidopsis Acyl c
115	10.4	61.2	21	24	ABD29090	Bovine fertility a
116	10.4	61.2	22	18	AA765512	Oligonucleotide 8L
117	10.4	61.2	22	21	AAZ39899	PCR primer 7 for s
118	10.4	61.2	22	21	AA685898	Primer AD173. Syn
119	10.4	61.2	24	24	ABK89038	RT-PCR primer, #4,
120	10.2	60.0	18	15	AA066783	L6 mRNA function s
121	10.2	60.0	18	24	ABK51920	Mouse Caenq2, PCR
122	10.2	60.0	19	14	AA050990	Human prothidin g
123	10.2	60.0	20	16	AA075159	RAR-alpha-1 primer
124	10.2	60.0	20	17	AA12421	Activital phosphor
125	10.2	60.0	20	17	AA12435	Activital phosphor
126	10.2	60.0	20	18	AAV01149	Homeobox 7 PCR pri
127	10.2	60.0	20	19	AAV70936	PCR primer used to
128	10.2	60.0	20	20	AAZ03809	PCR primer used to
129	10.2	60.0	20	20	AAZ03285	PCR primer used to
130	10.2	60.0	20	21	AAZ92608	Primer 6, a murine
131	10.2	60.0	20	22	AAK95204	Human cDNA clone-s
132	10.2	60.0	20	22	AAH25292	Antisense oligonuc
133	10.2	60.0	20	22	AA692836	Human P13 Kinase p
134	10.2	60.0	20	24	AAAD27995	Escherichia coli c
135	10.2	60.0	20	24	ABL52396	Mouse FLIP-c chime
136	10.2	60.0	21	19	AAV70926	PCR primer used to
137	10.2	60.0	21	19	AAV65913	Regulatory element
138	10.2	60.0	21	19	AAV65914	Regulatory element
139	10.2	60.0	21	21	AAAS3839	Rat c-Rel coding s
140	10.2	60.0	21	22	AAH24663	Nucleotide sequenc
141	10.2	60.0	21	24	ABK65616	Human single nucle
142	10.2	60.0	22	20	AAZ07591	Primer for detecti
143	10.2	60.0	22	24	ABA94946	Soybean KAS II DNA
144	10.2	60.0	24	14	AAO35526	5'-3' primer seque
145	10.2	60.0	24	22	AA513057	Probe #3 used in g
146	10.2	60.0	24	24	ABQ61253	Human aquaporin 5
147	10.2	60.0	24	24	ABQ01004	Oligonucleotide ad
148	10.2	60.0	24	24	ABQ05964	Oligonucleotide ad
149	10.2	60.0	24	24	ABQ06005	Oligonucleotide ad
150	10.2	60.0	24	24	AA519005	Oligonucleotide ad
151	10.2	60.0	24	24	AA519018	Wheat library acet
152	10.2	60.0	25	15	AAQ45170	Factor IX gene pri
153	10.2	60.0	25	17	AA12423	Activital phosphor
154	10.2	60.0	25	20	AA57102	Human mutant KCMQ2
155	10.2	60.0	25	24	ABQ61862	Human aquaporin 5
156	10.2	60.0	25	24	ABQ61864	Human aquaporin 5
157	10.2	60.0	25	24	ABQ61866	Human aquaporin 5
158	10.2	60.0	25	24	ABQ61868	Human aquaporin 5
159	10.2	60.0	25	24	ABQ61870	Human aquaporin 5
160	10.2	60.0	25	24	ABQ61872	Human aquaporin 5
161	10.2	60.0	25	24	ABQ61874	Human aquaporin 5
162	10.2	60.0	25	24	ABQ61876	Human aquaporin 5
163	10.2	60.0	25	24	ABQ61878	Human aquaporin 5
164	10.2	60.0	25	24	ABQ61880	Human aquaporin 5
165	10.2	60.0	25	24	ABQ61882	Human aquaporin 5
166	10.2	60.0	25	24	ABQ61915	Human aquaporin 5
167	10.2	60.0	25	24	ABQ61917	Human aquaporin 5
168	10.2	60.0	25	24	ABQ61919	Human aquaporin 5
169	10.2	60.0	25	24	ABQ61921	Human aquaporin 5
170	10.2	60.0	25	24	ABQ61923	Human aquaporin 5
171	10.2	60.0	25	24	ABQ61925	Human aquaporin 5
172	10.2	60.0	25	24	ABQ61927	Human aquaporin 5
173	10.2	60.0	25	24	ABQ61929	Human aquaporin 5
174	10.2	60.0	25	24	ABQ61931	Human aquaporin 5
175	10.2	58.8	15	24	AA139510	CCBP2 detecting AS
176	10.2	58.8	17	24	ABN99544	Fungi probe SEQ ID
177	10.2	58.8	17	24	ABN99554	Fungi probe SEQ ID
178	10.2	58.8	17	24	ABN99566	Fungi probe SEQ ID
179	10.2	58.8	17	24	ABN99579	Fungi probe SEQ ID
180	10.2	58.8	17	24	ABN99585	Fungi probe SEQ ID
181	10.2	58.8	17	24	ABK26259	Increased starch p
182	10.2	58.8	17	24	ABK26260	Increased starch p
183	10.2	58.8	17	24	ABK26261	Increased starch p
184	10.2	58.8	17	24	ABK26292	Increased starch p
185	10.2	58.8	17	24	ABK29141	Penicillium specie
186	10.2	58.8	17	24	ABK29151	Penicillium specie
187	10.2	58.8	17	24	ABK29163	Penicillium specie
188	10.2	58.8	17	24	ABK29176	Penicillium madric
189	10.2	58.8	17	24	ABK29182	Penicillium roquet
190	10.2	58.8	17	24	ABK29274	Aspergillus parado
191	10.2	58.8	17	24	ABK29340	Aspergillus acetic
192	10.2	58.8	17	24	ABK29346	Penicillium aurant
193	10.2	58.8	17	24	ABK29361	Penicillium crusto
194	10.2	58.8	17	24	ABK29364	Penicillium digit
195	10.2	58.8	17	24	ABK29373	Penicillium freii
196	10.2	58.8	17	24	ABK29376	Penicillium glandi
197	10.2	58.8	17	24	ABK29382	Penicillium hirsut
198	10.2	58.8	17	24	ABK29422	Penicillium verruc
199	10.2	58.8	18	21	AA658353	Human PRO1710 hybr
200	10.2	58.8	19	21	AAV81798	Granulocyte Ehr11
201	10.2	58.8	19	21	AAV49021	PCR primer #2 targ
202	10.2	58.8	20	20	AAK95765	PCR primer used to
203	10.2	58.8	20	20	AAK95770	PCR primer used to
204	10.2	58.8	20	24	AB197505	Capture oligonucle
205	10.2	58.8	21	24	ABN99450	Fungi probe SEQ ID
206	10.2	58.8	21	24	ABK29047	Aspergillus fumiga
207	10.2	58.8	21	24	ABK29258	Aspergillus clavac
208	10.2	58.8	22	19	AAV20903	PCR primer used to
209	10.2	58.8	24	24	ABO03775	Oligonucleotide ad
210	10.2	58.8	24	24	AB191002	Capture oligonucle
211	10.2	58.8	24	24	AB191003	Capture oligonucle
212	10.2	58.8	24	24	AB191580	Capture oligonucle
213	10.2	58.8	24	24	AB191581	Capture oligonucle
214	9.8	57.6	13	23	ABG81812	Oligonucleotide SE
215	9.8	57.6	13	23	ABG81813	Oligonucleotide SE
216	9.8	57.6	13	23	ABG85786	Oligonucleotide SE
217	9.8	57.6	13	23	ABG85787	Oligonucleotide SE
218	9.8	57.6	13	23	ABG85954	Oligonucleotide SE
219	9.8	57.6	13	23	ABG85955	Oligonucleotide SE
220	9.8	57.6	13	23	ABG86230	Oligonucleotide SE
221	9.8	57.6	13	23	ABG86231	Oligonucleotide SE
222	9.8	57.6	13	23	ABG86232	Oligonucleotide SE
223	9.8	57.6	13	23	ABG86233	Oligonucleotide SE
224	9.8	57.6	13	23	ABG86702	Oligonucleotide SE
225	9.8	57.6	13	23	ABG86703	Oligonucleotide SE
226	9.8	57.6	14	19	AAV95593	Human c-fos target
227	9.8	57.6	15	19	AAV31870	Human c-fos target
228	9.8	57.6	15	24	ABK15154	Human HNF3A allele

C 229	9.8	57.6	16	22	AAH42495	PCR primer used to
C 230	9.8	57.6	17	20	AAH91368	Primer for RT-PCR
C 231	9.8	57.6	17	21	AAA36448	Human genomic SNP
C 232	9.8	57.6	17	21	AAA34768	Oestrogen receptor
C 233	9.8	57.6	17	22	ABA77289	Adenosine deaminas
C 234	9.8	57.6	17	22	ABA77290	Adenosine deaminas
C 235	9.8	57.6	17	22	ABA77293	Adenosine deaminas
C 236	9.8	57.6	17	22	ABA77294	T. gondii immunoge
C 237	9.8	57.6	17	22	ASA43691	Flavonoid-3',5'-hy
C 238	9.8	57.6	18	14	AAO47859	Flavonoid-3',5'-hy
C 239	9.8	57.6	18	14	AAO47862	Flavonoid-3',5'-hy
C 240	9.8	57.6	18	14	AAO47864	Flavonoid-3',5'-hy
C 241	9.8	57.6	18	15	AAO97316	Primer amplifying
C 242	9.8	57.6	18	15	AAO97316	Delta-9 desaturase
C 243	9.8	57.6	18	18	AAH63294	Paracoccus denitrif
C 244	9.8	57.6	18	21	AAH75332	Human diallelic ma
C 245	9.8	57.6	18	21	AAH75332	TRADD antisense ol
C 246	9.8	57.6	18	16	AAH01526	Human hepatitis
C 247	9.8	57.6	19	16	AAH088028	Cytomegalovirus de
C 248	9.8	57.6	19	16	AAH088028	Oligonucleotide pr
C 249	9.8	57.6	19	16	AAH087298	Epstein-Barr virus
C 250	9.8	57.6	19	16	AAH90090	Primer T96-pr1 for
C 251	9.8	57.6	19	18	AAH8121	Primer P51-3.2 for
C 252	9.8	57.6	19	18	AAH8121	Primer P51-3.2 for
C 253	9.8	57.6	19	19	AAH51598	Zea mays genome fo
C 254	9.8	57.6	19	19	AAH51598	Cyclin G1 ribozyme
C 255	9.8	57.6	19	21	AAH60139	Cyclin G1 ribozyme
C 256	9.8	57.6	19	21	AAH60139	Primer Epl. Synth
C 257	9.8	57.6	20	13	AAH26636	Staphylococcus aur
C 258	9.8	57.6	20	13	AAH26636	Primer used to det
C 259	9.8	57.6	20	15	AAH08450	Primer for porcine
C 260	9.8	57.6	20	18	AAH89502	Murine B7-1 target
C 261	9.8	57.6	20	19	AAH08026	PCR primer used to
C 262	9.8	57.6	20	20	AAH05791	BF-tu gene region
C 263	9.8	57.6	20	20	AAH99796	PCR primer used to
C 264	9.8	57.6	20	20	AAH93437	PCR primer used to
C 265	9.8	57.6	20	20	AAH93437	Human FUT3 antigen
C 266	9.8	57.6	20	21	AAH68755	PCR primer U320 us
C 267	9.8	57.6	20	21	AAH68755	pBR322 5' primer.
C 268	9.8	57.6	20	21	AAH63684	Human E-Cadherin r
C 269	9.8	57.6	20	22	AAH505678	Transcription fact
C 270	9.8	57.6	20	22	AAH87576	S aureus detection
C 271	9.8	57.6	20	22	AAH87576	S aureus gene spec
C 272	9.8	57.6	20	22	AAH58932	Integrin-linked Ki
C 273	9.8	57.6	20	22	AAH79828	Human hnRNP A1 pho
C 274	9.8	57.6	20	22	AAH69314	Murine B7-1 mRNA a
C 275	9.8	57.6	20	22	AAH69314	py644 primer used
C 276	9.8	57.6	20	22	AAH32868	Mouse C/EBP beta p
C 277	9.8	57.6	20	24	AAH35809	Primer TetR1 for m
C 278	9.8	57.6	20	24	AAH34425	Oligonucleotide us
C 279	9.8	57.6	20	24	AAH34425	Third-generation p
C 280	9.8	57.6	21	21	AAH34288	Human gene single
C 281	9.8	57.6	21	21	AAH3672	Salmonella typhimu
C 282	9.8	57.6	21	22	AAH56899	MAGE-1 PCR primer
C 283	9.8	57.6	21	22	AAH56899	Human polymorphic
C 284	9.8	57.6	21	23	AAH89159	MAGE-1 PCR primer
C 285	9.8	57.6	22	17	AAH1401	Salmonella typhimu
C 286	9.8	57.6	22	18	AAH92083	MAGE-1 gene specif
C 287	9.8	57.6	22	20	AAH28055	Probe for Candida
C 288	9.8	57.6	22	20	AAH27083	PCR primer used to
C 289	9.8	57.6	22	21	AAH64235	MAGE-1 PCR primer
C 290	9.8	57.6	22	21	AAH39235	PCR primer for MAG
C 291	9.8	57.6	22	21	AAH49184	Sense PCR primer f
C 292	9.8	57.6	22	21	AAH35532	Forward PCR primer
C 293	9.8	57.6	22	22	AAH1414	MAGE-A1 sense PCR
C 294	9.8	57.6	22	22	AAH84232	MAGE tumour reject
C 295	9.8	57.6	22	22	AAH67089	Mouse trkA gene am
C 296	9.8	57.6	23	16	AAH87643	Primer2 for amplif
C 297	9.8	57.6	23	20	AAH80650	E. coli FMS patia
C 298	9.8	57.6	23	22	AAH81965	Mycobacterium tube
C 299	9.8	57.6	24	19	AAH63997	PCR primer for clo
C 300	9.8	57.6	24	20	AAH81053	Oligonucleotide TNG
C 301	9.8	57.6	24	20	AAH15831	
C 302	9.8	57.6	24	22	AAH43310	Escherichia coli m
C 303	9.8	57.6	24	24	ABT03551	Human Ach-5 gene p
C 304	9.8	57.6	24	24	ABT01435	Oligonucleotide ad
C 305	9.8	57.6	24	24	ABT01504	Oligonucleotide ad
C 306	9.8	57.6	24	24	ABT03043	Oligonucleotide ad
C 307	9.8	57.6	24	24	ABT03985	Oligonucleotide ad
C 308	9.8	57.6	24	24	ABT06797	Oligonucleotide ad
C 309	9.8	57.6	24	24	ABT06818	Oligonucleotide ad
C 310	9.8	57.6	24	24	ABT06948	Oligonucleotide ad
C 311	9.8	57.6	24	24	ABT06989	Oligonucleotide ad
C 312	9.8	57.6	24	24	ABT06995	Oligonucleotide ad
C 313	9.8	57.6	24	24	ABT010016	Oligonucleotide ad
C 314	9.8	57.6	24	24	ABT188470	Capture oligonucle
C 315	9.8	57.6	24	24	ABT188471	Capture oligonucle
C 316	9.8	57.6	25	15	AAH81095	Mutagenic primer t
C 317	9.8	57.6	25	18	AAH02448	Rat type G protein
C 318	9.8	57.6	25	20	AAH76087	A. gossypii ADB4 p
C 319	9.8	57.6	25	20	AAH15541	PCR primer rRECR u
C 320	9.8	57.6	25	22	AAH23988	Tumour antigen 17-
C 321	9.8	57.6	25	24	ABT01858	Human aquaporin 5
C 322	9.8	57.6	25	24	ABT061860	Human aquaporin 5
C 323	9.8	57.6	25	24	ABT061911	Human aquaporin 5
C 324	9.8	57.6	25	24	ABT061913	Human aquaporin 5
C 325	9.8	57.6	25	24	ABT061933	NET-4 amplification
C 326	9.8	57.6	25	24	AAH72298	Pseudomonas aerugi
C 327	9.8	57.6	25	24	AAH72298	Human NCOG 100zyme
C 328	9.8	57.6	25	24	ABT01008	Human NCOG G-Cleav
C 329	9.8	57.6	25	24	ABT00633	Linker #1 used for
C 330	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 331	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 332	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 333	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 334	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 335	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 336	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 337	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 338	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 339	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 340	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 341	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 342	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 343	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 344	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 345	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 346	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 347	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 348	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 349	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 350	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 351	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 352	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 353	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 354	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 355	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 356	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 357	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 358	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 359	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 360	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 361	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 362	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 363	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 364	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 365	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 366	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 367	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 368	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 369	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 370	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 371	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 372	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 373	9.8	57.6	25	24	ABT00633	Human chromosome 1
C 374	9.8	57.6	25	24	ABT00633	Human chromosome 1

C 375	9.6	56.5	24	24	ABO02005	Oligonucleotide ad	C 448	9.4	55.3	20	19	AAV61121	l. brevis 16S ribo
C 376	9.6	56.5	24	24	ABO02970	Oligonucleotide ad	C 449	9.4	55.3	20	20	AA205032	PCR primer used to
C 377	9.6	56.5	24	24	ABO03189	Oligonucleotide ad	C 450	9.4	55.3	20	20	AA205032	PCR primer used to
C 378	9.6	56.5	24	24	ABO03719	Oligonucleotide ad	C 451	9.4	55.3	20	21	AA273652	Human biallelic ma
C 379	9.6	56.5	24	24	ABO03723	Oligonucleotide ad	C 452	9.4	55.3	20	21	AA292055	Mammalian Lhx3 PCR
C 380	9.6	56.5	24	24	ABO04010	Oligonucleotide ad	C 453	9.4	55.3	20	21	AA248067	Human IGF-II antis
C 381	9.6	56.5	24	24	ABO04047	Oligonucleotide ad	C 454	9.4	55.3	20	22	AA293934	Immunostimulatory
C 382	9.6	56.5	24	24	ABO06884	Oligonucleotide ad	C 455	9.4	55.3	20	22	AA293934	Immunostimulatory
C 383	9.6	56.5	24	24	ABO06925	Oligonucleotide ad	C 456	9.4	55.3	20	24	AA248176	Human HLA DPB1 10c
C 384	9.6	56.5	24	24	ABO07862	Oligonucleotide ad	C 457	9.4	55.3	20	24	AA248192	Human HLA DPB1 10c
C 385	9.6	56.5	24	24	ABO07903	Oligonucleotide ad	C 458	9.4	55.3	20	24	AA248192	Bacillus sp novel
C 386	9.6	56.5	24	24	ABO07939	Oligonucleotide ad	C 459	9.4	55.3	20	24	AA248192	Mouse C/EBP beta P
C 387	9.6	56.5	24	24	ABO07980	Oligonucleotide ad	C 460	9.4	55.3	20	24	AA248192	Chimeric phosphoro
C 388	9.6	56.5	24	24	ABO09822	Oligonucleotide ad	C 461	9.4	55.3	20	24	AA248192	Marimastat Type II G
C 389	9.6	56.5	24	24	ABO09863	Oligonucleotide ad	C 462	9.4	55.3	20	24	AA248192	Capture oligonucle
C 390	9.6	56.5	24	24	ABO10241	Oligonucleotide ad	C 463	9.4	55.3	20	24	AA248192	Penicillium purpur
C 391	9.6	56.5	24	24	ABO10282	Oligonucleotide ad	C 464	9.4	55.3	20	24	AA248192	Immunostimulatory
C 392	9.6	56.5	24	24	ABO14765	Capture oligonucle	C 465	9.4	55.3	20	24	AA248192	Immunostimulatory
C 393	9.6	56.5	24	24	ABO14765	Capture oligonucle	C 466	9.4	55.3	20	24	AA248192	Human megakaryocy
C 394	9.6	56.5	24	24	AA175968	GAlectin 10 3' PCR	C 467	9.4	55.3	21	15	AA056652	Glutathione peroxi
C 395	9.6	56.5	25	18	AAV29824	GAlectin 10 3' PCR	C 468	9.4	55.3	21	15	AA072457	Hepatitis C virus
C 396	9.6	56.5	25	19	AAV29831	Chimeric Ig gamma1	C 469	9.4	55.3	21	16	AA099347	Human polymorphic
C 397	9.6	56.5	25	19	AAV21359	Composite CRB-CAR	C 470	9.4	55.3	21	19	AA226304	Human polymorphic
C 398	9.6	56.5	25	19	AAV04090	HLA DPB1 gene PCR	C 471	9.4	55.3	21	19	AA226305	Regulatory element
C 399	9.6	56.5	25	21	AAV06349	Antisense oligonuc	C 472	9.4	55.3	21	19	AA226305	Regulatory element
C 400	9.6	56.5	25	21	AAV07768	Primer #2 used to	C 473	9.4	55.3	21	19	AA226305	Regulatory element
C 401	9.6	56.5	25	22	AAH49550	Human Ash-1 gene P	C 474	9.4	55.3	21	20	AAV55712	PCR primer for glu
C 402	9.6	56.5	25	24	ABT03543	Human colon cancer	C 475	9.4	55.3	21	20	AAV83825	PCR primer used to
C 403	9.6	56.5	25	24	AA141672	Oligonucleotide pr	C 476	9.4	55.3	21	21	AA269271	Human ABC1 gene ex
C 404	9.4	55.3	12	23	ABH98514	Oligonucleotide pr	C 477	9.4	55.3	21	21	AA269271	5' PCR primer used
C 405	9.4	55.3	13	18	AA165510	Oligonucleotide SL	C 478	9.4	55.3	21	21	AA269271	Human tumour suppr
C 406	9.4	55.3	13	23	ABCS2580	Oligonucleotide SE	C 479	9.4	55.3	21	21	AA269271	Human gene single
C 407	9.4	55.3	13	23	ABCS2581	Oligonucleotide SE	C 480	9.4	55.3	21	22	AA269271	Human gene single
C 408	9.4	55.3	13	23	ABCS2581	Oligonucleotide SE	C 481	9.4	55.3	21	22	AA269271	Partial exon 7 pub
C 409	9.4	55.3	13	23	ABCS2581	Oligonucleotide SE	C 482	9.4	55.3	21	22	AA269271	PCR primer used to
C 410	9.4	55.3	13	23	ABCS2581	Oligonucleotide SE	C 483	9.4	55.3	21	22	AA269271	Sequence of PCR pr
C 411	9.4	55.3	13	23	ABCS2581	Oligonucleotide SE	C 484	9.4	55.3	21	22	AA269271	meo-lacZ fusion c
C 412	9.4	55.3	14	20	AAV92826	Oligonucleotide SE	C 485	9.4	55.3	22	15	AA054952	Primer to amplify
C 413	9.4	55.3	14	20	AAV92826	Oligonucleotide SE	C 486	9.4	55.3	22	15	AA054952	Primer 3-S1 for ta
C 414	9.4	55.3	14	21	AA264817	Substrate for hair	C 487	9.4	55.3	22	18	AA264817	Arabidopsis RAP2.7
C 415	9.4	55.3	15	21	AA264817	Substrate for hair	C 488	9.4	55.3	22	18	AA264817	RAP2.7 gene specif
C 416	9.4	55.3	15	21	AA264817	Substrate for hair	C 489	9.4	55.3	22	20	AA264817	RAP2.7 Ap2 domain
C 417	9.4	55.3	15	21	AA264817	Substrate for hair	C 490	9.4	55.3	22	21	AA264817	aac(6)-Ic resist
C 418	9.4	55.3	15	22	AAFS0492	IGF-1 oligonucleot	C 491	9.4	55.3	22	21	AA264817	aac(6)-Ic resist
C 419	9.4	55.3	15	22	AAFS0492	IGF-1 oligonucleot	C 492	9.4	55.3	22	21	AA264817	Sequence of probe
C 420	9.4	55.3	15	22	AAFS0492	IGF-1 oligonucleot	C 493	9.4	55.3	22	21	AA264817	Neuroblastoma spec
C 421	9.4	55.3	15	22	AAFS0492	IGF-1 oligonucleot	C 494	9.4	55.3	22	21	AA264817	Human tumour necro
C 422	9.4	55.3	15	22	AAFS0492	IGF-1 oligonucleot	C 495	9.4	55.3	22	21	AA264817	PCR primer corresp
C 423	9.4	55.3	15	22	AAFS0492	IGF-1 oligonucleot	C 496	9.4	55.3	22	21	AA264817	Oligonucleotide ad
C 424	9.4	55.3	15	24	ABK95956	Human LIPF gene po	C 497	9.4	55.3	24	24	ABO02919	Oligonucleotide ad
C 425	9.4	55.3	15	24	ABK95956	Human LIPF gene po	C 498	9.4	55.3	24	24	ABO02919	Oligonucleotide ad
C 426	9.4	55.3	15	24	ABK95956	Human LIPF gene po	C 499	9.4	55.3	24	24	ABO02919	Oligonucleotide ad
C 427	9.4	55.3	15	24	ABK95956	Human LIPF gene po	C 500	9.4	55.3	24	24	ABO02919	Human basophil gra
C 428	9.4	55.3	15	24	ABK95956	Human LIPF gene po	C 501	9.4	55.3	24	24	ABO02919	Capture oligonucle
C 429	9.4	55.3	17	19	AAV43302	Primer JB627 for a	C 502	9.4	55.3	24	24	ABO02919	Capture oligonucle
C 430	9.4	55.3	17	19	AAV43302	Primer JB627 for a	C 503	9.4	55.3	24	24	ABO02919	Capture oligonucle
C 431	9.4	55.3	18	14	AAO52919	Primer for pertuss	C 504	9.4	55.3	24	24	ABO02919	Capture oligonucle
C 432	9.4	55.3	18	14	AAO52919	Primer for pertuss	C 505	9.4	55.3	24	24	ABO02919	Capture oligonucle
C 433	9.4	55.3	18	20	AAZ41105	Human G-alpha-11 p	C 506	9.4	55.3	25	16	AA207062	Novel method of de
C 434	9.4	55.3	18	20	AAZ41105	Human G-alpha-11 p	C 507	9.4	55.3	25	16	AA207062	Primer C3E2 for Cm
C 435	9.4	55.3	18	20	AAZ41105	Human G-alpha-11 p	C 508	9.4	55.3	25	16	AA207062	PCR primer LB42M u
C 436	9.4	55.3	18	21	AAZ73526	Human biallelic ma	C 509	9.4	55.3	25	21	AA207062	Cytomegalovirus et
C 437	9.4	55.3	18	22	AAZ73526	Human biallelic ma	C 510	9.4	55.3	25	21	AA207062	SNP specific SNP
C 438	9.4	55.3	18	22	AAZ73526	Human biallelic ma	C 511	9.4	55.3	25	22	AA207062	Human rela hamme
C 439	9.4	55.3	18	24	AAZ73526	Human biallelic ma	C 512	9.4	55.3	25	22	AA207062	Mouse rela hamme
C 440	9.4	55.3	19	9	AAH80321	Synthetic oligo LB	C 513	9.2	54.1	15	16	AA207062	IGF-1 oligonucleot
C 441	9.4	55.3	19	21	AAH80321	Synthetic oligo LB	C 514	9.2	54.1	15	16	AA207062	IGF-1 oligonucleot
C 442	9.4	55.3	19	21	AAH80321	Synthetic oligo LB	C 515	9.2	54.1	15	16	AA207062	IGF-1 oligonucleot
C 443	9.4	55.3	19	22	AAH80321	Synthetic oligo LB	C 516	9.2	54.1	15	16	AA207062	IGF-1 oligonucleot
C 444	9.4	55.3	19	22	AAH80321	Synthetic oligo LB	C 517	9.2	54.1	15	16	AA207062	IGF-1 oligonucleot
C 445	9.4	55.3	20	15	AAO71662	Human chromosom	C 518	9.2	54.1	16	14	AA207062	Vibrio cholerae 16
C 446	9.4	55.3	20	15	AAO71662	Human chromosom	C 519	9.2	54.1	16	14	AA207062	Human rela hamme
C 447	9.4	55.3	20	19	AAV57074	Human Notch3 mutan	C 520	9.2	54.1	16	16	AA207062	Human rela hamme

C 521	9.2	54.1	16	16	AAT55608	Mouse relA hairpin	594	9.2	54.1	20	24	ABN74928	Mouse caspase 2 an
C 522	9.2	54.1	16	24	ABK96855	Preyn1 diphosphate	595	9.2	54.1	20	24	AA514411	Reverse PCR primer
C 523	9.2	54.1	16	24	ABA9572	Acidobacterium Tag	596	9.2	54.1	20	24	AA597424	Murine SMC1 gene-8
C 524	9.2	54.1	16	24	ABA89658	Serial analysis of	597	9.2	54.1	20	24	AA516653	Human inhibitor of
C 525	9.2	54.1	16	24	ABA89768	Serial analysis of	598	9.2	54.1	20	24	AB182301	p53 mutation detec
C 526	9.2	54.1	17	14	AAQ37997	Reverse PCR primer	599	9.2	54.1	20	24	AB193470	Capture oligonucle
C 527	9.2	54.1	17	14	AAQ38490	Reverse PCR primer	600	9.2	54.1	20	24	AB194404	Capture oligonucle
C 528	9.2	54.1	17	18	AAK68973	Human fil1 VEGF re	601	9.2	54.1	20	24	AB194601	Capture oligonucle
C 529	9.2	54.1	17	18	AAK68973	Rat Ha-ras targete	602	9.2	54.1	20	24	AB194662	Capture oligonucle
C 530	9.2	54.1	17	19	AAK21341	Integrin alpha 6 s	603	9.2	54.1	20	24	AB194677	Capture oligonucle
C 531	9.2	54.1	17	20	AAA21342	Integrin alpha 6 s	604	9.2	54.1	20	24	AB195236	Capture oligonucle
C 532	9.2	54.1	17	20	AAA21343	Integrin alpha 6 s	605	9.2	54.1	20	24	AB196060	Capture oligonucle
C 533	9.2	54.1	17	20	AAA21343	Integrin subunit b	606	9.2	54.1	20	24	AB196635	Capture oligonucle
C 534	9.2	54.1	17	21	AAFO2799	Hammerhead ribozym	607	9.2	54.1	20	24	AB197345	Capture oligonucle
C 535	9.2	54.1	17	21	AAFO2799	Hammerhead ribozym	608	9.2	54.1	20	24	AB197345	Capture oligonucle
C 536	9.2	54.1	17	22	ABA79980	HBAl mutation corr	609	9.2	54.1	20	24	AB197345	Human chromosome 1
C 537	9.2	54.1	17	22	ABA79981	HBAl mutation corr	610	9.2	54.1	21	13	AAQ25066	DNA for modulating
C 538	9.2	54.1	17	24	ABK26555	Waxy starch produc	611	9.2	54.1	21	16	AAQ40205	Sequence of primer
C 539	9.2	54.1	17	24	ABK26556	Waxy starch produc	612	9.2	54.1	21	16	AAT12012	CMV DNA polymerase
C 540	9.2	54.1	17	24	ABK26559	Waxy starch produc	613	9.2	54.1	21	17	AAT32891	Bovine leukaemia v
C 541	9.2	54.1	17	24	ABK26592	Waxy starch produc	614	9.2	54.1	21	18	AAT61610	Humicola lanuginos
C 542	9.2	54.1	17	24	ABK26615	Waxy starch produc	615	9.2	54.1	21	18	AAT61599	Humicola lanuginos
C 543	9.2	54.1	17	24	ABK26616	Waxy starch produc	616	9.2	54.1	21	19	AAZ26154	Humicola lanuginos
C 544	9.2	54.1	18	16	AAQ93389	Mycosphaerella mus	617	9.2	54.1	21	19	AAZ17929	Humicola lanuginos
C 545	9.2	54.1	18	18	AAT60440	Mouse fil-1 VEGF r	618	9.2	54.1	21	20	AAZ29253	LCI leukaemia-asso
C 546	9.2	54.1	18	18	AAT60440	Mouse fil-1 VEGF r	619	9.2	54.1	21	20	AAZ29253	Human alpha-Gal A
C 547	9.2	54.1	18	19	AAV62059	Mouse Aop2 gene ex	620	9.2	54.1	21	21	AAZ70680	PCR primer used to
C 548	9.2	54.1	18	19	AAV62537	M. musicola specie	621	9.2	54.1	21	21	AAZ75436	PCR primer used to
C 549	9.2	54.1	18	19	AAT99647	Human SCA2 gene SC	622	9.2	54.1	21	21	AAZ48511	Nethesteria meningit
C 550	9.2	54.1	18	21	AAAI1067	Antisense oligonuc	623	9.2	54.1	21	21	AAZ47035	Primer #2 for huma
C 551	9.2	54.1	18	21	AAZ89240	Rat ribosomal prot	624	9.2	54.1	21	22	AAH45625	PCR primer Crei sp
C 552	9.2	54.1	18	22	ABA82411	Zmaxi gene region	625	9.2	54.1	21	22	AAD09514	Human SGP08 fragm
C 553	9.2	54.1	18	24	ABK23208	Human Zmaxi cDNA r	626	9.2	54.1	21	22	AAH26050	Typanosoma cruzi
C 554	9.2	54.1	18	24	ABK30680	Human HLA genotypi	627	9.2	54.1	21	22	AAH80194	PCR primer used to
C 555	9.2	54.1	18	24	AA520413	RT-PCR reverse pri	628	9.2	54.1	21	22	AAH97564	Human gene single
C 556	9.2	54.1	19	14	AAQ43123	HCV NS-4 antisense	629	9.2	54.1	21	22	AAH97564	Human polymorphic
C 557	9.2	54.1	19	14	AAQ36094	C. trachomatis det	630	9.2	54.1	21	23	AAH89078	C. lustrantiae 18S r
C 558	9.2	54.1	19	19	AAV22644	PCR primer specifi	631	9.2	54.1	21	24	AAH47009	Bombix mori R2 ele
C 559	9.2	54.1	19	20	AAZ27664	PCR primer specifi	632	9.2	54.1	21	24	ABK51445	Human single nucle
C 560	9.2	54.1	19	20	AAZ10784	Retroviral tagged	633	9.2	54.1	21	24	ABK65514	Human single nucle
C 561	9.2	54.1	19	21	AAAG9515	Primer used to amp	634	9.2	54.1	21	24	ABK65514	Human single nucle
C 562	9.2	54.1	19	24	ABL89147	HIV-1 related bind	635	9.2	54.1	21	24	ABK65514	Primer 2v for huma
C 563	9.2	54.1	19	24	ABK14616	Linked linear ampl	636	9.2	54.1	22	17	AAT35492	Oligonucleotide BL
C 564	9.2	54.1	20	13	AAQ20250	Hepatitis C primer	637	9.2	54.1	22	18	AAT65513	Primer for mouse X
C 565	9.2	54.1	20	13	AAQ24095	Primer DNA 3. Syn	638	9.2	54.1	22	18	AAT84421	Primer for mouse Z
C 566	9.2	54.1	20	13	AAQ24104	HCV NS-4 type 3 de	639	9.2	54.1	22	20	AAH84069	Primer for mouse Z
C 567	9.2	54.1	20	14	AAQ43136	C. trachomatis det	640	9.2	54.1	22	20	AAH80709	Oligonucleotide ta
C 568	9.2	54.1	20	14	AAQ36093	C. trachomatis det	641	9.2	54.1	22	21	AAH63574	Primer 2 L for SSC
C 569	9.2	54.1	20	16	AAT00877	Murine m26 struct	642	9.2	54.1	22	21	AAH07608	Forward primer for
C 570	9.2	54.1	20	16	AAQ79663	Primer OTG5024 to	643	9.2	54.1	22	21	AAH07670	Primer A #42 used
C 571	9.2	54.1	20	18	AAT95328	Phytophthora palmi	644	9.2	54.1	22	22	AAZ32728	Streptomyces sp. C
C 572	9.2	54.1	20	18	AAT76473	Chymase antisense	645	9.2	54.1	22	24	ABN88918	Streptomyces sp. C
C 573	9.2	54.1	20	20	AAZ06137	PCR primer used to	646	9.2	54.1	22	24	ABN88922	Streptomyces sp. C
C 574	9.2	54.1	20	20	AAZ04304	PCR primer used to	647	9.2	54.1	22	24	ABN88923	Streptomyces sp. C
C 575	9.2	54.1	20	20	AAZ02869	PCR primer used to	648	9.2	54.1	22	24	ABN88923	DNA-kinase gene am
C 576	9.2	54.1	20	20	AAZ02869	PCR primer used to	649	9.2	54.1	22	24	ABN88923	Lactococcus lactis
C 577	9.2	54.1	20	20	AAZ02869	PCR primer used to	650	9.2	54.1	23	19	AAV64142	Rat activin recept
C 578	9.2	54.1	20	20	AAZ02869	PCR primer used to	651	9.2	54.1	23	19	AAV64142	Primer DBR40 for b
C 579	9.2	54.1	20	20	AAZ02869	PCR primer used to	652	9.2	54.1	23	19	AAV12287	HSV-2 Xho-2 transf
C 580	9.2	54.1	20	20	AAZ02869	PCR primer used to	653	9.2	54.1	23	19	AAV12287	PCR primer used to
C 581	9.2	54.1	20	20	AAZ02869	PCR primer used to	654	9.2	54.1	23	21	AAZ02869	Alzheimer's diseas
C 582	9.2	54.1	20	21	AAZ02869	Chymase antisense	655	9.2	54.1	23	21	AAZ02869	Gene specific prim
C 583	9.2	54.1	20	21	AAZ02869	Human chymase poly	656	9.2	54.1	23	21	AAZ02869	Human mitochondria
C 584	9.2	54.1	20	21	AAZ02869	Human KIX-L1 PCR p	657	9.2	54.1	23	21	AAZ02869	Bovine MLC (BOLA)
C 585	9.2	54.1	20	21	AAZ02869	Dog genomic marker	658	9.2	54.1	23	22	AAZ02869	Human C12orf1386
C 586	9.2	54.1	20	21	AAZ02869	BanHI adapter. SEO	659	9.2	54.1	23	22	AAZ02869	Human TNFRSF11B ge
C 587	9.2	54.1	20	21	AAZ02869	BanHI adapter. SEO	660	9.2	54.1	23	22	AAZ02869	Human TNFRSF11B ge
C 588	9.2	54.1	20	21	AAZ02869	Low adenosine anti	661	9.2	54.1	23	22	AAZ02869	Human TNFRSF11B ge
C 589	9.2	54.1	20	21	AAZ02869	PCR primer used to	662	9.2	54.1	23	22	AAZ02869	Human TNFRSF11B ge
C 590	9.2	54.1	20	21	AAZ02869	PCR primer used to	663	9.2	54.1	23	22	AAZ02869	Human TNFRSF11B ge
C 591	9.2	54.1	20	21	AAZ02869	Human TRAP100 PCR	664	9.2	54.1	23	24	AAZ02869	Human TNFRSF11B ge
C 592	9.2	54.1	20	22	AAH00833	Typanosoma detect	665	9.2	54.1	23	24	AAZ02869	Human TNFRSF11B ge
C 593	9.2	54.1	20	22	AAH00833	Antisense IGFBP-5	666	9.2	54.1	23	24	AAZ02869	Human TNFRSF11B ge
C 594	9.2	54.1	20	22	AAH00833	Human PERK-cytoso	667	9.2	54.1	23	24	AAZ02869	Sequence of primer

667	9.2	54.1	24	15	AA045043	Oligomer comprisin	C 740	9.2	54.1	25	21	AA095878	HHA HHA-A gene PCR
668	9.2	54.1	24	15	AA071900	Lo-CD2a VH leader	C 741	9.2	54.1	25	21	AA095958	HHA HHA-B gene PCR
669	9.2	54.1	24	16	AA067942	Sense oligonucleot	C 742	9.2	54.1	25	21	AA096190	16s rRNA gene PCR
670	9.2	54.1	24	18	AAV01095	Human insulin PCR	C 743	9.2	54.1	25	21	AA096660	HHA HHA-A gene PCR
671	9.2	54.1	24	18	AA06106	Primer for light c	C 744	9.2	54.1	25	21	AA066066	PCR primer for mut
672	9.2	54.1	24	19	AA067034	Mouse Ikaro5 oligo	C 745	9.2	54.1	25	21	AA066067	PCR primer for mut
673	9.2	54.1	24	19	AAV42170	Mouse Ikaro5 isofo	C 746	9.2	54.1	25	21	AA066067	Sense PCR primer
674	9.2	54.1	24	19	AAV62519	Lo-CD2a chimeric a	C 747	9.2	54.1	25	21	AA066068	Antisense PCR prim
675	9.2	54.1	24	19	AAV53719	Nucleotide sequenc	C 748	9.2	54.1	25	21	AA066068	PCR primer for C.
676	9.2	54.1	24	19	AAV28795	Lo-CD2a primer VH	C 749	9.2	54.1	25	22	AA066100	Human proinsulin m
677	9.2	54.1	24	19	AAV18681	Human immunoglobul	C 750	9.2	54.1	25	22	AA066100	Human proinsulin m
678	9.2	54.1	24	20	AAI10144	PCR primer used to	C 751	9.2	54.1	25	22	AA066100	Human COL1A2 PCR p
679	9.2	54.1	24	20	AA022476	Receptor specific	C 752	9.2	54.1	25	22	AA066100	A. mediterranei ha
680	9.2	54.1	24	20	AA080529	DBS module 1 engi	C 753	9.2	54.1	25	22	AA066100	Human aquaporin 5
681	9.2	54.1	24	21	AA075347	PCR primer COLTPCR	C 754	9.2	54.1	25	24	AA066100	Human SRCR domain
682	9.2	54.1	24	21	AA059566	Hepatitis C virus	C 755	9.2	54.1	25	24	AA066100	Human MTG16 gene,
683	9.2	54.1	24	21	AA054499	SPINK5 5' splice d	C 756	9.2	54.1	25	24	AA066100	Human insulin, mut
684	9.2	54.1	24	22	AA05890	Human split comple	C 757	9.2	54.1	25	24	AA066100	Oligonucleotide ad
685	9.2	54.1	24	22	AA01373	aac(3'')-Vira resist	C 758	9.2	54.1	25	24	AA066100	Oligonucleotide ad
686	9.2	54.1	24	22	AA030587	Human Factor IX ge	C 759	9.2	54.1	25	24	AA066100	Oligonucleotide ad
687	9.2	54.1	24	22	AA029722	Human alpha1,2-man	C 760	9.2	54.1	25	24	AA066100	Transcript tag DNA
688	9.2	54.1	24	22	AA084662	Degenerate PCR pri	C 761	9.2	54.1	25	24	AA066100	Oligonucleotide pr
689	9.2	54.1	24	24	AA098425	Human V gene libra	C 762	9.2	54.1	25	23	AA066100	Oligonucleotide pr
690	9.2	54.1	24	24	AA056804	Replication start	C 763	9.2	54.1	25	23	AA066100	Oligonucleotide SE
691	9.2	54.1	24	24	AA000011	Oligonucleotide ad	C 764	9.2	54.1	25	23	AA066100	Oligonucleotide SE
692	9.2	54.1	24	24	AA000842	Oligonucleotide ad	C 765	9.2	54.1	25	23	AA066100	Oligonucleotide SE
693	9.2	54.1	24	24	AA000900	Oligonucleotide ad	C 766	9.2	54.1	25	23	AA066100	Oligonucleotide SE
694	9.2	54.1	24	24	AA001746	Oligonucleotide ad	C 767	9.2	54.1	25	23	AA066100	Oligonucleotide SE
695	9.2	54.1	24	24	AA002102	Oligonucleotide ad	C 768	9.2	54.1	25	23	AA066100	Oligonucleotide SE
696	9.2	54.1	24	24	AA004011	Oligonucleotide ad	C 769	9.2	54.1	25	23	AA066100	Oligonucleotide SE
697	9.2	54.1	24	24	AA004048	Oligonucleotide ad	C 770	9.2	54.1	25	23	AA066100	Oligonucleotide SE
698	9.2	54.1	24	24	AA005638	Oligonucleotide ad	C 771	9.2	54.1	25	23	AA066100	Oligonucleotide SE
699	9.2	54.1	24	24	AA005679	Oligonucleotide ad	C 772	9.2	54.1	25	23	AA066100	Oligonucleotide SE
700	9.2	54.1	24	24	AA005737	Oligonucleotide ad	C 773	9.2	54.1	25	23	AA066100	Oligonucleotide SE
701	9.2	54.1	24	24	AA005778	Oligonucleotide ad	C 774	9.2	54.1	25	23	AA066100	Oligonucleotide SE
702	9.2	54.1	24	24	AA007435	Oligonucleotide ad	C 775	9.2	54.1	25	22	AA066100	IGF-I oligonucleot
703	9.2	54.1	24	24	AA007476	Oligonucleotide ad	C 776	9.2	54.1	25	24	AA066100	IGF-I oligonucleot
704	9.2	54.1	24	24	AA008116	Oligonucleotide ad	C 777	9.2	54.1	25	24	AA066100	Human P450(cytochr
705	9.2	54.1	24	24	AA008157	Oligonucleotide ad	C 778	9.2	54.1	25	24	AA066100	ASO primer #6 to d
706	9.2	54.1	24	24	AA010339	Oligonucleotide ad	C 779	9.2	54.1	25	24	AA066100	Streptomyces sp. r
707	9.2	54.1	24	24	AA010376	Oligonucleotide ad	C 780	9.2	54.1	25	16	AA066100	Human IL4 receptor
708	9.2	54.1	24	24	AA018310	Oligonucleotide ad	C 781	9.2	54.1	25	16	AA066100	Human IL4 receptor
709	9.2	54.1	24	24	AA018351	Capture oligonucle	C 782	9.2	54.1	25	16	AA066100	Human IL4 receptor
710	9.2	54.1	24	24	AA018425	Capture oligonucle	C 783	9.2	54.1	25	16	AA066100	Low adenocarcin anti
711	9.2	54.1	24	24	AA018455	Capture oligonucle	C 784	9.2	54.1	25	17	AA066100	Aryl hydrocarbon n
712	9.2	54.1	24	24	AA018458	Capture oligonucle	C 785	9.2	54.1	25	17	AA066100	Integrin subunit b
713	9.2	54.1	24	24	AA018459	Capture oligonucle	C 786	9.2	54.1	25	17	AA066100	Integrin subunit b
714	9.2	54.1	24	24	AA018472	Capture oligonucle	C 787	9.2	54.1	25	17	AA066100	Hammerhead ribozym
715	9.2	54.1	24	24	AA018473	Capture oligonucle	C 788	9.2	54.1	25	17	AA066100	Oestrogen receptor
716	9.2	54.1	24	24	AA018572	Capture oligonucle	C 789	9.2	54.1	25	17	AA066100	Streptococcus pyog
717	9.2	54.1	24	24	AA018573	Capture oligonucle	C 790	9.2	54.1	25	17	AA066100	Human KTM1a portl
718	9.2	54.1	24	24	AA018589	Capture oligonucle	C 791	9.2	54.1	25	17	AA066100	Mouse E2 CDNA ampl
719	9.2	54.1	24	24	AA018595	Capture oligonucle	C 792	9.2	54.1	25	17	AA066100	Rgh PCR primer, to
720	9.2	54.1	24	24	AA018592	Capture oligonucle	C 793	9.2	54.1	25	17	AA066100	Mouse E4 protein,
721	9.2	54.1	24	24	AA018595	Capture oligonucle	C 794	9.2	54.1	25	17	AA066100	Increased stretch p
722	9.2	54.1	24	24	AA018610	Capture oligonucle	C 795	9.2	54.1	25	17	AA066100	Increased stretch p
723	9.2	54.1	24	24	AA018621	Capture oligonucle	C 796	9.2	54.1	25	17	AA066100	Increased stretch p
724	9.2	54.1	24	24	AA018702	Capture oligonucle	C 797	9.2	54.1	25	18	AA066100	Primer 5 for Hepat
725	9.2	54.1	24	24	AA018703	Capture oligonucle	C 798	9.2	54.1	25	18	AA066100	Calcium ion channe
726	9.2	54.1	24	24	AA018743	Capture oligonucle	C 799	9.2	54.1	25	18	AA066100	Calcium ion channe
727	9.2	54.1	24	24	AA018891	Capture oligonucle	C 800	9.2	54.1	25	18	AA066100	Sequencing primer
728	9.2	54.1	24	24	AA018940	Capture oligonucle	C 801	9.2	54.1	25	18	AA066100	Human prostate-rel
729	9.2	54.1	24	24	AA018941	Capture oligonucle	C 802	9.2	54.1	25	18	AA066100	Prostate-specific
730	9.2	54.1	24	24	AA019126	Capture oligonucle	C 803	9.2	54.1	25	18	AA066100	Human Smd6 antis
731	9.2	54.1	24	24	AA019126	Capture oligonucle	C 804	9.2	54.1	25	18	AA066100	Forward PCR primer
732	9.2	54.1	25	13	AA021242	PCR primer GH46' f	C 805	9.2	54.1	25	18	AA066100	Klebsiella pneumon
733	9.2	54.1	25	15	AA042244	PCR primer Geloc-5	C 806	9.2	54.1	25	18	AA066100	PCR primer for Bov
734	9.2	54.1	25	15	AA064546	Chromosome 11 (loc	C 807	9.2	54.1	25	19	AA066100	PCR primer for Bov
735	9.2	54.1	25	16	AA082566	Nucleotide sequenc	C 808	9.2	54.1	25	19	AA066100	Human beta1a1c ma
736	9.2	54.1	25	19	AA041659	Nucleotide sequenc	C 809	9.2	54.1	25	19	AA066100	Rabbit KAP61r PCR
737	9.2	54.1	25	19	AA041670	SNRPN gene flankin	C 810	9.2	54.1	25	24	AA066100	Human G protein-co
738	9.2	54.1	25	20	AA010132	Primer 6A4_Rc4. U	C 811	9.2	54.1	25	24	AA066100	Esophageal adenoca
739	9.2	54.1	25	21	AA083337		C 812	9.2	54.1	25	24	AA066100	Esophageal adenoca

C 813	52.9	20	18	AA92784	Primer #1 for c-Kit	C 886	52.9	22	14	AA051893	PML mRNA ribozyme
C 814	52.9	20	18	AA78883	Primer 788NUTR for	C 887	52.9	22	19	AAV60619	PCR primer used to
C 815	52.9	20	18	AA751024	Primer #1 for env	C 888	52.9	22	19	AAV20905	PCR primer used to
C 816	52.9	20	19	AAV52781	c-Kit PCR primer K	C 889	52.9	22	21	AA62117	Agrobacterium Ti-p
C 817	52.9	20	19	AAV40367	Maize oligonucleot	C 890	52.9	22	21	ABT04234	Human G-protein co
C 818	52.9	20	19	AAV37070	PCR primer for ant	C 891	52.9	22	24	ABO8630	Human GPCR revers
C 819	52.9	20	20	AAZ02304	PCR primer used to	C 892	52.9	22	24	ABK14927	Bovine poly(ADP-ri
C 820	52.9	20	20	AAV93684	PCR primer used to	C 893	52.9	22	24	ABK14945	Bovine poly(ADP-ri
C 821	52.9	20	20	AAV93302	PCR primer used to	C 894	52.9	22	24	ABK14951	Oryza sativa promo
C 822	52.9	20	20	AAV9405	Control oligonucle	C 895	52.9	23	15	AAQ45021	Oligomer compresin
C 823	52.9	20	20	AAV84236	Human CAX phosph	C 896	52.9	23	17	AAV42148	Primer P4 for apol
C 824	52.9	20	21	AAV93176	Human STAT3 phosp	C 897	52.9	23	19	AAV36836	Mouse Ikafos isolo
C 825	52.9	20	21	AAV62948	JNK antisense olig	C 898	52.9	23	21	AAV63556	Oligonucleotide sp
C 826	52.9	20	21	AAV97514	Streptomyces albu	C 899	52.9	23	22	AAV65525	Primer ZC21, 076
C 827	52.9	20	21	AAV63844	PCR primer used to	C 900	52.9	23	24	ABK66773	Human gene specif
C 828	52.9	20	21	AAV63848	PCR primer used to	C 901	52.9	23	24	AAQ05781	pol primer of HIV
C 829	52.9	20	21	AAV72550	PCR primer CB3-TM	C 902	52.9	24	11	AAQ05781	1.1ASML CKOR olig
C 830	52.9	20	21	AAV72550	PCR primer CB3-TM	C 903	52.9	24	18	AAV62575	Telomerase reverse
C 831	52.9	20	21	AAV71144	PCR primer specif	C 904	52.9	24	19	AAV09149	Human calcium chan
C 832	52.9	20	21	AAV9256	PCR primer DHRD.91	C 905	52.9	24	20	AAV01489	Primer STS sy243 1
C 833	52.9	20	21	AAV9256	Primer 1 for human	C 906	52.9	24	21	AAV96930	PCR primer used to
C 834	52.9	20	21	AAV9256	Human neurofilin m	C 907	52.9	24	21	AAV96930	Hepevirus expres
C 835	52.9	20	22	AAV95007	Human CDNA clone-s	C 908	52.9	24	21	AAV96930	Murine VH IIB fro
C 836	52.9	20	22	AAV95007	Human CDNA clone-s	C 909	52.9	24	21	AAV96930	Human Y-specific S
C 837	52.9	20	22	AAV95007	PCR primer for an	C 910	52.9	24	22	AAV96930	DNA fragment used
C 838	52.9	20	22	AAV95007	Human MHC S DNA PC	C 911	52.9	24	22	AAV96930	Rat fibroblast
C 839	52.9	20	22	AAV95007	Human MHC S DNA PC	C 912	52.9	24	22	AAV96930	Primer #2 used to
C 840	52.9	20	22	AAV95007	Human MHC S DNA PC	C 913	52.9	24	24	ABK67214	Human gene specif
C 841	52.9	20	22	AAV95007	Human MHC S DNA PC	C 914	52.9	24	24	ABK67214	Oligonucleotide ad
C 842	52.9	20	22	AAV95007	Human MHC S DNA PC	C 915	52.9	24	24	ABK67214	Oligonucleotide ad
C 843	52.9	20	22	AAV95007	Human MHC S DNA PC	C 916	52.9	24	24	ABK67214	Oligonucleotide ad
C 844	52.9	20	22	AAV95007	Human MHC S DNA PC	C 917	52.9	24	24	ABK67214	Oligonucleotide ad
C 845	52.9	20	22	AAV95007	Human MHC S DNA PC	C 918	52.9	24	24	ABK67214	Oligonucleotide ad
C 846	52.9	20	22	AAV95007	Human MHC S DNA PC	C 919	52.9	24	24	ABK67214	Oligonucleotide ad
C 847	52.9	20	22	AAV95007	Human MHC S DNA PC	C 920	52.9	24	24	ABK67214	Oligonucleotide ad
C 848	52.9	20	22	AAV95007	Human MHC S DNA PC	C 921	52.9	24	24	ABK67214	Oligonucleotide ad
C 849	52.9	20	22	AAV95007	Human MHC S DNA PC	C 922	52.9	24	24	ABK67214	Oligonucleotide ad
C 850	52.9	20	22	AAV95007	Human MHC S DNA PC	C 923	52.9	24	24	ABK67214	Oligonucleotide ad
C 851	52.9	20	22	AAV95007	Human MHC S DNA PC	C 924	52.9	24	24	ABK67214	Oligonucleotide ad
C 852	52.9	20	22	AAV95007	Human MHC S DNA PC	C 925	52.9	24	24	ABK67214	Oligonucleotide ad
C 853	52.9	20	22	AAV95007	Human MHC S DNA PC	C 926	52.9	24	24	ABK67214	Oligonucleotide ad
C 854	52.9	20	22	AAV95007	Human MHC S DNA PC	C 927	52.9	24	24	ABK67214	Oligonucleotide ad
C 855	52.9	20	22	AAV95007	Human MHC S DNA PC	C 928	52.9	24	24	ABK67214	Oligonucleotide ad
C 856	52.9	20	22	AAV95007	Human MHC S DNA PC	C 929	52.9	24	24	ABK67214	Oligonucleotide ad
C 857	52.9	20	22	AAV95007	Human MHC S DNA PC	C 930	52.9	24	24	ABK67214	Oligonucleotide ad
C 858	52.9	20	22	AAV95007	Human MHC S DNA PC	C 931	52.9	24	24	ABK67214	Oligonucleotide ad
C 859	52.9	20	22	AAV95007	Human MHC S DNA PC	C 932	52.9	24	24	ABK67214	Oligonucleotide ad
C 860	52.9	20	22	AAV95007	Human MHC S DNA PC	C 933	52.9	24	24	ABK67214	Oligonucleotide ad
C 861	52.9	20	22	AAV95007	Human MHC S DNA PC	C 934	52.9	24	24	ABK67214	Oligonucleotide ad
C 862	52.9	20	22	AAV95007	Human MHC S DNA PC	C 935	52.9	24	24	ABK67214	Oligonucleotide ad
C 863	52.9	20	22	AAV95007	Human MHC S DNA PC	C 936	52.9	24	24	ABK67214	Oligonucleotide ad
C 864	52.9	20	22	AAV95007	Human MHC S DNA PC	C 937	52.9	24	24	ABK67214	Oligonucleotide ad
C 865	52.9	20	22	AAV95007	Human MHC S DNA PC	C 938	52.9	24	24	ABK67214	Oligonucleotide ad
C 866	52.9	20	22	AAV95007	Human MHC S DNA PC	C 939	52.9	24	24	ABK67214	Oligonucleotide ad
C 867	52.9	20	22	AAV95007	Human MHC S DNA PC	C 940	52.9	24	24	ABK67214	Oligonucleotide ad
C 868	52.9	20	22	AAV95007	Human MHC S DNA PC	C 941	52.9	24	24	ABK67214	Oligonucleotide ad
C 869	52.9	20	22	AAV95007	Human MHC S DNA PC	C 942	52.9	24	24	ABK67214	Oligonucleotide ad
C 870	52.9	20	22	AAV95007	Human MHC S DNA PC	C 943	52.9	24	24	ABK67214	Oligonucleotide ad
C 871	52.9	20	22	AAV95007	Human MHC S DNA PC	C 944	52.9	24	24	ABK67214	Oligonucleotide ad
C 872	52.9	20	22	AAV95007	Human MHC S DNA PC	C 945	52.9	24	24	ABK67214	Oligonucleotide ad
C 873	52.9	20	22	AAV95007	Human MHC S DNA PC	C 946	52.9	24	24	ABK67214	Oligonucleotide ad
C 874	52.9	20	22	AAV95007	Human MHC S DNA PC	C 947	52.9	24	24	ABK67214	Oligonucleotide ad
C 875	52.9	20	22	AAV95007	Human MHC S DNA PC	C 948	52.9	24	24	ABK67214	Oligonucleotide ad
C 876	52.9	20	22	AAV95007	Human MHC S DNA PC	C 949	52.9	24	24	ABK67214	Oligonucleotide ad
C 877	52.9	20	22	AAV95007	Human MHC S DNA PC	C 950	52.9	24	24	ABK67214	Oligonucleotide ad
C 878	52.9	20	22	AAV95007	Human MHC S DNA PC	C 951	52.9	24	24	ABK67214	Oligonucleotide ad
C 879	52.9	20	22	AAV95007	Human MHC S DNA PC	C 952	52.9	24	24	ABK67214	Oligonucleotide ad
C 880	52.9	20	22	AAV95007	Human MHC S DNA PC	C 953	52.9	24	24	ABK67214	Oligonucleotide ad
C 881	52.9	20	22	AAV95007	Human MHC S DNA PC	C 954	52.9	24	24	ABK67214	Oligonucleotide ad
C 882	52.9	20	22	AAV95007	Human MHC S DNA PC	C 955	52.9	24	24	ABK67214	Oligonucleotide ad
C 883	52.9	20	22	AAV95007	Human MHC S DNA PC	C 956	52.9	24	24	ABK67214	Oligonucleotide ad
C 884	52.9	20	22	AAV95007	Human MHC S DNA PC	C 957	52.9	24	24	ABK67214	Oligonucleotide ad
C 885	52.9	20	22	AAV95007	Human MHC S DNA PC	C 958	52.9	24	24	ABK67214	Oligonucleotide ad

[illegible]

RESULT 1

1D ABK29246 standard; DNA; 22 BP.
YY

23-APR-2002 (first entry)

aspergillus auricomus probe.
XX
XX

XX bacterial detection; probe; primer; ss.

~~Aspergillus~~ auricomus.

PM WO200106613

PD 20-DEC-2001.

13-JUN-2001; 2001WO-US18892.

13-JUN-2000; 2000US-0593012.
PR
XX

U.S. ENVIRONMENTAL PROTECTION AGENCY.

PI Haugland R, Vesper SJ;

XX:

PT Detecting and quantifying fungi and bacteria, involves obtaining a
PT sequence of the fungus, extracting the DNA from the sample, and
PT subjecting the DNA to polymerase chain reaction and fluorescent probe
PT analysis.

PS. Disclosure; Page 23; 110pp; English

The invention relates to a method of detecting and quantifying fungi and bacteria, involving obtaining a sequence of the microorganism to be detected and quantified, extracting the DNA from the sample, and subjecting the DNA to polymerase chain reaction (PCR) and fluorescent probe analysis. The method is useful for identifying and quantifying specific fungi and bacteria using specific DNA sequences. The specific DNA sequences are useful for the real time detection of PCR products with a fluorescent probe system or other molecular probes like hybridisation. *AKR3026-ABK329474* represent fungal and bacterial PCR primers and probes used in the method of the invention.

sequence 22 B; 1 A; 8 C; 6 G; 1 T; 0 other;

Query Match	Score	DB	Length
Best Local Similarity	100.0%	Pred. No. 4.9e+02	
Matches	14	Conservative 0	Mismatches 0
			Indels

QY	1	GTTGCTTCGGCGGG	14
Db	14	GTTGCTTCGGCGGG	1

RESULT 2

ABK29280 standard; DNA; 22 BP.

AC ABK29280;

23-APR-2002 (first entry)

respergillus sclerotiorum f.

----- bacterial detection; probe; primer; 58.

Aspergillus sclerotiorum.

PN WO200196612-A2

20-DEC-2001.

13-JUN-2001; 2001WO-US18892.

13-JUN-2000; 2000US-0593012

(USSI) US ENVIRONMENTAL PROTECTION AGENCY

Haugland R, Vesper SJ;

WPI; 2002-098078/13.

Detecting and quantifying fungi and bacteria. involves obtaining a

subjecting the DNA to polymerase chain reaction and fluorescent probe

Claim 87: Page 25: English

C. The invention relates to a method of detecting and quantifying

detected and obtaining a sequence of the microorganism to be

subjecting the DNA to polymerase chain reaction (PCR) and electro-

probe analysis. The method is useful for identifying and quantifying specific fungi and bacteria.

DNA sequences are useful for the real time detection of PCB products with

CC a fluorogenic probe system or other molecular probes like hybridisation.
CC ABK29026-ABK29474 represent fungal and bacterial PCR primers and probes
CC used in the method of the invention.

XX Sequence 22 BP; 7 A; 8 C; 6 G; 1 T; 0 other;

Query Match 82.4%; Score 14; DB 24; Length 22;

Best Local Similarity 100.0%; Pred. No. 4.9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTGCTTCGCGCGG 14

DB 14 GTTGCTTCGCGCGG 1

RESULT 3
ID ABK29289/c
ABK29289 standard; DNA; 22 BP.

XX ABK29289;

DT 23-APR-2002 (first entry)

XX Aspergillus wentii probe.

XX Fungal detection; bacterial detection; probe; primer; ss.

XX Aspergillus wentii.

XX WO200196612-A2.

PD 20-DEC-2001.

PF 13-JUN-2001; 2001WO-US18892.

PR 13-JUN-2000; 2000US-0593012.

XX (USST) US ENVIRONMENTAL PROTECTION AGENCY.

XX Haugland R, Vesper SJ;

XX WPI; 2002-098078/13.

PT Detecting and quantifying fungi and bacteria, involves obtaining a

PT sequence of the fungus, extracting the DNA from the sample, and

PT subjecting the DNA to polymerase chain reaction and fluorescent probe

PT analysis

PS Claim 90; Page 26; 110pp; English.

XX The invention relates to a method of detecting and quantifying fungi and

XX bacteria, involving obtaining a sequence of the microorganism to be

XX detected and quantified, extracting the DNA from the sample, and

XX subjecting the DNA to polymerase chain reaction (PCR) and fluorescent

XX probe analysis. The method is useful for identifying and quantifying

XX specific fungi and bacteria using specific DNA sequences. The specific

XX DNA sequences are useful for the real time detection of PCR products with

XX a fluorogenic probe system or other molecular probes like hybridisation.

XX ABK29026-ABK29474 represent fungal and bacterial PCR primers and probes

XX used in the method of the invention.

XX Sequence 22 BP; 7 A; 8 C; 6 G; 1 T; 0 other;

Query Match 82.4%; Score 14; DB 24; Length 22;

Best Local Similarity 100.0%; Pred. No. 4.9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTGCTTCGCGCGG 14

DB 14 GTTGCTTCGCGCGG 1

RESULT 4

ABK29262
ID ABK29262 standard; DNA; 16 BP.

XX ABK29262;

DT 23-APR-2002 (first entry)

XX Aspergillus flavipes probe.

XX Fungal detection; bacterial detection; probe; primer; ss.

XX Aspergillus flavipes

XX WO200196612-A2.

PD 20-DEC-2001.

PF 13-JUN-2001; 2001WO-US18892.

PR 13-JUN-2000; 2000US-0593012.

XX (USST) US ENVIRONMENTAL PROTECTION AGENCY.

XX Haugland R, Vesper SJ;

XX WPI; 2002-098078/13.

PT Detecting and quantifying fungi and bacteria, involves obtaining a

PT sequence of the fungus, extracting the DNA from the sample, and

PT subjecting the DNA to polymerase chain reaction and fluorescent probe

PT analysis

PS Claim 81; Page 24; 110pp; English.

XX The invention relates to a method of detecting and quantifying fungi and

XX bacteria, involving obtaining a sequence of the microorganism to be

XX detected and quantified, extracting the DNA from the sample, and

XX subjecting the DNA to polymerase chain reaction (PCR) and fluorescent

XX probe analysis. The method is useful for identifying and quantifying

XX specific fungi and bacteria using specific DNA sequences. The specific

XX DNA sequences are useful for the real time detection of PCR products with

XX a fluorogenic probe system or other molecular probes like hybridisation.

XX ABK29026-ABK29474 represent fungal and bacterial PCR primers and probes

XX used in the method of the invention.

XX Sequence 16 BP; 0 A; 6 C; 6 G; 4 T; 0 other;

Query Match 76.5%; Score 13; DB 24; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.7e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTGCTTCGCGCGG 14

DB 1 TTGCTTCGCGCGG 13

RESULT 5
ID ABK29265
ABK29265 standard; DNA; 16 BP.

XX ABK29265;

DT 23-APR-2002 (first entry)

XX Aspergillus niveus probe.

XX Fungal detection; bacterial detection; probe; primer; ss.

XX Aspergillus niveus.

XX WO200196612-A2.

PD 20-DEC-2001.

XX PF 13-JUN-2001; 2001WO-US18892.
XX PF 13-JUN-2000; 2000US-0593012.
XX PA (USSI) US ENVIRONMENTAL PROTECTION AGENCY.
XX PI Haugland R, Vesper SJ;
XX DR WPI; 2002-098078/13.
XX PT Detecting and quantifying fungi and bacteria, involves obtaining a
XX PT sequence of the fungus, extracting the DNA from the sample, and
XX PT subjecting the DNA to polymerase chain reaction and fluorescent probe
XX PT analysis
XX PS Claim 82; Page 24; 110pp; English.
XX CC The invention relates to a method of detecting and quantifying fungi and
XX CC bacteria, involving obtaining a sequence of the microorganism to be
XX CC detected and quantified, extracting the DNA from the sample, and
XX CC subjecting the DNA to polymerase chain reaction (PCR) and fluorescent
XX CC probe analysis. The method is useful for identifying and quantifying
XX CC specific fungi and bacteria using specific DNA sequences. The specific
XX CC DNA sequences are useful for the real time detection of PCR products with
XX CC a fluorescent probe system or other molecular probes like hybridisation.
XX CC ABR29026-ABK29474 represent fungal and bacterial PCR primers and probes
XX CC used in the method of the invention.
XX SQ Sequence 16 BP; 0 A; 6 C; 6 G; 4 T; 0 other;
XX
XX Query Match 76.5%; Score 13; DB 24; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+03;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 TTGCTTCGCGCGG 14
XX Db 1 TTGCTTCGCGCGG 13
XX
XX RESULT 6
XX ABR29249
XX ID ABR29249 standard; DNA; 23 BP.
XX AC ABR29249;
XX XX
XX DT 23-APR-2002 (first entry)
XX XX
XX DE Aspergillus caespitosus probe.
XX XX
XX KM Fungal detection; bacterial detection; probe; primer; ss.
XX OS Aspergillus caespitosus.
XX PN WO200196612-A2.
XX PD 20-DEC-2001.
XX PF 13-JUN-2001; 2001WO-US18892.
XX PR 13-JUN-2000; 2000US-0593012.
XX PA (USSI) US ENVIRONMENTAL PROTECTION AGENCY.
XX PI Haugland R, Vesper SJ;
XX DR WPI; 2002-098078/13.
XX PT Detecting and quantifying fungi and bacteria, involves obtaining a
XX PT sequence of the fungus, extracting the DNA from the sample, and
XX PT subjecting the DNA to polymerase chain reaction and fluorescent probe
XX PT analysis

PS Claim 77; Page 23; 110pp; English.
XX CC The invention relates to a method of detecting and quantifying fungi and
XX CC bacteria, involving obtaining a sequence of the microorganism to be
XX CC detected and quantified, extracting the DNA from the sample, and
XX CC subjecting the DNA to polymerase chain reaction (PCR) and fluorescent
XX CC probe analysis. The method is useful for identifying and quantifying
XX CC specific fungi and bacteria using specific DNA sequences. The specific
XX CC DNA sequences are useful for the real time detection of PCR products with
XX CC a fluorescent probe system or other molecular probes like hybridisation.
XX CC ABR29026-ABK29474 represent fungal and bacterial PCR primers and probes
XX CC used in the method of the invention.
XX SQ Sequence 23 BP; 3 A; 7 C; 8 G; 5 T; 0 other;
XX
XX Query Match 75.3%; Score 12.8; DB 24; Length 23;
XX Best Local Similarity 87.5%; Pred. No. 2.2e+03;
XX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1 GTTGCTTCGCGCGGAA 16
XX Db 5 GTTGCTTCGCGCGAGA 20
XX
XX RESULT 7
XX ABR29286
XX ID ABR29286 standard; DNA; 23 BP.
XX AC ABR29286;
XX XX
XX DT 23-APR-2002 (first entry)
XX XX
XX DE Aspergillus unguis probe.
XX XX
XX KM Fungal detection; bacterial detection; probe; primer; ss.
XX OS Aspergillus unguis.
XX PN WO200196612-A2.
XX PD 20-DEC-2001.
XX PF 13-JUN-2001; 2001WO-US18892.
XX PR 13-JUN-2000; 2000US-0593012.
XX PA (USSI) US ENVIRONMENTAL PROTECTION AGENCY.
XX PI Haugland R, Vesper SJ;
XX DR WPI; 2002-098078/13.
XX PT Detecting and quantifying fungi and bacteria, involves obtaining a
XX PT sequence of the fungus, extracting the DNA from the sample, and
XX PT subjecting the DNA to polymerase chain reaction and fluorescent probe
XX PT analysis
XX PS Claim 89; Page 25; 110pp; English.
XX CC The invention relates to a method of detecting and quantifying fungi and
XX CC bacteria, involving obtaining a sequence of the microorganism to be
XX CC detected and quantified, extracting the DNA from the sample, and
XX CC subjecting the DNA to polymerase chain reaction (PCR) and fluorescent
XX CC probe analysis. The method is useful for identifying and quantifying
XX CC specific fungi and bacteria using specific DNA sequences. The specific
XX CC DNA sequences are useful for the real time detection of PCR products with
XX CC a fluorescent probe system or other molecular probes like hybridisation.
XX CC ABR29026-ABK29474 represent fungal and bacterial PCR primers and probes
XX CC used in the method of the invention.
XX SQ Sequence 23 BP; 3 A; 7 C; 8 G; 5 T; 0 other;
XX
XX Query Match 75.3%; Score 12.8; DB 24; Length 23;

Best Local Similarity 87.5%; Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GTTGCTTCGGCGGGA 16
|||
DB 5 GTTGCTTCGGCGGGA 20

RESULT 8

ABN99623 ID ABN99623 standard; DNA; 15 BP.

AC ABN99623;

DT 05-AUG-2002 (first entry)

DE Fungi PCR primer SEQ ID NO 195.

KM Fungus; bacteria; quantification; detection; infection; gastroenteritis;
ulcer; asthma; allergy; sinusitis; PCR; primer; ss.

OS Trichoderma harzianum.

PN US6387652-B1.

PD 14-MAY-2002.

PF 13-JUN-2000; 2000US-0593012.

PR 15-APR-1998; 98US-081773P.

PR 14-APR-1999; 99US-0290990.

XX (USSI) US ENVIRONMENTAL PROTECTION AGENCY.

PI Haugland R. Vesper S;

DR WPI; 2002-462353/49.

CC Detection and quantification of specific fungi or bacteria useful e.g.
in medical diagnosis and treatment of fungal and bacterial conditions,
by hybridizing and amplifying DNA using sequences unique to the species
or group of species -
Claim 65; Column 97, 55pp; English.

CC The invention relates to specific fungi or bacteria detected and
quantified in a sample by extracting and recovering DNA from the organism
in the sample and hybridizing and amplifying the DNA sequence using
sequences unique to the species/group of species but common to all
isolates of the species/group of species. The method especially employs
sequences selected from 225 fungal and bacterial primer and probe
sequences (ABN99429-ABN99653) for detection of specified fungi/fungal
groups or specified bacteria. The method enables detection and
quantification of specific fungi or bacteria, or groups of
fungal/bacterial species, useful medically for diagnosis and treatment of
fungi or bacteria associated with health problems such as infections,
gastroenteritis, ulcers, asthma, allergies and sinusitis. It is also
useful to detect and/or quantify microorganisms in the environment e.g.
to establish the risk of adverse health effects (e.g. pulmonary
haemorrhage from levels of Stachybotrys chartarum in air samples in
houses).

XX Sequence 15 BP; 1 A; 4 C; 6 G; 4 T; 0 other;

Query Match 72.9%; Score 12.4; DB 24; Length 15;

Best Local Similarity 92.9%; Pred. No. 3.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TTGCTTCGGCGGGA 15
|||
DB 1 TTGCTTCGGCGGGA 14

RESULT 9
ABK29220 ID ABK29220 standard; DNA; 15 BP.

AC ABK29220;

DT 23-APR-2002 (first entry)

DE Trichoderma harzianum forward PCR primer.

KM Fungal detection; bacterial detection; probe; primer; ss.

OS Trichoderma harzianum.

PN WO200196612-A2.

PD 20-DEC-2001.

PF 13-JUN-2001; 2001WO-US18892.

PR 13-JUN-2000; 2000US-0593012.

XX (USSI) US ENVIRONMENTAL PROTECTION AGENCY.

PI Haugland R. Vesper S;

DR WPI; 2002-098078/13.

CC Detecting and quantifying fungi and bacteria, involves obtaining a
sequence of the fungus, extracting the DNA from the sample, and
subjecting the DNA to polymerase chain reaction and fluorescent probe
analysis -
Claim 65; Page 21; 110pp; English.

CC The invention relates to a method of detecting and quantifying fungi and
bacteria, involving obtaining a sequence of the microorganism to be
detected and quantified, extracting the DNA from the sample, and
subjecting the DNA to polymerase chain reaction (PCR) and fluorescent
probe analysis. The method is useful for identifying and quantifying
specific fungi and bacteria using specific DNA sequences. The specific
DNA sequences are useful for the real time detection of PCR products with
a fluorescent probe system or other molecular probes like hybridisation.
CC ABK29026-ABK29474 represent fungal and bacterial PCR primers and probes
used in the method of the invention.

XX Sequence 15 BP; 1 A; 4 C; 6 G; 4 T; 0 other;

Query Match 72.9%; Score 12.4; DB 24; Length 15;

Best Local Similarity 92.9%; Pred. No. 3.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TTGCTTCGGCGGGA 15
|||
DB 1 TTGCTTCGGCGGGA 14

RESULT 10

ABK29366/c ID ABK29366 standard; DNA; 16 BP.

AC ABK29366;

DT 23-APR-2002 (first entry)

DE Penicillium expansum reverse PCR primer.

KM Fungal detection; bacterial detection; probe; primer; ss.

OS Penicillium expansum.

PN WO200196612-A2.

CC The invention relates to specific fungi or bacteria detected and
 CC quantified in a sample by extracting and recovering DNA from the organism
 CC in the sample and hybridizing and amplifying the DNA sequence using
 CC sequences unique to the species/group of species but common to all
 CC isolates of the species/group of species. The method especially employs
 CC sequences selected from 225 fungal and bacterial primer and probe
 CC sequences (ABN99429-ABN99653) for detection of specified fungi/fungal
 CC groups or specified bacteria. The method enables detection and
 CC quantification of specific fungi or bacteria, or groups of
 CC fungi/bacterial species, useful medically for diagnosis and treatment of
 CC fungi or bacteria associated with health problems such as infections,
 CC gastroenteritis, ulcers, asthma, allergies and sinusitis. It is also
 CC useful to detect and/or quantify microorganisms in the environment e.g.
 CC to establish the risk of adverse health effects (e.g. pulmonary
 CC haemorrhage from levels of *Stachybotrys chartarum* in air samples in
 CC houses).

SO Sequence 21 BP; 3 A; 7 C; 7 G; 4 T; 0 other;

Query Match 72.9%; Score 12.4; DB 24; Length 21;
 Best Local Similarity 92.9%; Pred. No. 3.5e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GTTGCTTCGGCGGG 14
 |||||
 8 GTTGCTTCGGCGGG 21

DB

RESULT 13
 ABN99631
 ID ABN99631 standard; DNA; 21 BP.
 AC ABN99631;
 DT 05-AUG-2002 (first entry)
 XX
 XX Fungal probe SEQ ID NO 203.
 DE
 XX Fungus; bacteria; quantification; detection; infection; gastroenteritis;
 KW ulcer; asthma; allergy; sinusitis; probe; ss.
 XX
 OS *Trichoderma viride*.
 OS *Trichoderma atroviride*.
 OS *Trichoderma koningii*.
 XX
 XX US6387652-B1.
 XX
 XX 14-MAY-2002.
 PD
 XX
 XX 13-JUN-2000; 2000US-0593012.
 PF
 XX 15-APR-1998; 98US-081773P.
 PR 14-APR-1999; 99US-0290990.
 XX
 XX (USSI) US ENVIRONMENTAL PROTECTION AGENCY.
 PA
 XX
 XX Haugland R, Vesper S;
 PI
 XX WPI, 2002-462353/49.
 DR
 XX
 XX Detection and quantification of specific fungi or bacteria useful e.g.
 PT in medical diagnosis and treatment of fungal and bacterial conditions,
 PT by hybridizing and amplifying DNA using sequences unique to the species
 PT or group of species -
 XX
 XX Claim 67; Column 98; 55pp; English.
 PS
 XX The invention relates to specific fungi or bacteria detected and
 CC quantified in a sample by extracting and recovering DNA from the organism
 CC in the sample and hybridizing and amplifying the DNA sequence using
 CC sequences unique to the species/group of species but common to all
 CC isolates of the species/group of species. The method especially employs
 CC sequences selected from 225 fungal and bacterial primer and probe

CC sequences (ABN99429-ABN99653) for detection of specified fungi/fungal
 CC groups or specified bacteria. The method enables detection and
 CC quantification of specific fungi or bacteria, or groups of
 CC fungi/bacterial species, useful medically for diagnosis and treatment of
 CC fungi or bacteria associated with health problems such as infections,
 CC gastroenteritis, ulcers, asthma, allergies and sinusitis. It is also
 CC useful to detect and/or quantify microorganisms in the environment e.g.
 CC to establish the risk of adverse health effects (e.g. pulmonary
 CC haemorrhage from levels of *Stachybotrys chartarum* in air samples in
 CC houses).

SO Sequence 21 BP; 3 A; 7 C; 7 G; 4 T; 0 other;

Query Match 72.9%; Score 12.4; DB 24; Length 21;
 Best Local Similarity 92.9%; Pred. No. 3.5e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GTTGCTTCGGCGGG 14
 |||||
 8 GTTGCTTCGGCGGG 21

DB

RESULT 14
 ABK29216
 ID ABK29216 standard; DNA; 21 BP.
 AC ABK29216;
 XX
 XX 23-APR-2002 (first entry)
 DT
 XX
 XX *Trichoderma asperellum*/hamatum probe.
 DE
 XX
 XX Fungal detection; bacterial detection; probe; primer; ss.
 KW
 XX
 OS *Trichoderma asperellum*.
 OS *Trichoderma hamatum*.
 XX
 XX WO200196612-A2.
 PN
 XX
 XX 20-DEC-2001.
 PD
 XX
 XX 13-JUN-2001; 2001WO-US18892.
 PF
 XX 13-JUN-2000; 2000US-0593012.
 PR
 XX
 XX (USSI) US ENVIRONMENTAL PROTECTION AGENCY.
 PA
 XX
 XX Haugland R, Vesper SJ;
 PI
 XX WPI, 2002-098078/13.
 DR
 XX
 XX Detecting and quantifying fungi and bacteria, involves obtaining a
 PT sequence of the fungus, extracting the DNA from the sample, and
 PT subjecting the DNA to polymerase chain reaction and fluorescent probe
 PT analysis -
 XX
 XX Claim 63; Page 21; 110pp; English.
 PS
 XX The invention relates to a method of detecting and quantifying fungi and
 CC bacteria, involving obtaining a sequence of the microorganism to be
 CC detected and quantified, extracting the DNA from the sample, and
 CC subjecting the DNA to polymerase chain reaction (PCR) and fluorescent
 CC probe analysis. The method is useful for identifying and quantifying
 CC specific fungi and bacteria using specific DNA sequences. The specific
 CC DNA sequences are useful for the real time detection of PCR products with
 CC a fluorescent probe system or other molecular probes like hybridisation.
 CC ABK29026-ABK29474 represent fungal and bacterial PCR primers and probes
 CC used in the method of the invention.
 CC
 XX
 XX Sequence 21 BP; 3 A; 7 C; 7 G; 4 T; 0 other;
 SO
 Query Match 72.9%; Score 12.4; DB 24; Length 21;
 Best Local Similarity 92.9%; Pred. No. 3.5e+03;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GTTGCTTCGGCGG 14
 |||||
 8 GTTGCTTCGGCGG 21

Db 8 GTTGCTTCGGCGG 21

RESULT 15
 ABRK29219
 ID ABRK29219 standard; DNA; 21 BP.
 XX
 AC ABRK29219;
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE Trichoderma asperellum/hamatum/viride probe.
 XX
 KM Fungal detection; bacterial detection; probe; primer; ss.
 XX
 OS Trichoderma asperellum.
 XX
 OS Trichoderma hamatum.
 XX
 PN WO200196612-A2.
 XX
 PD 20-DEC-2001.
 XX
 PF 13-JUN-2001; 2001WO-US18892.
 XX
 PR 13-JUN-2000; 2000US-0593012.
 XX
 PA (USST) US ENVIRONMENTAL PROTECTION AGENCY.
 XX
 PI Haugland R, Vesper SJ;
 XX
 DR WPI; 2002-098078/13.
 XX
 PT Detecting and quantifying fungi and bacteria, involves obtaining a
 PT sequence of the fungus, extracting the DNA from the sample, and
 PT subjecting the DNA to polymerase chain reaction and fluorescent probe
 PT analysis -
 XX
 PS Claim 64; Page 21; 110pp; English.
 XX
 CC The invention relates to a method of detecting and quantifying fungi and
 CC bacteria, involving obtaining a sequence of the microorganism to be
 CC detected and quantified, extracting the DNA from the sample, and
 CC subjecting the DNA to polymerase chain reaction (PCR) and fluorescent
 CC probe analysis. The method is useful for identifying and quantifying
 CC specific fungi and bacteria using specific DNA sequences. The specific
 CC DNA sequences are useful for the real time detection of PCR products with
 CC a fluorogenic probe system or other molecular probes like hybridisation.
 CC ABRK29026-ABRK29474 represent fungal and bacterial PCR primers and probes
 CC used in the method of the invention.
 CC
 SQ Sequence 21 BP; 3 A; 7 C; 7 G; 4 T; 0 other;

Query Match 72.9%; Score 12.4; DB 24; Length 21;
 Best Local Similarity 92.9%; Pred. No. 3.5e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GTTGCTTCGGCGG 14
 |||||
 8 GTTGCTTCGGCGG 21

Db 8 GTTGCTTCGGCGG 21

RESULT 16
 ABRK29228
 ID ABRK29228 standard; DNA; 21 BP.
 XX
 AC ABRK29228;
 XX
 DT 23-APR-2002 (first entry)

DE Trichoderma viride/atrovride/Xonlingii probe.
 XX
 KM Fungal detection; bacterial detection; probe; primer; ss.
 XX
 OS Trichoderma sp.
 XX
 PN WO200196612-A2.
 XX
 PD 20-DEC-2001.
 XX
 PF 13-JUN-2001; 2001WO-US18892.
 XX
 PR 13-JUN-2000; 2000US-0593012.
 XX
 PA (USST) US ENVIRONMENTAL PROTECTION AGENCY.
 XX
 PI Haugland R, Vesper SJ;
 XX
 DR WPI; 2002-098078/13.
 XX
 PT Detecting and quantifying fungi and bacteria, involves obtaining a
 PT sequence of the fungus, extracting the DNA from the sample, and
 PT subjecting the DNA to polymerase chain reaction and fluorescent probe
 PT analysis -
 XX
 PS Claim 67; Page 22; 110pp; English.
 XX
 CC The invention relates to a method of detecting and quantifying fungi and
 CC bacteria, involving obtaining a sequence of the microorganism to be
 CC detected and quantified, extracting the DNA from the sample, and
 CC subjecting the DNA to polymerase chain reaction (PCR) and fluorescent
 CC probe analysis. The method is useful for identifying and quantifying
 CC specific fungi and bacteria using specific DNA sequences. The specific
 CC DNA sequences are useful for the real time detection of PCR products with
 CC a fluorogenic probe system or other molecular probes like hybridisation.
 CC ABRK29026-ABRK29474 represent fungal and bacterial PCR primers and probes
 CC used in the method of the invention.
 CC
 SQ Sequence 21 BP; 3 A; 7 C; 7 G; 4 T; 0 other;

Query Match 72.9%; Score 12.4; DB 24; Length 21;
 Best Local Similarity 92.9%; Pred. No. 3.5e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GTTGCTTCGGCGG 14
 |||||
 8 GTTGCTTCGGCGG 21

Db 8 GTTGCTTCGGCGG 21

RESULT 17
 ABRN99459
 ID ABRN99459 standard; DNA; 22 BP.
 XX
 AC ABRN99459;
 XX
 DT 05-AUG-2002 (first entry)
 XX
 DE Fungi probe SEQ ID NO 31.
 XX
 KM Fungus; bacteria; quantification; detection; infection; gastroenteritis;
 KM ulcer; asthma; allergy; sinusitis; probe; ss.
 XX
 OS Aspergillus ochraceus.
 XX
 OS Aspergillus ocellatus.
 XX
 OS Aspergillus auricomus.
 XX
 PN US6387652-B1.
 XX
 PD 14-MAY-2002.
 XX
 PF 13-JUN-2000; 2000US-0593012.
 XX
 PR 15-APR-1998; 98US-081773P.

XX	14-APR-1999;	99US-0290990.
XX	(USSI) US ENVIRONMENTAL PROTECTION AGENCY.	
XX	Haugland R, Vesper S;	
DR	WPI; 2002-462353/49.	
PT	Detection and quantification of specific fungi or bacteria useful e.g.	
PT	In medical diagnosis and treatment of fungal and bacterial conditions,	
PT	by hybridizing and amplifying DNA using sequences unique to the species	
XX	or group of species	
PS	Claim 12; Column 91; 55dp; English.	
XX	The invention relates to specific fungi or bacteria detected and	
CC	quantified in a sample by extracting and recovering DNA from the organism	
CC	in the sample and hybridising and amplifying the DNA sequence using	
CC	sequences unique to the species/group of species but common to all	
CC	isolates of the species/group of species. The method especially employs	
CC	sequences selected from 225 fungal and bacterial primer and probe	
CC	sequences (ABN99429-ABN99653) for detection of specified fungi/fungal	
CC	groups or specified bacteria. The method enables detection and	
CC	quantification of specific fungi or bacteria, or groups of	
CC	fungal/bacterial species, useful medically for diagnosis and treatment of	
CC	fungi or bacteria associated with health problems such as infections,	
CC	gastroenteritis, ulcers, asthma, allergies and sinusitis. It is also	
CC	useful to detect and/or quantify microorganisms in the environment e.g.	
CC	to establish the risk of adverse health effects (e.g. pulmonary	
CC	haemorrhage from levels of Stachybotrys chartarum in air samples in	
CC	houses).	
XX	Sequence 22 BP; 2 A; 8 C; 6 G; 6 T; 0 other;	
SQ		
XX	Query Match	72.9%; Score 12.4; DB 24; Length 22;
XX	Best Local Similarity	92.9%; Pred. No. 3.5e+03;
XX	Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0	
QY	1 GTTGCTTCGCGCGG 14 6 GTTGCCTTCGCGCAG 19	
DB		
RESULT 18		
ID	ABK29056	
AC	ABK29056 standard; DNA; 22 BP.	
XX	ABK29056;	
DT	23-APR-2002 (first entry)	
XX	Aspergillus ochraceus/oslanus/auricomus probe.	
DE	Fungal detection; bacterial detection; probe; primer; ss.	
XX	Aspergillus sp.	
OS	WO200196612-A2.	
XX	20-DEC-2001.	
PD	13-JUN-2001; 2001WO-US18892.	
PF	13-JUN-2000; 2000US-0593012.	
XX	(USSI) US ENVIRONMENTAL PROTECTION AGENCY.	
FA	Haugland R, Vesper SJ;	
XX	WPI; 2002-098078/13.	
DR	Detecting and quantifying fungi and bacteria, involves obtaining a	
XX	sequence of the fungus, extracting the DNA from the sample, and	
PT		

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PT  subjecting the DNA to polymerase chain reaction and fluorescent probe
XX  analysis
XX  Claim 12; Page 8; 110pp; English.
XX
CC  The invention relates to a method of detecting and quantifying fungi and
CC  bacteria, involving obtaining a sequence of the microorganism to be
CC  detected and quantified, extracting the DNA from the sample, and
CC  subjecting the DNA to polymerase chain reaction (PCR) and fluorescent
CC  probe analysis. The method is useful for identifying and quantifying
CC  specific fungi and bacteria using specific DNA sequences. The specific
CC  DNA sequences are useful for the real time detection of PCR products with
CC  a fluorogenic probe system or other molecular probes like hybridisation.
CC  ABK29026-ABK29474 represent fungal and bacterial PCR primers and probes
CC  used in the method of the invention.
XX
SQ  Sequence 22 BP; 2 A; 8 C; 6 G; 6 T; 0 other;
XX
Query Match          72.9%; Score 12.4; DB 24; Length 22;
Best Local Similarity 92.9%; Pred. No. 3.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY  1 GTTGCTTCGGCGGG 14
    |||||
Db   6 GTTGCTTCGGCGAG 19
XX
RESULT 19
ABK29268
ID  ABK29268 standard; DNA; 22 BP.
XX
AC  ABK29268;
XX
DT  23-APR-2002 (first entry)
XX
XX  Aspergillus ochraceus probe.
DE  Aspergillus ochraceus.
XX
XX  Fungal detection; bacterial detection; probe; primer; ss.
XX
XX  Aspergillus ochraceus.
XX
XX  WO200196612-A2.
PN  WO200196612-A2.
XX
PD  20-DEC-2001.
XX
PF  13-JUN-2001; 2001WO-US18892.
XX
PR  13-JUN-2000; 2000US-0593012.
XX
PA  (USSI ) US ENVIRONMENTAL PROTECTION AGENCY.
XX
PI  Haugland R, Vesper SJ;
XX
DR  WPI; 2002-098076/13.
XX
XX  Detecting and quantifying fungi and bacteria, involves obtaining a
XX  sequence of the fungus, extracting the DNA from the sample, and
XX  subjecting the DNA to polymerase chain reaction and fluorescent probe
XX  analysis
XX
XX  Claim 83; Page 24; 110pp; English.
XX
XX  The invention relates to a method of detecting and quantifying fungi and
XX  bacteria, involving obtaining a sequence of the microorganism to be
XX  detected and quantified, extracting the DNA from the sample, and
XX  subjecting the DNA to polymerase chain reaction (PCR) and fluorescent
XX  probe analysis. The method is useful for identifying and quantifying
XX  specific fungi and bacteria using specific DNA sequences. The specific
XX  DNA sequences are useful for the real time detection of PCR products with
XX  a fluorogenic probe system or other molecular probes like hybridisation.
XX  ABK29026-ABK29474 represent fungal and bacterial PCR primers and probes
XX  used in the method of the invention.
XX

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SQ Sequence 22 BP; 2 A; 8 C; 6 G; 6 T; 0 other;
  Query Match          72.9%; Score 12.4; DB 24; Length 22;
  Best Local Similarity 92.9%; Pred. No. 3.5e+03;
  Matches 13; Conservative 0; Mismatches 1; Intels 0; Gaps 0;
  Oy 1 GTTGCTTCGGCGGG 14
      |||||
      |||||
  Db 6 GTTGCTTCGGCGAG 19

RESULT 20
ID ABK29271 standard; DNA; 22 BP.
XX ABK29271;
AC ABK29271;
XX 23-APR-2002 (first entry)
DT 23-APR-2002 (first entry)
XX Aspergillus ochraceus probe.
DE Aspergillus ochraceus probe.
KW Fungal detection; bacterial detection; probe; primer; ss.
XX Aspergillus ochraceus.
OS WO200196612-A2.
XX WO200196612-A2.
PD 20-DEC-2001.
XX 20-DEC-2001.
PE 13-JUN-2001; 2001WO-US18892.
XX 13-JUN-2001; 2001WO-US18892.
PR 13-JUN-2000; 2000US-0593012.
XX 13-JUN-2000; 2000US-0593012.
PA (USSI ) US ENVIRONMENTAL PROTECTION AGENCY.
XX (USSI ) US ENVIRONMENTAL PROTECTION AGENCY.
PI Haugland R, Vesper SJ;
XX Haugland R, Vesper SJ;
DR WPI; 2002-098078/13.
XX WPI; 2002-098078/13.
PT Detecting and quantifying fungi and bacteria, involves obtaining a
PT sequence of the fungus, extracting the DNA from the sample, and
PT subjecting the DNA to polymerase chain reaction and fluorescent probe
PT analysis
XX
XX Claim 84; Page 24; 110pp; English.
PS
XX
CC The invention relates to a method of detecting and quantifying fungi and
CC bacteria, involving obtaining a sequence of the microorganism to be
CC detected and quantified, extracting the DNA from the sample, and
CC subjecting the DNA to polymerase chain reaction (PCR) and fluorescent
CC probe analysis. The method is useful for identifying and quantifying
CC specific fungi and bacteria using specific DNA sequences. The specific
CC DNA sequences are useful for the real time detection of PCR products with
CC a fluorescent probe system or other molecular probes like hybridisation.
CC ABK29026-ABK29474 represent fungal and bacterial PCR primers and probes
CC used in the method of the invention.
XX
SQ Sequence 22 BP; 2 A; 8 C; 6 G; 6 T; 0 other;
  Query Match          72.9%; Score 12.4; DB 24; Length 22;
  Best Local Similarity 92.9%; Pred. No. 3.5e+03;
  Matches 13; Conservative 0; Mismatches 1; Intels 0; Gaps 0;
  Oy 1 GTTGCTTCGGCGGG 14
      |||||
      |||||
  Db 6 GTTGCTTCGGCGAG 19

RESULT 21
ID AAQ94376
XX AAQ94376 standard; DNA; 20 BP.
AC AAQ94376;

```

04-JUN-1996 (first entry)
Mycosphaerella fijiensis ITS primer JB548.
Plant pathogen; fungus; Septoria nodorum; Septoria tritici; Fusarium; Pseudocercospora herpotrichoides; Mycosphaerella fijiensis; PCR; Mycosphaerella muscicola; amplification; primer; ribosomal RNA gene; internal transcribed region; strain; capture; colourimetric assay; isolate; development; population; ss.
Synthetic.
WO9529260-A2.
02-NOV-1995.
19-APR-1995; 95WO-US04712.
25-APR-1994; 94US-0233608.
(CIBA) CIBA GEIGY AG.
Beck JY, Ligon JM;
WPI, 1995-383005/49.
DNA encoding intervening transcribed sequence - used for detection of plant fungal pathogens
Claim 3; Page 15; 65pp; English.
A novel method for the detection of plant pathogenic strains of fungi e.g. Septoria nodorum, S. tritici, Pseudocercospora herpotrichoides, Mycosphaerella fijiensis, M. muscicola or Fusarium spp, involves the PCR amplification of sequences found in the internal transcribed region (ITS) of the 18S, 5.8S and 28S ribosomal RNA genes by the primers AAQ4359-93 and AAT05357-72. These primers are derived from the ITS sequences of these fungi (AAT05394-105404 and AAQ43598) and are strain specific. The amplification products of the reactions using these primers can be used with the capture primers AAT05378-93 in colourimetric assays. The primers and ITS DNA can be used for the detection of specific fungal pathogen isolates and in monitoring disease development in plant populations.
Sequence 20 BP; 1 A; 5 C; 9 G; 5 T; 0 other;
Query Match 71.8%; Score 12.2; DB 16; Length 20;
Best Local Similarity 82.4%; Pred. No. 4.5e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
1 GTTGCTTCGGCGGAC 17
1 GTTGCTTCGGCGGAC 17
RESULT 22
AAV62524
ID AAV62524 standard; DNA; 20 BP.
AAV62524;
17-DEC-1998 (first entry)
M. fijiensis species specific primer JB548.
Internal transcribed spacer; ITS; ribosomal RNA; Fusarium avenaceum; Fusarium culmorum; Fusarium graminearum; Fusarium moniliforme; plant; Septoria avenae; Microdochium nivale; Fusarium poae; fungal pathogen; PCR; nucleic acid detection; PCR primer; ss.
Synthetic.
Mycosphaerella fijiensis.

PT Detection and quantification of specific fungi or bacteria useful e.g.
 PT in medical diagnosis and treatment of fungal and bacterial conditions,
 PT by hybridizing and amplifying DNA using sequences unique to the species
 PT or group of species
 XX
 PS Claim 41; Column 94; 55pp; English.
 CC The invention relates to specific fungi or bacteria detected and
 CC quantified in a sample by extracting and recovering DNA from the organism
 CC in the sample and hybridizing and amplifying the DNA sequence using
 CC sequences unique to the species/group of species but common to all
 CC isolates of the species/group of species. The method especially employs
 CC sequences selected from 325 fungal and bacterial primer and probe
 CC sequences (ABN99429-ABN99653) for detection of specified fungi/fungal
 CC groups or specified bacteria. The method enables detection and
 CC quantification of specific fungi or bacteria, or groups of
 CC fungal/bacterial species, useful medically for diagnosis and treatment of
 CC fungi or bacteria associated with health problems such as infections,
 CC gastroenteritis, ulcers, asthma, allergies and sinusitis. It is also
 CC useful to detect and/or quantify microorganisms in the environment e.g.
 CC to establish the risk of adverse health effects (e.g. pulmonary
 CC haemorrhage from levels of *Stachybotrys chartarum* in air samples in
 CC houses).
 CC
 SQ Sequence 17 BP; 1 A; 5 C; 5 G; 6 T; 0 other;
 XX
 Query Match 70.6%; Score 12; DB 24; Length 17;
 Best Local Similarity 100.0%; Pred. No. 5.7e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTGCTTCGGCG 12
 |||||
 5 GTTGCTTCGGCG 16
 Db
 RESULT 25
 ABK29145
 ID ABK29145 standard; DNA; 17 BP.
 XX
 XX ABK29145;
 AC
 XX
 DT 23-APR-2002 (first entry)
 XX
 XX Penicillium brevicompactum/alberechii forward PCR primer.
 DE
 XX Fungal detection; bacterial detection; probe; primer; ss.
 KM
 XX Penicillium brevicompactum.
 OS
 OS Penicillium alberechii.
 XX
 XX WO200196612-A2.
 PN
 XX
 XX 20-DEC-2001.
 PD
 XX 13-JUN-2001; 2001WO-US18892.
 PP
 XX 13-JUN-2000; 2000US-0593012.
 PR
 XX (USST) US ENVIRONMENTAL PROTECTION AGENCY.
 PA
 XX (USST) US ENVIRONMENTAL PROTECTION AGENCY.
 XX
 XX Haugland R, Vesper SJ;
 PI
 XX
 XX WPI, 2002-098078/13.
 DR
 XX
 XX Detecting and quantifying fungi and bacteria, involves obtaining a
 PT sequence of the fungus, extracting the DNA from the sample, and
 PT subjecting the DNA to polymerase chain reaction and fluorescent probe
 PT analysis
 XX
 XX Claim 41; Page 15; 110pp; English.
 XX
 CC The invention relates to a method of detecting and quantifying fungi and
 CC bacteria, involving obtaining a sequence of the microorganism to be

CC detected and quantified, extracting the DNA from the sample, and
 CC subjecting the DNA to polymerase chain reaction (PCR) and fluorescent
 CC probe analysis. The method is useful for identifying and quantifying
 CC specific fungi and bacteria using specific DNA sequences. The specific
 CC DNA sequences are useful for the real time detection of PCR products with
 CC a fluorogenic probe system or other molecular probes like hybridisation.
 CC ABK29026-ABK29474 represent fungal and bacterial PCR primers and probes
 CC used in the method of the invention.
 CC
 SQ Sequence 17 BP; 1 A; 5 C; 5 G; 6 T; 0 other;
 XX
 Query Match 70.6%; Score 12; DB 24; Length 17;
 Best Local Similarity 100.0%; Pred. No. 5.7e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTGCTTCGGCG 12
 |||||
 5 GTTGCTTCGGCG 16
 Db
 RESULT 26
 AA202872/C
 ID AA202872 standard; DNA; 20 BP.
 XX
 XX AA202872;
 AC
 XX
 DT 07-OCT-1999 (first entry)
 XX
 XX PCR primer used to amplify an ORF of *Chlamydia trachomatis*.
 DE
 XX Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
 KM paratrachoma; inclusion conjunctivitis; genital disease; peritrophic;
 KM nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
 KM Bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
 XX
 OS Synthetic.
 OS *Chlamydia trachomatis*.
 XX
 XX WO9928475-A2.
 PN
 XX
 XX 10-JUN-1999.
 PD
 XX 27-NOV-1998; 98WO-IB01939.
 PP
 XX 04-NOV-1998; 98US-0107077.
 PR 28-NOV-1997; 97FR-0015041.
 PR 17-DEC-1997; 97FR-0016034.
 XX
 XX (GEST) GENSET.
 PA
 XX Griffais R;
 PI
 XX
 XX WPI, 1999-371125/31.
 DR
 XX
 XX Genome sequence of *Chlamydia trachomatis*
 PT
 XX
 XX Disclosure; Page 1560; 1755pp; English.
 PS
 XX
 XX PCR primers AA201426-206209 were used to amplify open reading frames
 CC (ORFs) of the genome of *Chlamydia trachomatis* (see AA201425). These ORFs
 CC encode polypeptides (see AA136754-Y37949) which can be used as vaccines
 CC against *Chlamydia trachomatis*. Antisense and ribozyme sequences
 CC can also be used to control growth of the microorganism. *Chlamydia*
 CC trachomatis is responsible for a large number of diseases, e.g. eye
 CC diseases such as conventional trachoma, nonendemic trachoma,
 CC paratrachoma, and inclusion conjunctivitis; genital diseases such as
 CC nongonococcal urethritis, epididymitis, cervicitis, salpingitis;
 CC peritrophic, Bartholinitis; pneumopathy; in breast feeding infants;
 CC and venereal lymphogranulomatosis. The polypeptides of the
 CC invention may be of use in treating these diseases.
 CC
 SQ Sequence 20 BP; 6 A; 7 C; 3 G; 4 T; 0 other;
 XX

Query Match 70.6%; Score 12; DB 20; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.8e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TTGCTTCGGCGG 13
 DB 14 TTGCTTCGGCGG 3

RESULT 27
 AAF61866
 ID AAF61866 standard; DNA; 19 BP.

XX AAF61866;

AC 26-JUL-2001 (first entry)

DE Soybean leccin PCR primer LECr1.

XX Amplification; genetically modified organism; GMO; soya; maize; plant;
 KW detection; leccin; invertase; 35S-promoter; NOS terminator; NPTII;
 KM nopaline synthase; neomycin phosphotransferase; EPSPS; CryIA(b);
 KM enol-pyruvyl-shikimate-3-phosphate synthase; PCR primer; ss.

OS Glycine max.

PN W0200132919-A2.

PD 10-MAY-2001.

PP 27-OCT-2000; 2000MO-AT00283.

PR 29-OCT-1999; 99AT-0001820.

PA (OSTP) OESTERR FORSCH SEIBERSDORF.

PI Vollenhofer S, Mansfeld M, Knoch H;

DR WPI; 2001-308749/32.

PT New primer pairs for polymerase chain reaction, useful for detecting
 PT genetically modified plant materials in e.g. foods, have high annealing
 PT temperature for increased sensitivity.

PS Claim 10; Page 15; 37PP; German.

XX This invention describes a novel group of primer pairs for polymerase
 CC chain reaction (PCR) amplification of at least one genetic element (A),
 CC introduced by genetic modification of soya, maize or other plants,
 CC present in crude plant materials or derived compositions. The new primers
 CC and probes are used (i) to detect and/or quantify genetically modified
 CC plant materials in seeds, animal and human foodstuffs, especially where
 CC these have been processed so that DNA is extensively degraded and (ii)
 CC for monitoring the amplification of (A). The probes may also be used to
 CC confirm a successful PCR amplification. The high annealing temperature of
 CC the primers ensures high specificity and sensitivity, even with badly
 CC degraded samples, and facilitates analysis by restriction analysis, since
 CC only inexpensive restriction enzymes are required, reducing costs and
 CC making the method suitable for routine use. The process reliably
 CC detects/quantifies even very small amounts of genetically modified
 CC materials. AAF61845-AAF61868 represent the PCR primers used in the method
 CC of the invention which amplify the soybean (Glycine max) leccin gene, Zea
 CC mays invertase gene, Cauliflower Mosaic virus (CaMV) 35S-promoter,
 CC Agrobacterium tumefaciens NOS (nopaline synthase) terminator, an
 CC unidentified NPTII (neomycin phosphotransferase) gene, Petunia hybrida
 CC EPSPS (enol-pyruvyl-shikimate-3-phosphate synthase) CIP-fragment and the
 CC Bacillus thuringiensis modified CryIA(b) gene.

XX Sequence 19 BP; 3 A; 5 C; 5 G; 6 T; 0 other;

Query Match 69.4%; Score 11.8; DB 22; Length 19;
 Best Local Similarity 86.7%; Pred. No. 7.4e+03;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 TGCTTCGGCGGAAC 17
 DB 1 TGCTTCGGCGGAAC 15

RESULT 28
 AAF69341/C
 ID AAF69341 standard; DNA; 20 BP.

XX AAF69341;

AC 18-APR-2001 (first entry)

DE Integrin-linked kinase coding region targeted oligonucleotide #54.

XX Antisense; integrin-linked kinase; htk; infection; tumour;
 KM inflammation; ss.

OS Homo sapiens.

PN US6177273-B1.

PD 23-JAN-2001.

PP 26-OCT-1999; 99US-0428219.

PR 26-OCT-1999; 99US-0428219.

PA (ISIS-) ISIS PHARM INC.

PI Bennett CF, Cowseert LM;

DR WPI; 2001-137069/14.

PT Novel antisense compounds capable of modulating expression of human
 PT Integrin-linked kinase, useful for diagnosis, prophylaxis and treatment
 PT of disease, e.g. tumours, associated with expression of the kinase

PS Claim 3; Column 43; 40PP; English.

XX The present invention relates to an antisense compound 8 to
 CC 30 bases in length targeted to the 5' untranslated (UTR) region,
 CC the coding region or the 3' UTR region human integrin-linked
 CC kinase (htk). The antisense oligonucleotides are useful for
 CC inhibiting the expression of human htk in human cells or tissues,
 CC in vitro. The oligonucleotides can be utilized for diagnostics,
 CC therapeutics for the treatment of diseases associated with
 CC the expression of htk, prophylaxis e.g. to prevent or delay infection,
 CC inflammation or tumor formation and as research reagent.

XX Sequence 20 BP; 6 A; 8 C; 3 G; 3 T; 0 other;

Query Match 69.4%; Score 11.8; DB 22; Length 20;
 Best Local Similarity 86.7%; Pred. No. 7.4e+03;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 TGCTTCGGCGGAAC 17
 DB 18 TGCTTCGGCGGAAC 4

RESULT 29
 AB194529/C
 ID AB194529 standard; DNA; 20 BP.

XX AB194529;

AC 16-FEB-2002 (first entry)

DE Capture oligonucleotide zip ID#1616 oligo #9.

KM Human; K-ras; PCR primer; probe; capture probe; mutation detection;

KM ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
 KM infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
 KM cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
 KM environmental monitoring; food industry; feed industry; ss.
 XX
 OS Synthetic.
 XX
 PN WO200179548-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 04-APR-2001; 2001WO-US10958.
 XX
 PR 14-APR-2000; 2000US-197271P.
 XX
 PA (CORR) CORNELL RES FOUND INC.
 XX
 PI Barany F, Zivri M, Gerry NP, Favie R, Kliman R;
 XX
 DR WPI; 2002-034366/04.
 XX
 PT Designing capture oligonucleotide probes for use on a support to which
 PT complementary oligonucleotides hybridize with little mismatch -
 XX
 PS Example 5; Fig 29; 300pp; English.
 XX
 CC The present invention describes a method (M1) for designing capture
 CC oligonucleotide probes (I) for use on a support to which complementary
 CC oligonucleotide probes (II) will hybridize with little mismatch, where
 CC (I) have melting temperatures within a narrow range. The method is useful
 CC for detecting infectious diseases caused by bacterial infectious agents
 CC e.g. Salmonella, listeria monocytogenes and Haemophilus influenza, fungal
 CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
 CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
 CC Epstein-Barr virus and polio virus, and parasitic infectious agents
 CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
 CC medinensis. The method is also useful for detecting genetic diseases such
 CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
 CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
 CC involved in DNA amplification, replication, recombination or repair, the
 CC cancer is specifically associated with a gene selected from BRCA1 gene,
 CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
 CC method is also used for environmental monitoring, forensics and the food
 CC and feed industry, detecting comprises scanning (using e.g. a scanning
 CC electron microscope and infrared microscope) the support at the
 CC particular sites and identifying if ligation of the oligonucleotide probe
 CC sets occurred and correlating (using a computer) identified ligation to a
 CC presence or absence of the target nucleotide sequences. AB182074 to
 CC AB197546 represent oligonucleotide sequences used in the exemplification
 CC of the present invention.
 CC
 CC
 SQ Sequence 20 BP; 7 A; 6 C; 5 G; 2 T; 0 other;
 Query Match 69.4%; Score 11.8; DB 24; Length 20;
 Best Local Similarity 86.7%; Pred. No. 7.4e+03;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 TTGCTTCGGCGGAA 16
 DB 20 TTGCTTCGGCTGCA 6
 RESULT 30
 AB185628/c
 ID AB185628 standard; DNA; 24 BP.
 XX
 AC AB185628;
 XX
 DT 15-FEB-2002 (first entry)
 XX
 DE Capture oligonucleotide zip ID#1616 oligo #1.
 XX
 KM Human; K-ras; PCR primer; probe; capture probe; mutation detection;

KM ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
 KM infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
 KM cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
 KM environmental monitoring; food industry; feed industry; ss.
 XX
 OS Synthetic.
 XX
 PN WO200179548-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 04-APR-2001; 2001WO-US10958.
 XX
 PR 14-APR-2000; 2000US-197271P.
 XX
 PA (CORR) CORNELL RES FOUND INC.
 XX
 PI Barany F, Zivri M, Gerry NP, Favie R, Kliman R;
 XX
 DR WPI; 2002-034366/04.
 XX
 PT Designing capture oligonucleotide probes for use on a support to which
 PT complementary oligonucleotides hybridize with little mismatch -
 XX
 PS Example 5; Fig 25; 300pp; English.
 XX
 CC The present invention describes a method (M1) for designing capture
 CC oligonucleotide probes (I) for use on a support to which complementary
 CC oligonucleotide probes (II) will hybridize with little mismatch, where
 CC (I) have melting temperatures within a narrow range. The method is useful
 CC for detecting infectious diseases caused by bacterial infectious agents
 CC e.g. Salmonella, listeria monocytogenes and Haemophilus influenza, fungal
 CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
 CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
 CC Epstein-Barr virus and polio virus, and parasitic infectious agents
 CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
 CC medinensis. The method is also useful for detecting genetic diseases such
 CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
 CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
 CC involved in DNA amplification, replication, recombination or repair, the
 CC cancer is specifically associated with a gene selected from BRCA1 gene,
 CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
 CC method is also used for environmental monitoring, forensics and the food
 CC and feed industry, detecting comprises scanning (using e.g. a scanning
 CC electron microscope and infrared microscope) the support at the
 CC particular sites and identifying if ligation of the oligonucleotide probe
 CC sets occurred and correlating (using a computer) identified ligation to a
 CC presence or absence of the target nucleotide sequences. AB182074 to
 CC AB197546 represent oligonucleotide sequences used in the exemplification
 CC of the present invention.
 CC
 CC
 SQ Sequence 24 BP; 7 A; 7 C; 7 G; 3 T; 0 other;
 Query Match 69.4%; Score 11.8; DB 24; Length 24;
 Best Local Similarity 86.7%; Pred. No. 7.4e+03;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 TTGCTTCGGCGGAA 16
 DB 20 TTGCTTCGGCTGCA 6
 RESULT 31
 AB185629
 ID AB185629 standard; DNA; 24 BP.
 XX
 AC AB185629;
 XX
 DT 15-FEB-2002 (first entry)
 XX
 DE Capture oligonucleotide zip ID#1616 oligo #2.
 XX
 KM Human; K-ras; PCR primer; probe; capture probe; mutation detection;

KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
 KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
 KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
 KW environmental monitoring; food industry; feed industry; ss.
 OS Synthetic.
 XX WO200179548-A2.
 XX PN
 XX 25-OCT-2001.
 XX PD
 XX 04-APR-2001; 2001WO-US10958.
 XX PP
 XX 14-APR-2000; 2000US-197271P.
 XX PR
 XX (CORR) CORNELL RES FOUND INC.
 XX PA
 XX Barany F, Zivri M, Gerry NP, Favls R, Kliman R;
 XX PI
 XX WPI; 2002-034366/04.
 XX DR
 XX Designing capture oligonucleotide probes for use on a support to which
 XX PT complementary oligonucleotides hybridize with little mismatch -
 XX PT
 XX Example 5; Fig 25; 300pp; English.
 XX PS
 XX The present invention describes a method (M1) for designing capture
 XX CC oligonucleotide probes (I) for use on a support to which complementary
 XX CC oligonucleotide probes (II) will hybridise with little mismatch, where
 XX CC (I) have melting temperatures within a narrow range. The method is useful
 XX CC for detecting infectious diseases caused by bacterial infectious agents
 XX CC e.g. Salmonella, listeria monocytogenes and Haemophilus influenza, fungal
 XX CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
 XX CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
 XX CC Epstein-Barr virus and polio virus, and parasitic infectious agents
 XX CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
 XX CC medinensis. The method is also useful for detecting genetic diseases such
 XX CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
 XX CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
 XX CC involved in DNA amplification, replication, recombination or repair, the
 XX CC cancer is specifically associated with a gene selected from BRCA1 gene,
 XX CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
 XX CC method is also used for environmental monitoring, forensics and the food
 XX CC and feed industry, detecting comprises scanning (using e.g. a scanning
 XX CC electron microscope and infrared microscope) the support at the
 XX CC particular sites and identifying if ligation of the oligonucleotide probe
 XX CC sets occurred and correlating (using a computer) identified ligation to a
 XX CC presence or absence of the target nucleotide sequences. AB182074 to
 XX CC AB197546 represent oligonucleotide sequences used in the exemplification
 XX CC of the present invention.
 XX CC
 XX SQ Sequence 24 BP; 3 A; 7 C; 7 G; 7 T; 0 other;
 XX
 XX Query Match 69.4%; Score 11.8; DB 24; Length 24;
 XX Best Local Similarity 86.7%; Pred. No. 7.4e+03;
 XX Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 XX QY 2 TTGCTGGCGCGGAA 16
 XX |||||
 XX 5 TTGCTGGCGCTGCAA 19
 XX
 XX Db
 XX
 XX RESULT 32
 XX AAF80069/c
 XX ID AAF80069 standard; DNA; 25 BP.
 XX AC
 XX AAF80069;
 XX
 XX 11-JUN-2001 (first entry)
 XX DT
 XX PCR primer for a maize seed-specific gene promoter.
 XX DE
 XX pZ840 gene; seed-specific promoter; maize; fatty acid metabolism;

KW protein metabolism; carbohydrate metabolism; phytohormone biosynthesis;
 KW cell cycle regulation; transgenic plant; PCR primer; ss.
 XX Zea mays.
 XX OS
 XX WO200121783-A2.
 XX PN
 XX 29-MAR-2001.
 XX PD
 XX 22-SEP-2000; 2000WO-US26131.
 XX PF
 XX 24-SEP-1999; 99US-0155859.
 XX PR
 XX (PION-) PIONEER HI-BRED INT INC.
 XX PI
 XX Jiao S, Habben JE, Niu X;
 XX PI
 XX WPI; 2001-257981/26.
 XX DR
 XX Novel seed-preferred promoter sequence useful for selectively
 XX PT expressing a fire nucleotide sequence in a plant seed and for
 XX PT transgenic plant production -
 XX PT
 XX Example 1; Page 19; 31pp; English.
 XX PS
 XX PCR primers AAF80067-69 were used to amplify a maize promoter that
 XX CC is capable of driving transcription in a seed-preferred manner. The
 XX CC promoter is isolated from a gene which is homologous to the Dairley pZ840
 XX CC gene. The seed-specific promoter is used for selectively expressing a
 XX CC nucleotide sequence encoding a polypeptide involved in fatty acid
 XX CC metabolism, protein metabolism, carbohydrate metabolism, phytohormone
 XX CC biosynthesis or in cell cycle regulation. The promoter may be used
 XX CC to produce transgenic plants. The genes of interest expressed by the
 XX CC promoter are also useful for varying the phenotype of seeds.
 XX CC
 XX SQ Sequence 25 BP; 5 A; 8 C; 6 G; 6 T; 0 other;
 XX
 XX Query Match 69.4%; Score 11.8; DB 22; Length 25;
 XX Best Local Similarity 86.7%; Pred. No. 7.5e+03;
 XX Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 XX QY 2 TTGCTGGCGCGGAA 16
 XX |||||
 XX 15 TTGCTGGCGCGGCAA 1
 XX
 XX Db
 XX
 XX RESULT 33
 XX ABQ61935/c
 XX ID ABQ61935 standard; DNA; 25 BP.
 XX AC
 XX ABQ61935;
 XX
 XX 03-OCT-2002 (first entry)
 XX DT
 XX Human aquaporin 5 (AQ5) gene oligonucleotide (OGN) chip PCR primer 674.
 XX DE
 XX Human; ss; PCR; primer; aquaporin; AQ5; AQP; water channel protein;
 XX KW oligonucleotide chip; OGN chip; cDNA chip; lung cancer;
 XX KW mutation detection; polymorphism detection; gene expression.
 XX
 XX OS Homo sapiens.
 XX XX
 XX WO200220787-A1.
 XX PN
 XX 14-MAR-2002.
 XX PD
 XX 10-SEP-2001; 2001WO-KR01528.
 XX PF
 XX 09-SEP-2000; 2000KR-0053821.
 XX PR
 XX (GOOD-) GOODGENE INC.
 XX PA
 XX (MOON/) MOON W.
 XX PA
 XX (MOON/) MOON C.

XX Moon W, Moon C, Moon Y, Kim B, Kim D, Shin C, Um T, Kim H,
 PI Song M, Kim H, Song S;
 XX WPI; 2002-393647/42.
 DR Novel aquaporin 5 gene mutant useful for diagnosing lung, stomach,
 PT colon, prostate, or head or neck cancer -
 XX Claim 9; Fig 20; 154pp; English.
 XX The invention comprises a mutant form of the human aquaporin 5 (AQP5)
 CC gene. Aquaporin (AQP) is a family of water channel proteins, through
 CC which water is transported into and out of cells - ten types of mammalian
 CC AQP have been identified so far. The invention also comprises an
 CC oligonucleotide (OGN) chip having 902 oligonucleotide primer sequences
 CC and a cDNA chip comprising one or more sequences from the human AQP5
 CC gene. The mutant AQP5 gene is useful for diagnosing cancer (i.e lung
 CC cancer). The OGN chip is useful for detecting mutations and polymorphisms
 CC in AQP5 and the cDNA chip is useful for analysis of gene expression. The
 CC present DNA sequence represents a human aquaporin 5 (AQP5) gene
 CC oligonucleotide (OGN) chip PCR primer.
 XX Sequence 25 BP; 3 A; 12 C; 6 G; 4 T; 0 other;
 SQ
 Query Match 69.4%; Score 11.8; DB 24; Length 25;
 Best Local Similarity 86.7%; Pred. No. 7.5e+03;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GTTGCTTCGGCGGGA 15
 Db 15 GTTGCTTCGGCGGGA 1
 RESULT 34
 AAF51334/C
 ID AAF51334 standard; DNA; 15 BP.
 XX AAF51334;
 AC 30-MAR-2001 (first entry)
 XX IGF-1 oligonucleotide #2294.
 DE IGF-1 oligonucleotide #2294.
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KM cytoskeletal; dermatological; cardiac; vitreous; ophthalmological; keloid;
 KM skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KM IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KM growth factor mediated cell proliferation; ichthyosis; seborrhoea; rube;
 KM keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KM hyperneovascular condition; hyperplasia; kidney disease;
 KM neovascular condition of the retina; ss.
 XX Homo sapiens.
 OS
 XX WO200078341-A1.
 PN 28-DEC-2000.
 XX 21-JUN-2000; 2000WO-AU00693.
 PF 21-JUN-1999; 99US-0140345.
 PR 21-JUN-1999; 99US-0140345.
 XX (MURDOCH CHILDRENS RES INST.
 PA Wright CJ, Werther GA, Edmondson SR,
 PI WPI; 2001-041421/05.
 DR WPI; 2001-041421/05.
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by
 PT administering UV (ultra-violet) treatment (optional) and an antisense
 PT nucleic acid that inhibits or reduces growth factor mediated cell
 PT proliferation and/or inflammation -

XX Example 8; Page 75; 201pp; English.
 PS The present invention relates to a method for ameliorating the effects
 CC of skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor (IGF)-1
 CC receptor, IGF binding protein (IGFBP)-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation.
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF5151 and
 CC AAF5153-FAS161). The method is useful for ameliorating the effects of
 CC psoriasis, ichthyosis, pityriasis, rube, pilaris, seborrhoea, keloids,
 CC keratosis, neoplasias, scleroderma, wart, benign growths, cancers of the
 CC skin, a hyperneovascular condition such as a neovascular condition of the
 CC retina, brain or skin, growth factor-mediated malignancies, other
 CC sclerotic disease, kidney disease, hyperproliferation of the inside of
 CC blood vessels or any other hyperplasia.
 XX Sequence 15 BP; 4 A; 5 C; 4 G; 2 T; 0 other;
 SQ
 Query Match 67.1%; Score 11.4; DB 22; Length 15;
 Best Local Similarity 92.3%; Pred. No. 1.2e+04;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 TGCTTCGGCGGGA 15
 Db 15 TGCTTCGGCGGGA 3
 RESULT 35
 AAF51335/C
 ID AAF51335 standard; DNA; 15 BP.
 XX AAF51335;
 AC 30-MAR-2001 (first entry)
 XX IGF-1 oligonucleotide #2295.
 DE IGF-1 oligonucleotide #2295.
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KM cytoskeletal; dermatological; cardiac; vitreous; ophthalmological; keloid;
 KM skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KM IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KM growth factor mediated cell proliferation; ichthyosis; seborrhoea; rube;
 KM keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KM hyperneovascular condition; hyperplasia; kidney disease;
 KM neovascular condition of the retina; ss.
 XX Homo sapiens.
 OS
 XX WO200078341-A1.
 PN 28-DEC-2000.
 XX 21-JUN-2000; 2000WO-AU00693.
 PF 21-JUN-1999; 99US-0140345.
 PR 21-JUN-1999; 99US-0140345.
 XX (MURDOCH CHILDRENS RES INST.
 PA Wright CJ, Werther GA, Edmondson SR,
 PI WPI; 2001-041421/05.
 DR WPI; 2001-041421/05.
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by
 PT administering UV (ultra-violet) treatment (optional) and an antisense
 PT nucleic acid that inhibits or reduces growth factor mediated cell
 PT proliferation and/or inflammation -
 XX Example 8; Page 75; 201pp; English.
 PS The present invention relates to a method for ameliorating the effects
 CC

CC inhibiting or reducing growth factor mediated cell proliferation,

Sequence 16 BP; 1 A; 5 C; 6 G; 4 T; 0 other;

Query Match 67.1%; Score 11.4; DB 16; Length 16;
 Best Local Similarity 92.3%; Pred. No. 1.2e+04;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GTTGCTTCGGCGG 13
 1 GTTGCTTCGGCGG 13
 DB 1 GTTGCTTCGGCGG 13

RESULT 38

AAT05364 standard; DNA, 16 BP.

XX AAT05364;
 XX AAT05364;
 XX 04-JUN-1996 (first entry)
 XX
 XX Fusarium spp. ITS primer JB570.
 XX
 XX Plant pathogen; fungus; Septoria nodorum; Septoria tritici; Fusarium;
 KM Pseudocercospora herpeticoides; Mycosphaerella filijensis; PCR;
 KM Mycosphaerella muscicola; amplification; primer; ribosomal RNA gene;
 KM Internal transcribed region; strain; capture; colourimetric assay;
 KM isolate; development; population; ss.
 XX
 XX Synthetic.
 XX
 XX MO9529260-A2.
 XX
 XX 02-NOV-1995.
 XX
 XX 19-APR-1995; 95WO-US04712.
 XX
 XX 25-APR-1994; 94US-0233608.
 XX
 XX (CIBA) CIBA GEIGY AG.
 XX
 XX Beck JJ, Ligon JM;
 XX WPI; 1995-383005/49.
 XX
 XX DNA encoding intervening transcribed sequence - used for detection
 PT of plant fungal pathogens
 XX
 XX Claim 3; Page 15; 65pp; English.

CC A novel method for the detection of plant pathogenic strains of fungi
 CC e.g. Septoria nodorum, S.tritici, Pseudocercospora herpeticoides,
 CC Mycosphaerella filijensis, M.muscicola or Fusarium spp, involves the PCR
 CC amplification of sequences found in the internal transcribed region
 CC (ITS) of the 18S, 5.8S and 28S ribosomal RNA genes by the primers
 CC AA09459-93 and AAT05357-72. These primers are derived from the ITS
 CC sequences of these fungi (AAT05394-105404 and AAQ94398) and are strain
 CC specific. The amplification products of the reactions using these
 CC primers can be used with the capture primers AAT05379-93 in
 CC colourimetric assays. The primers and ITS DNA can be used for the
 CC detection of specific fungal pathogen isolates and in monitoring disease
 CC development in plant populations.
 CC
 XX Sequence 16 BP; 1 A; 4 C; 6 G; 5 T; 0 other;

Query Match 67.1%; Score 11.4; DB 16; Length 16;
 Best Local Similarity 92.3%; Pred. No. 1.2e+04;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GTTGCTTCGGCGG 13
 1 GTTGCTTCGGCGG 13
 DB 4 GTTGCTTCGGCGG 16

RESULT 39
 AAT55603/c

ID AAT55603 standard; RNA, 16 BP.
 XX
 AC AAT55603;
 XX
 XX 15-APR-1997 (first entry)
 DT
 XX
 XX Mouse relA hairpin ribozyme target sequence (Int. position 137).

XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KM gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KM intercellular adhesion molecule; rel A; tumour necrosis factor;
 KM TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KM translocation; chronic myelogenous leukaemia; CML; cancer;
 KM Philadelphia chromosome; inflammation; autoimmune disease;
 KM atherosclerosis; myocardial infarction; stroke; resenosis;
 KM transplant rejection; rheumatoid arthritis; psoriasis;
 KM myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KM human immunodeficiency virus; acquired immune deficiency syndrome;
 KM AIDS; ss.

XX Mus musculus.

XX MO9523225-A2.

XX 31-AUG-1995.

XX 23-FEB-1995; 95WO-IB00156.

XX 30-JAN-1995; 95US-0380734.

XX 23-FEB-1994; 94US-0201109.

XX 22-MAR-1994; 94US-0218934.

XX 04-APR-1994; 94US-0222795.

XX 07-APR-1994; 94US-0224483.

XX 15-APR-1994; 94US-0227958.

XX 18-MAY-1994; 94US-0228041.

XX 06-JUL-1994; 94US-0245736.

XX 15-AUG-1994; 94US-0291932.

XX 16-AUG-1994; 94US-0291433.

XX 17-AUG-1994; 94US-0292620.

XX 19-AUG-1994; 94US-0293520.

XX 02-SEP-1994; 94US-0300000.

XX 08-SEP-1994; 94US-0303039.

XX 23-SEP-1994; 94US-0311486.

XX 28-SEP-1994; 94US-0311749.

XX 03-OCT-1994; 94US-0316771.

XX 07-OCT-1994; 94US-0319492.

XX 11-OCT-1994; 94US-0321993.

XX 04-NOV-1994; 94US-0334847.

XX 10-NOV-1994; 94US-0337608.

XX 28-NOV-1994; 94US-0345516.

XX 16-DEC-1994; 94US-0357577.

XX 23-DEC-1994; 94US-0363233.

(RIBO-) RIBOZYME PHARM INC.

XX Stinchcomb DT, Chowitra B, Dizezio A, Draper KG, Dudycz LW;

XX Grimm S, Karpelesky A, Kisch K, Matulic-Adamic J;

XX McSwigen JA, Modak A, Pavco P, Beigelman L, Sullivan SM;

XX Swedler D, Thompson JD, Tracz D, Ueman N, Wincott FE;

XX Woolf T;

XX WPI; 1995-351090/45.

XX Ribozymes having modified bases and methods for producing them

XX for use in inhibiting disease related genes

XX Claim 2; Page 240; 407pp; English.

XX The present sequence represents a preferred target sequence for an

XX enzymatic nucleic acid (i.e. a ribozyme) which cleaves relA

XX mRNA at the nucleotide base position indicated in the DE line.

CC The *relA* gene product is a subunit of the transcriptional
 CC regulator NF-kappaB and is implicated specifically in the induction
 CC of inflammatory responses. Regions of the mRNA that do not form
 CC secondary folding structures and that contain potential hammerhead
 CC and hairpin ribozyme cleavage sites were identified by computer
 CC analysis. Ribozymes directed against these mRNA sequences were
 CC designed and synthesised with modifications that improve their
 CC nuclease resistance. The ribozymes are designed to cleave the
 CC target sequences and thereby inhibit *relA* expression, making them
 CC potentially useful for treating rheumatoid arthritis, restenosis
 CC and asthma as well as for increasing tolerance to transplanted
 CC tissues. The potential immunosuppressive properties of a ribozyme
 CC that cleaves *relA* mRNA means that uses are limited to local
 CC delivery, acute indications or *ex vivo* treatment.

SQ Sequence 16 BP; 7 A; 5 C; 4 G; 0 U; 0 other;

Query Match 67.1%; Score 11.4; DB 16; Length 16;
 Best Local Similarity 92.3%; Pred. No. 1.2e+04;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGG 13
 |||||
 DB 16 GTTGCTTCGGCTG 4

RESULT 40

AAV62556 AAV62556 standard; DNA; 16 BP.

AAV62556;

17-DEC-1998 (first entry)

Fusarium species specific primer JB577.

Internal transcribed spacer; ITS; ribosomal RNA; *Fusarium avenaceum*;
Fusarium culmorum; *Fusarium graminearum*; *Fusarium moniliforme*; plant;
Septoria avenae; *Microdochium nivale*; *Fusarium poae*; fungal pathogen;
 PCR; nucleic acid detection; PCR primer; ss.

Synthetic.

Fusarium sp.

US5814453-A.

29-SEP-1998.

02-JUL-1997; 97US-0887480.

02-JUL-1997; 97US-0887480.

19-APR-1995; 95WO-US04712.

15-OCT-1996; 96US-0722187.

(NOVS) NOVARTIS FINANCE CORP.

Beck JU;

WPI; 1998-541745/46.

DNA isolated from fungal RNA, and its internal transcribed spacer

sequence - used for detecting fungal pathogens in plant tissue

Claim 3; Column 17; 56pp; English.

Sequences AAV62507 to AAV62566 represent species specific PCR primers
 for various fungal isolates used for fungal detection in the course of
 the invention. The primers are designed based on the internal
 transcribed spacer (ITS) sequences of the various fungal species. The
 invention provides a DNA molecule isolated from the ribosomal RNA gene
 region of a fungal pathogen, where the DNA molecule consists of an ITS
 sequence selected from ITS1 and ITS2 of *Fusarium culmorum*, *Fusarium*
graminearum, *Fusarium moniliforme*, *Septoria avenae* or *Microdochium*

CC *nivale*. A method for detecting *F. graminearum*, *F. culmorum*, *F.*
 CC *moniliforme*, *F. poae*, *F. avenaceum* and *M. nivale* isolates is also
 CC provided which comprises isolating DNA from a plant leaf infected with at
 CC least one of the above pathogens and amplifying parts of the ITS sequence
 CC of the pathogen(s) by PCR using specific primers from within these
 CC sequences. The pathogen(s) are detected by visualising the amplified part
 CC of the ITS sequence.

SQ Sequence 16 BP; 1 A; 5 C; 6 G; 4 T; 0 other;

Query Match 67.1%; Score 11.4; DB 19; Length 16;
 Best Local Similarity 92.3%; Pred. No. 1.2e+04;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGG 13
 |||||
 DB 1 GTTGCTTCGGCGG 13

Search completed: June 7, 2003, 08:30:21
 Job time: 157.018 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 7, 2003, 07:18:59 ; Search time 148.255 Seconds

(without alignments)
273.421 Million cell updates/sec

Title: US-10-080-959A-5

Sequence: 1 ctgagccgcgcgcgcgcgc 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 1698378

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1000 summaries

Database :

1: N_Geneseq_101002:.*
2: /SID2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
3: /SID2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
4: /SID2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
5: /SID2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
6: /SID2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
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22: /SID2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
23: /SID2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
24: /SID2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
25: /SID2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	24	ABN99616
2	18	100.0	18	24	ABK29213
3	12.8	71.1	17	24	ABN99534
4	12.8	71.1	17	24	ABK29131
5	12.4	68.9	15	22	AAFS1791
6	12.4	68.9	15	22	AAFS1792
7	12.4	68.9	24	24	ABAL42362
8	12.4	68.9	24	24	ABA96574
9	12.2	67.8	21	20	AAK59160

C	10	12.2	67.8	21	24	ABK94173	Endothelin recepto
C	11	12.2	67.8	21	24	ABK94174	Endothelin recepto
C	12	12.2	67.8	24	20	AAK24822	Oligonucleotide ZC
C	13	12.2	67.8	24	21	AAK44122	PCR primer for the
C	14	12.2	67.8	25	24	AAK19807	ASO primer #65 to
C	15	12	66.7	21	14	AAO40880	Apptase gene rever
C	16	12	66.7	21	15	AAO64130	Apptase gene PCR p
C	17	12	66.7	25	15	AAO61767	HEV strain BUR-121
C	18	12	66.7	25	17	AAAT27478	HEV ORF proteins e
C	19	12	66.7	25	19	AAV71688	Bacillus lichenifo
C	20	11.8	65.6	18	15	AAO68697	Alkaline protease
C	21	11.8	65.6	18	16	AAO80932	Human CDC27 gene 5
C	22	11.8	65.6	24	17	AAK41772	Primer 48 for sequ
C	23	11.6	64.4	19	24	ABK98282	Human polymorphic
C	24	11.6	64.4	21	19	AAK26752	CAPL 3' splice sit
C	25	11.6	64.4	21	20	AAK17717	US5877308 Seq ID 2
C	26	11.6	64.4	21	24	ABK94171	Endothelin recepto
C	27	11.6	64.4	21	24	ABK94172	Endothelin recepto
C	28	11.6	64.4	21	24	ABK94175	Endothelin recepto
C	29	11.6	64.4	21	24	ABK94176	Endothelin recepto
C	30	11.6	64.4	21	24	AAV41141	CAPL 3' splice sit
C	31	11.6	64.4	22	19	AAV41142	CAPL 3' splice sit
C	32	11.6	64.4	22	20	AAK17697	Antisense oligo to
C	33	11.6	64.4	22	20	AAK17698	Antisense oligo to
C	34	11.6	64.4	22	21	AAK58261	Human PRO212 hybr
C	35	11.6	64.4	23	22	AAH78624	PCR primer RFC780
C	36	11.6	64.4	15	22	AAFS1793	IGF-1 oligonucleot
C	37	11.4	63.3	15	22	AAV24377	Chimeric antibody
C	38	11.4	63.3	19	19	AAK00122	Human antibody PCR
C	39	11.4	63.3	19	20	AAK58902	PCR primer MBCLVR
C	40	11.4	63.3	19	21	AAH75095	Nucleotide sequenc
C	41	11.4	63.3	19	22	AAH74274	Nucleotide sequenc
C	42	11.4	63.3	19	22	AAH76633	Humanised anti-PTH
C	43	11.4	63.3	19	22	AAK69118	Human L chain V re
C	44	11.4	63.3	19	22	AAK69174	Human L chain V re
C	45	11.4	63.3	19	22	AAK69230	Human L chain V re
C	46	11.4	63.3	19	22	AAK69410	Joint disease rela
C	47	11.4	63.3	20	20	AAK06762	Lymphocyte activat
C	48	11.4	63.3	20	22	AAK6704	Human cytohesin-2
C	49	11.4	63.3	20	22	AAK6704	Human gene single
C	50	11.4	63.3	21	22	AAK62834	Beta subunit of AT
C	51	11.4	63.3	24	14	AAK62834	Granule bound star
C	52	11.2	62.2	16	18	AAK62836	Hammerhead ribozym
C	53	11.2	62.2	17	21	AAK02847	Human GDMMP-1 17-m
C	54	11.2	62.2	17	24	ABN00659	Human GDMMP-1 17-m
C	55	11.2	62.2	17	24	ABN00659	Human GDMMP-1 17-m
C	56	11.2	62.2	17	24	ABN00659	Human GDMMP-1 17-m
C	57	11.2	62.2	18	18	AAK62746	Granule bound star
C	58	11.2	62.2	19	24	ABK99522	Fungi probe SEQ ID
C	59	11.2	62.2	19	24	ABK29119	Memnoniella echina
C	60	11.2	62.2	20	24	ABK96263	Capture oligonucle
C	61	11.2	62.2	21	21	AAK91937	Sequence surroundi
C	62	11.2	62.2	21	24	ABK70329	Synthetic antisens
C	63	11.2	62.2	22	19	AAV43066	Amplification prim
C	64	11.2	62.2	22	24	ABK85825	Myotonic dystrophy
C	65	11.2	62.2	23	19	AAV43100	Primer B14 for 1i
C	66	11.2	62.2	23	22	AAK04323	Dog leukocyte inte
C	67	11.2	62.2	23	24	ABK28778	H5V-1 capture sequ
C	68	11.2	62.2	24	24	ABK89097	Capture oligonucle
C	69	11.2	62.2	24	24	ABK89097	Capture oligonucle
C	70	11.2	62.2	25	24	ABN03588	Human GDMMP-1 25-m
C	71	11.2	62.2	25	24	ABN03589	Human GDMMP-1 25-m
C	72	11.2	62.2	25	24	ABN03590	Human GDMMP-1 25-m
C	73	11.2	62.2	25	24	ABN03591	Human GDMMP-1 25-m
C	74	11.2	62.2	25	24	ABN03592	Human GDMMP-1 25-m
C	75	11.2	62.2	25	24	ABN03593	Human GDMMP-1 25-m
C	76	11.2	62.2	25	24	ABN03594	Human GDMMP-1 25-m
C	77	11.2	62.2	25	24	ABN03595	Human GDMMP-1 25-m
C	78	11.2	62.2	25	24	ABN03596	Human GDMMP-1 25-m
C	79	11.2	62.2	25	24	ABN03597	Human GDMMP-1 25-m
C	80	11.1	61.1	21	24	AAK27211	Mouse Skp2 promote
C	81	11	61.1	21	21	AAK27211	Primer used in con
C	82	11	61.1	23	21	AAK27211	Primer used in con

C 83	11	61.1	25	10	AA97005	Herpes simplex Vir
84	11	61.1	25	18	AA75208	Primer 1 used to a
85	11	61.1	25	18	AAV00130	Human glucose regu
86	11	61.1	25	18	AAV00095	Human glucose regu
87	11	61.1	25	18	AA75048	Human glucose regu
88	11	61.1	25	21	AA655737	PCR primer for hum
89	11	61.1	25	22	AA658822	Human glucose regu
90	10.8	60.0	18	22	AAH37286	SNP specific lower
91	10.8	60.0	18	22	AA688331	Primer CDX2-0048P
92	10.8	60.0	18	24	ABN99616	Fungi probe SEQ ID
93	10.8	60.0	18	24	ABL30636	Human HLA genocyp
94	10.8	60.0	19	24	ABK29213	Stachyotrys chart
95	10.8	60.0	19	24	AAQ06434	Oligonucleotide pr
96	10.8	60.0	19	18	AA793031	Rat liver derived
97	10.8	60.0	19	22	AA684484	Cyclin E ribozyme
98	10.8	60.0	19	22	AA684484	P HyBeacon probe f
99	10.8	60.0	19	22	AA684484	Cyclin E ribozyme
100	10.8	60.0	20	19	AAV30525	HLA DQB1 typing pr
101	10.8	60.0	20	22	AAV37477	Primer P3 used to
102	10.8	60.0	20	22	AAV37477	Human BGR-1 transc
103	10.8	60.0	20	22	AAH29856	Murine Bax-alpha c
104	10.8	60.0	20	22	AAH29856	Oligonucleotide #5
105	10.8	60.0	21	21	AAH29856	Human p52 PCR prim
106	10.8	60.0	21	21	AAH29856	Human p52 PCR prim
107	10.8	60.0	21	21	AAH29856	PCR primer for the
108	10.8	60.0	21	22	AAH29856	Human gene single
109	10.8	60.0	21	22	AAH29856	AB54 PCR primer.
110	10.8	60.0	21	22	AAH29856	Human MIP-1 beta p
111	10.8	60.0	24	20	AAH29856	Human BGR-1 transc
112	10.8	60.0	24	22	AAH29856	DNA encoding VP16
113	10.8	60.0	24	22	AAH29856	Oligonucleotide ad
114	10.8	60.0	24	22	AAH29856	Oligonucleotide ad
115	10.8	60.0	24	24	AAH29856	Transduced RACC ge
116	10.8	60.0	24	24	AAH29856	Human regulatory sc
117	10.8	60.0	24	24	AAH29856	M. tuberculosis st
118	10.8	60.0	24	24	AAH29856	A. goessypii GUA2 P
119	10.8	60.0	25	17	AAH29856	HLA DOB gene PCR p
120	10.8	60.0	25	21	AAH29856	HLA DOB gene PCR p
121	10.8	60.0	25	21	AAH29856	Neisseria meningit
122	10.8	60.0	25	21	AAH29856	Neisseria meningit
123	10.8	60.0	25	22	AAH29856	Rat catalase (CAT)
124	10.8	60.0	25	22	AAH29856	N. meningitidis fu
125	10.8	60.0	25	22	AAH29856	Human GDMPL-1 17-m
126	10.8	60.0	25	22	AAH29856	Primer #2 for PCR/
127	10.8	60.0	25	22	AAH29856	E. coli 16S rRNA s
128	10.8	60.0	25	22	AAH29856	PCR primer used to
129	10.8	60.0	25	22	AAH29856	Primer for amplify
130	10.8	60.0	25	22	AAH29856	Human IGF-1 antis
131	10.8	60.0	25	22	AAH29856	Human mcpPCK phos
132	10.8	60.0	25	22	AAH29856	Sense PCR primer u
133	10.8	60.0	25	22	AAH29856	Corn zein 10 gene
134	10.8	60.0	25	22	AAH29856	Oryza sativa 10 ge
135	10.8	60.0	25	22	AAH29856	Human IGF-1 antis
136	10.8	60.0	25	22	AAH29856	Human mcpPCK phos
137	10.8	60.0	25	22	AAH29856	Sense PCR primer u
138	10.8	60.0	25	22	AAH29856	Corn zein 10 gene
139	10.8	60.0	25	22	AAH29856	Oryza sativa 10 ge
140	10.8	60.0	25	22	AAH29856	Human IGF-1 antis
141	10.8	60.0	25	22	AAH29856	Human mcpPCK phos
142	10.8	60.0	25	22	AAH29856	Sense PCR primer u
143	10.8	60.0	25	22	AAH29856	Corn zein 10 gene
144	10.8	60.0	25	22	AAH29856	Oryza sativa 10 ge
145	10.8	60.0	25	22	AAH29856	Human IGF-1 antis
146	10.8	60.0	25	22	AAH29856	Human mcpPCK phos
147	10.8	60.0	25	22	AAH29856	Sense PCR primer u
148	10.8	60.0	25	22	AAH29856	Corn zein 10 gene
149	10.8	60.0	25	22	AAH29856	Oryza sativa 10 ge
150	10.8	60.0	25	22	AAH29856	Human IGF-1 antis
151	10.8	60.0	25	22	AAH29856	Human mcpPCK phos
152	10.8	60.0	25	22	AAH29856	Sense PCR primer u
153	10.8	60.0	25	22	AAH29856	Corn zein 10 gene
154	10.8	60.0	25	22	AAH29856	Oryza sativa 10 ge
155	10.8	60.0	25	22	AAH29856	Human IGF-1 antis

229	10.4	57.8	25	18	AAV00502	Human alpha-(2) su	c 302	10.2	56.7	20	21	AA992292	16S ribosomal DNA
230	10.4	57.8	25	19	AAV59348	zif10 primer ZC13	c 303	10.2	56.7	20	21	AA922647	Bacterial DNA PCR
231	10.4	57.8	25	20	AAV64971	Human c-myc protei	c 304	10.2	56.7	20	21	AA915486	PCR primer for 16S
232	10.4	57.8	25	21	AAZ93273	Primer used in con	c 305	10.2	56.7	20	21	AA915486	Hepatitis GB virus
233	10.4	57.8	25	22	AAZ93273	3' FTR 5' PCR prim	c 306	10.2	56.7	20	21	AA915486	Treponema socransk
234	10.4	57.8	25	23	AAZ93273	Oligo #11 for clon	c 307	10.2	56.7	20	21	AA915486	Forward PCR primer
235	10.4	57.8	25	24	ABA03545	Relaxin/IGF/insuli	c 308	10.2	56.7	20	21	AA925945	PCR primer for L.
236	10.2	56.7	15	22	AAZ93273	Human TNFRSF1B ge	c 309	10.2	56.7	20	21	AA925945	PCR primer #1 for
237	10.2	56.7	15	22	AAZ93273	IGFBP2 oligonucleo	c 310	10.2	56.7	20	21	AA925945	Brevibacillus bore
238	10.2	56.7	15	22	AAZ93273	IGFBP2 oligonucleo	c 311	10.2	56.7	20	21	AA925945	PCR primer for 16S
239	10.2	56.7	15	22	AAZ93273	Human chorionic go	c 312	10.2	56.7	20	21	AA925945	MLC-2v PCR primer
240	10.2	56.7	15	22	AAZ93273	PNA probe sequence	c 313	10.2	56.7	20	21	AA925945	Brevibacillus bore
241	10.2	56.7	15	22	AAZ93273	Granule bound star	c 314	10.2	56.7	20	21	AA925945	Human caspase 8 mr
242	10.2	56.7	15	22	AAZ93273	Biosensor oligonuc	c 315	10.2	56.7	20	21	AA925945	Heart muscle cell
243	10.2	56.7	15	22	AAZ93273	PCR primer used to	c 316	10.2	56.7	20	21	AA925945	MLC-2v PCR primer
244	10.2	56.7	15	22	AAZ93273	Hammerhead ribozym	c 317	10.2	56.7	20	21	AA925945	Bacterial sequen
245	10.2	56.7	15	22	AAZ93273	Hepatitis B virus	c 318	10.2	56.7	20	21	AA925945	16S rRNA PCR primer
246	10.2	56.7	15	22	AAZ93273	Hepatitis B virus	c 319	10.2	56.7	20	21	AA925945	16S rRNA PCR primer
247	10.2	56.7	15	22	AAZ93273	Human ABC1 polymor	c 320	10.2	56.7	20	21	AA925945	Cycloclasticus pug
248	10.2	56.7	15	22	AAZ93273	Fungi probe SEQ ID	c 321	10.2	56.7	20	21	AA925945	Human DBP1 coding
249	10.2	56.7	15	22	AAZ93273	Human GMPLP-1 17-m	c 322	10.2	56.7	20	21	AA925945	its gene PCR prime
250	10.2	56.7	15	22	AAZ93273	Human GMPLP-1 17-m	c 323	10.2	56.7	20	21	AA925945	Bacterial 16S rRNA
251	10.2	56.7	15	22	AAZ93273	Human GMPLP-1 17-m	c 324	10.2	56.7	20	21	AA925945	PCR-restriction fr
252	10.2	56.7	15	22	AAZ93273	Human GMPLP-1 17-m	c 325	10.2	56.7	20	21	AA925945	Escherichia coli 1
253	10.2	56.7	15	22	AAZ93273	Human GMPLP-1 17-m	c 326	10.2	56.7	20	21	AA925945	Escherichia coli 1
254	10.2	56.7	15	22	AAZ93273	Human GMPLP-1 17-m	c 327	10.2	56.7	20	21	AA925945	Salinospira sp. 16
255	10.2	56.7	15	22	AAZ93273	Human GMPLP-1 17-m	c 328	10.2	56.7	20	21	AA925945	Nucleotide sequenc
256	10.2	56.7	15	22	AAZ93273	Chlorinated ethyle	c 329	10.2	56.7	20	21	AA925945	B. coli forward pr
257	10.2	56.7	15	22	AAZ93273	Bacterial 16S rRNA	c 330	10.2	56.7	20	21	AA925945	Mouse c/EBP beta p
258	10.2	56.7	15	22	AAZ93273	Myrothecium verticu	c 331	10.2	56.7	20	21	AA925945	Escherichia coli f
259	10.2	56.7	15	22	AAZ93273	Transforming growt	c 332	10.2	56.7	20	21	AA925945	Human TSP1 domain
260	10.2	56.7	15	22	AAZ93273	Otoferlin exon PCR	c 333	10.2	56.7	20	21	AA925945	Primer #1 relating
261	10.2	56.7	15	22	AAZ93273	Primer #1 to ampli	c 334	10.2	56.7	20	21	AA925945	PCR primer #5 for
262	10.2	56.7	15	22	AAZ93273	Bacterial ribosoma	c 335	10.2	56.7	20	21	AA925945	Primer #4. Undir
263	10.2	56.7	15	22	AAZ93273	Bloom's syndrome a	c 336	10.2	56.7	20	21	AA925945	Forward PCR primer
264	10.2	56.7	15	22	AAZ93273	Calcium ion channe	c 337	10.2	56.7	20	21	AA925945	Enterobacter 16S r
265	10.2	56.7	15	22	AAZ93273	Microorganism MO7	c 338	10.2	56.7	20	21	AA925945	DNA encoding Ribos
266	10.2	56.7	15	22	AAZ93273	PCR primer J11 for	c 339	10.2	56.7	20	21	AA925945	Rucophyllus fucoida
267	10.2	56.7	15	22	AAZ93273	5' primer used to	c 340	10.2	56.7	20	21	AA925945	Capture oligonucle
268	10.2	56.7	15	22	AAZ93273	MO9922023 probe 62	c 341	10.2	56.7	20	21	AA925945	Capture oligonucle
269	10.2	56.7	15	22	AAZ93273	Strain MO7 16S rDN	c 342	10.2	56.7	20	21	AA925945	PCR primer Kp115.
270	10.2	56.7	15	22	AAZ93273	Burkholderia sp. 1	c 343	10.2	56.7	20	21	AA925945	Burkitt's myc anti
271	10.2	56.7	15	22	AAZ93273	P. aeruginosa dect	c 344	10.2	56.7	20	21	AA925945	Burkitt's myc anti
272	10.2	56.7	15	22	AAZ93273	Burkholderia sp. 1	c 345	10.2	56.7	20	21	AA925945	PCR primer #1 for
273	10.2	56.7	15	22	AAZ93273	Rhodococcus erythr	c 346	10.2	56.7	20	21	AA925945	Antisense oligonuc
274	10.2	56.7	15	22	AAZ93273	Probe 1638 to the	c 347	10.2	56.7	20	21	AA925945	Human c-myc modifi
275	10.2	56.7	15	22	AAZ93273	Probe 1744 to the	c 348	10.2	56.7	20	21	AA925945	phosphonomonosete
276	10.2	56.7	15	22	AAZ93273	LAB RNA gene prim	c 349	10.2	56.7	20	21	AA925945	c-myc antisense co
277	10.2	56.7	15	22	AAZ93273	PCR primer for amp	c 350	10.2	56.7	20	21	AA925945	Phospholipase C-ga
278	10.2	56.7	15	22	AAZ93273	P. cepacia 16S rRNA	c 351	10.2	56.7	20	21	AA925945	Human nmr7-1 prime
279	10.2	56.7	15	22	AAZ93273	Hepatitis GB virus	c 352	10.2	56.7	20	21	AA925945	Vector-specific PC
280	10.2	56.7	15	22	AAZ93273	16S rRNA forward a	c 353	10.2	56.7	20	21	AA925945	Interleukin 5 rece
281	10.2	56.7	15	22	AAZ93273	Primer for amplifi	c 354	10.2	56.7	20	21	AA925945	PCR primer Ub15-2
282	10.2	56.7	15	22	AAZ93273	Control (1638) for	c 355	10.2	56.7	20	21	AA925945	PCR primer for Hum
283	10.2	56.7	15	22	AAZ93273	Burkholderia casid	c 356	10.2	56.7	20	21	AA925945	Bacterial 16S RNA
284	10.2	56.7	15	22	AAZ93273	Nucleotide sequen	c 357	10.2	56.7	20	21	AA925945	Human COL1A1 PCR p
285	10.2	56.7	15	22	AAZ93273	Primer 27F for bac	c 358	10.2	56.7	20	21	AA925945	Matte mDRS DNA amp
286	10.2	56.7	15	22	AAZ93273	16S rRNA Becherich	c 359	10.2	56.7	20	21	AA925945	Microorganism dect
287	10.2	56.7	15	22	AAZ93273	Eubacterial rRNA p	c 360	10.2	56.7	20	21	AA925945	Anti-c-myc oligonu
288	10.2	56.7	15	22	AAZ93273	PCR primer UD SEQ	c 361	10.2	56.7	20	21	AA925945	Lower PCR primer f
289	10.2	56.7	15	22	AAZ93273	Human Toso PCR pri	c 362	10.2	56.7	20	21	AA925945	c-myc targeted ant
290	10.2	56.7	15	22	AAZ93273	Forward primer for	c 363	10.2	56.7	20	21	AA925945	Mouse Huntington's
291	10.2	56.7	15	22	AAZ93273	Human chloroixin 16	c 364	10.2	56.7	20	21	AA925945	PCR primer for CDN
292	10.2	56.7	15	22	AAZ93273	M. tuberculosis 16	c 365	10.2	56.7	20	21	AA925945	PCR primer for CDN
293	10.2	56.7	15	22	AAZ93273	Human matrix metal	c 366	10.2	56.7	20	21	AA925945	Primer #1 used to
294	10.2	56.7	15	22	AAZ93273	PCR primer used to	c 367	10.2	56.7	20	21	AA925945	c-myc directed pho
295	10.2	56.7	15	22	AAZ93273	Human Toso protein	c 368	10.2	56.7	20	21	AA925945	
296	10.2	56.7	15	22	AAZ93273	Forward primer for	c 369	10.2	56.7	20	21	AA925945	
297	10.2	56.7	15	22	AAZ93273	PCR primer 1 used	c 370	10.2	56.7	20	21	AA925945	
298	10.2	56.7	15	22	AAZ93273	Pseudomonas sp. 01	c 371	10.2	56.7	20	21	AA925945	
299	10.2	56.7	15	22	AAZ93273		c 372	10.2	56.7	20	21	AA925945	
300	10.2	56.7	15	22	AAZ93273		c 373	10.2	56.7	20	21	AA925945	
301	10.2	56.7	15	22	AAZ93273		c 374	10.2	56.7	20	21	AA925945	

C 375	10.2	56.7	23	17	AA44282	5'-Guanosine-cappe	C 448	10	55.6	20	22	AAH20679	Human telomeric re
C 376	10.2	56.7	23	21	AAH39023	Unknown bacterial	C 449	10	55.6	20	22	AAH74084	Primer #18. Homo
C 377	10.2	56.7	23	21	ABL51612	Chimeric polymers	C 450	10	55.6	20	22	AAH73059	Human daxx inhibit
C 378	10.2	56.7	23	24	ABL51613	Chimeric polymers	C 451	10	55.6	20	22	AAH73059	PCR primer specific
C 379	10.2	56.7	24	9	AAH80289	Sequence of Arg 15	C 452	10	55.6	20	22	AAH92460	Capture oligonucle
C 380	10.2	56.7	24	9	AAH80289	Sequence of Arg 15	C 453	10	55.6	21	14	AAH97410	PCR primer #43 for
C 381	10.2	56.7	24	16	AAH82992	Primer for amplify	C 454	10	55.6	21	19	AAH26407	Human polymorphic
C 382	10.2	56.7	24	16	AAH81640	Salmonella typhimu	C 455	10	55.6	21	19	AAH19849	Primer for human i
C 383	10.2	56.7	24	18	AAH22943	Human cathepsin Y	C 456	10	55.6	21	21	AAH58850	Human gene single
C 384	10.2	56.7	24	19	AAH41361	M. catarrhalis str	C 457	10	55.6	21	22	AAH95420	Human gene single
C 385	10.2	56.7	24	19	AAH36102	Mismatch complemen	C 458	10	55.6	21	22	AAH95611	Human gene single
C 386	10.2	56.7	24	19	AAH22263	Primer used in pre	C 459	10	55.6	21	22	AAH96442	Primer 9 used in c
C 387	10.2	56.7	24	19	AAH22263	Primer used in pre	C 460	10	55.6	21	22	AAH83756	Barnase gene prime
C 388	10.2	56.7	24	22	AAH92421	Wild type 24-mer o	C 461	10	55.6	22	14	AAH42815	Barnase gene prime
C 389	10.2	56.7	24	22	AAH92421	Rice OsC1X2 PCR p	C 462	10	55.6	22	14	AAH42815	Barnase coding reg
C 390	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 463	10	55.6	22	19	AAH34988	Barnase gene PCR p
C 391	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 464	10	55.6	22	19	AAH34988	Barnase gene PCR p
C 392	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 465	10	55.6	22	19	AAH34988	Barnase gene PCR p
C 393	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 466	10	55.6	22	19	AAH34988	Barnase gene PCR p
C 394	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 467	10	55.6	22	19	AAH34988	Barnase coding reg
C 395	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 468	10	55.6	22	20	AAH90489	Vascular endotheli
C 396	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 469	10	55.6	22	21	AAH74693	Human lacciferin
C 397	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 470	10	55.6	22	21	AAH74693	Human G-protein co
C 398	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 471	10	55.6	22	22	AAH07977	Primer #1, to ampl
C 399	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 472	10	55.6	22	22	AAH07977	Mouse interferon g
C 400	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 473	10	55.6	22	22	AAH07977	PCR primer, YYB-B
C 401	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 474	10	55.6	22	24	AAH87949	Megaspinaera cerevi
C 402	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 475	10	55.6	22	24	AAH87949	Transforming growt
C 403	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 476	10	55.6	22	24	AAH87949	Plasmid pHPy PCR p
C 404	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 477	10	55.6	22	24	AAH87949	Primer used to iso
C 405	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 478	10	55.6	22	24	AAH87949	Primer used in con
C 406	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 479	10	55.6	22	24	AAH87949	Otiferlin RT-PCR p
C 407	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 480	10	55.6	22	24	AAH87949	Interferon-gamma R
C 408	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 481	10	55.6	22	24	AAH87949	Murine xpc gene PC
C 409	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 482	10	55.6	22	24	AAH87949	PCR primer for hls
C 410	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 483	10	55.6	22	24	AAH87949	PCR primer used to
C 411	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 484	10	55.6	22	24	AAH87949	Mouse KISS-1 PCR p
C 412	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 485	10	55.6	22	24	AAH87949	Human excitatory a
C 413	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 486	10	55.6	22	24	AAH87949	Human DNMT3L cDNA
C 414	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 487	10	55.6	22	24	AAH87949	Human GABA transpo
C 415	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 488	10	55.6	22	24	AAH87949	Alp1a(1)I subunit
C 416	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 489	10	55.6	22	24	AAH87949	Oligonucleotide ad
C 417	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 490	10	55.6	22	24	AAH87949	Oligonucleotide ad
C 418	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 491	10	55.6	22	24	AAH87949	Oligonucleotide ad
C 419	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 492	10	55.6	22	24	AAH87949	Oligonucleotide ad
C 420	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 493	10	55.6	22	24	AAH87949	Oligonucleotide ad
C 421	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 494	10	55.6	22	24	AAH87949	Oligonucleotide ad
C 422	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 495	10	55.6	22	24	AAH87949	Oligonucleotide ad
C 423	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 496	10	55.6	22	24	AAH87949	Oligonucleotide ad
C 424	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 497	10	55.6	22	24	AAH87949	Oligonucleotide ad
C 425	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 498	10	55.6	22	24	AAH87949	Oligonucleotide ad
C 426	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 499	10	55.6	22	24	AAH87949	Oligonucleotide ad
C 427	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 500	10	55.6	22	24	AAH87949	Oligonucleotide ad
C 428	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 501	10	55.6	22	24	AAH87949	Oligonucleotide ad
C 429	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 502	10	55.6	22	24	AAH87949	Oligonucleotide ad
C 430	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 503	10	55.6	22	24	AAH87949	Oligonucleotide ad
C 431	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 504	10	55.6	22	24	AAH87949	Oligonucleotide ad
C 432	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 505	10	55.6	22	24	AAH87949	Oligonucleotide ad
C 433	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 506	10	55.6	22	24	AAH87949	Oligonucleotide ad
C 434	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 507	10	55.6	22	24	AAH87949	Oligonucleotide ad
C 435	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 508	10	55.6	22	24	AAH87949	Oligonucleotide ad
C 436	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 509	10	55.6	22	24	AAH87949	Oligonucleotide ad
C 437	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 510	10	55.6	22	24	AAH87949	Oligonucleotide ad
C 438	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 511	10	55.6	22	24	AAH87949	Oligonucleotide ad
C 439	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 512	10	55.6	22	24	AAH87949	Oligonucleotide ad
C 440	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 513	10	55.6	22	24	AAH87949	Oligonucleotide ad
C 441	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 514	10	55.6	22	24	AAH87949	Oligonucleotide ad
C 442	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 515	10	55.6	22	24	AAH87949	Oligonucleotide ad
C 443	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 516	10	55.6	22	24	AAH87949	Oligonucleotide ad
C 444	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 517	10	55.6	22	24	AAH87949	Oligonucleotide ad
C 445	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 518	10	55.6	22	24	AAH87949	Oligonucleotide ad
C 446	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 519	10	55.6	22	24	AAH87949	Oligonucleotide ad
C 447	10.2	56.7	24	24	ABO02269	Oligonucleotide ad	C 520	10	55.6	22	24	AAH87949	Oligonucleotide ad

521	9.8	54.4	15	17	AAT37716	Apo(a) mRNA (nt. p	C 594	9.8	54.4	20	20	AA01433	Probe for Bacterol
522	9.8	54.4	15	17	AAT37626	Apo(a) mRNA (nt. p	C 595	9.8	54.4	20	21	AA068766	Human FUT6 antisen
523	9.8	54.4	15	17	AAT37587	Apo(a) mRNA (nt. p	C 596	9.8	54.4	20	21	AA040718	Mouse fibrinogen-1
524	9.8	54.4	15	17	AAT37564	Apo(a) mRNA (nt. p	C 597	9.8	54.4	20	21	AA286872	16S rRNA PCR prime
525	9.8	54.4	15	17	AAT37566	Apo(a) mRNA (nt. p	C 598	9.8	54.4	20	22	AA010991	Forward universal
526	9.8	54.4	15	17	AAT34531	Human Fas antigen	C 599	9.8	54.4	20	22	AA503151	Human EPO primary
527	9.8	54.4	15	17	AAT34533	Human Fas antigen	C 600	9.8	54.4	20	22	AA504839	Primer used for sp
C 528	9.8	54.4	15	22	AA045522	IGFBP2 oligonucleo	C 601	9.8	54.4	20	22	AA088343	Probe 432T. Unde
C 529	9.8	54.4	15	22	AA045524	IGFBP2 oligonucleo	C 602	9.8	54.4	20	22	AA067694	Oligonucleotide #5
C 530	9.8	54.4	15	22	AA045524	IGFBP2 oligonucleo	C 603	9.8	54.4	20	22	AA067695	Oligonucleotide #6
532	9.8	54.4	15	22	AA046672	IGFBP3 oligonucleo	C 604	9.8	54.4	20	24	AB055334	Eubacterial/univer
533	9.8	54.4	15	22	AA046674	IGFBP3 oligonucleo	C 605	9.8	54.4	20	24	AB055334	Arthrobacter sp. 1
534	9.8	54.4	15	24	AA048092	Human neurotrophide	C 606	9.8	54.4	20	24	AB080861	Human caspase 7 ph
535	9.8	54.4	16	16	AA094570	RNA "clamp" used t	C 607	9.8	54.4	20	24	AB069534	Rat phosphotyrase
536	9.8	54.4	16	20	AA020082	PCR primer for Pgi	C 608	9.8	54.4	20	24	AB069535	Rat phosphotyrase
537	9.8	54.4	16	20	AA030157	Detection probe SE	C 609	9.8	54.4	20	24	AB069513	Human phosphotyase
C 538	9.8	54.4	16	24	AB031304	HHA-QBI gene prob	C 610	9.8	54.4	20	24	AA029926	Forward primer use
C 539	9.8	54.4	17	14	AA039297	Glucocerebrosidase	C 611	9.8	54.4	20	24	AB096704	Manihela sp. 558
C 540	9.8	54.4	17	14	AA048259	Glucocerebrosidase	C 612	9.8	54.4	20	16	AA01017	Tomato exo-(1-4)de
C 541	9.8	54.4	17	18	AA048259	Mouse flt-1 VEGF r	C 613	9.8	54.4	21	20	AA023773	Vector pshuttle 3'
C 542	9.8	54.4	17	20	AA048259	Novamyl loop-speci	C 614	9.8	54.4	21	22	AA062469	GRAP polymorphism
C 543	9.8	54.4	17	20	AA048259	Novamyl loop-speci	C 615	9.8	54.4	21	22	AA062469	CHRNA7 polymorphi
C 544	9.8	54.4	17	20	AA048259	Human A-Raf subctr	C 616	9.8	54.4	21	22	AA095460	Human gene single
C 545	9.8	54.4	17	21	AA07163	Hammerhead ribozym	C 617	9.8	54.4	21	22	AA095460	Human gene single
C 546	9.8	54.4	17	21	AA07163	Hammerhead ribozym	C 618	9.8	54.4	21	24	AB073315	TPO mimetic antibo
547	9.8	54.4	17	21	AA070352	Hammerhead ribozym	C 619	9.8	54.4	21	24	AB073315	Human single nucle
548	9.8	54.4	17	21	AA080154	Hammerhead ribozym	C 620	9.8	54.4	22	18	AA074816	Porcine retrovirus
549	9.8	54.4	17	24	AB025589	Hepatitis B virus	C 621	9.8	54.4	22	18	AA074816	Porcine retrovirus
550	9.8	54.4	17	24	AB025590	Human GDMLP-1 17-m	C 622	9.8	54.4	22	18	AA074817	Porcine retrovirus
551	9.8	54.4	17	24	AB025591	Human GDMLP-1 17-m	C 623	9.8	54.4	22	18	AA074817	Porcine retrovirus
552	9.8	54.4	17	24	AB025591	Human GDMLP-1 17-m	C 624	9.8	54.4	22	18	AA074817	Porcine retrovirus
553	9.8	54.4	17	24	AB025591	Human GDMLP-1 17-m	C 625	9.8	54.4	22	20	AA0209309	Human macrophage s
C 554	9.8	54.4	18	13	AA026549	Human HLA genotypi	C 626	9.8	54.4	22	21	AA013227	PCR primer #8 used
C 555	9.8	54.4	18	15	AA026549	Control probe #4 f	C 627	9.8	54.4	22	22	AA073653	T cell receptor be
C 556	9.8	54.4	18	16	AA045595	Type II procollage	C 628	9.8	54.4	22	22	AA077732	Human MD36 CDNA PC
C 557	9.8	54.4	18	16	AA045595	Cosmid 46C7-T7 pri	C 629	9.8	54.4	22	22	AA077732	PCR primer #5. Un
C 558	9.8	54.4	18	18	AA035870	Human DNA polymera	C 630	9.8	54.4	22	22	AA077733	PCR primer #6. Un
C 559	9.8	54.4	18	18	AA035870	Delta-9 desaturase	C 631	9.8	54.4	22	22	AA077733	PCR primer #6. Un
560	9.8	54.4	18	20	AA022170	DNA repeat unit 1	C 632	9.8	54.4	22	24	AA043723	T-cell antigen rec
561	9.8	54.4	18	20	AA022170	Primer for amplify	C 633	9.8	54.4	22	24	AB086116	Human MD36 speci
C 562	9.8	54.4	18	20	AA022170	Human CPG2 PCR pri	C 634	9.8	54.4	23	16	AA082991	Human erythropoiet
563	9.8	54.4	18	20	AA022170	Human IYS17 3'-acc	C 635	9.8	54.4	23	18	AA082991	Human erythropoiet
564	9.8	54.4	18	20	AA022170	Human leukocyte an	C 636	9.8	54.4	23	18	AA082991	Human erythropoiet
565	9.8	54.4	18	20	AA022170	Human leukocyte an	C 637	9.8	54.4	23	18	AA082991	Human erythropoiet
566	9.8	54.4	18	20	AA022170	Group-specific seq	C 638	9.8	54.4	23	18	AA082991	Human erythropoiet
567	9.8	54.4	18	20	AA022170	Group-specific seq	C 639	9.8	54.4	23	18	AA082991	Human erythropoiet
568	9.8	54.4	18	21	AA049692	PCR primer for CDN	C 640	9.8	54.4	23	20	AA058213	Rose River virus N
569	9.8	54.4	18	21	AA049692	O. volvulus nOvPLA	C 641	9.8	54.4	23	20	AA058213	Rose River virus N
570	9.8	54.4	18	21	AA049692	Human CD44 antisen	C 642	9.8	54.4	23	21	AA063460	Human stem cell an
C 571	9.8	54.4	18	21	AA049692	PCR primer for hum	C 643	9.8	54.4	23	22	AA022272	Human growth hormo
C 572	9.8	54.4	18	21	AA049692	Synthetic bioelast	C 644	9.8	54.4	23	22	AA022272	Human growth hormo
573	9.8	54.4	18	22	AA042791	SLPI gene repeatin	C 645	9.8	54.4	23	22	AA022272	Human growth hormo
C 574	9.8	54.4	18	22	AA042791	Sequencing primer	C 646	9.8	54.4	23	22	AA022272	Human growth hormo
C 575	9.8	54.4	18	24	AB058292	Human Smad7 phosph	C 647	9.8	54.4	23	22	AA022272	Human growth hormo
576	9.8	54.4	18	24	AB058292	Human GLUT 10 SSCP	C 648	9.8	54.4	23	22	AA022272	Human growth hormo
577	9.8	54.4	18	24	AB058292	Human GLUT 10 SSCP	C 649	9.8	54.4	23	24	AB058292	Human growth hormo
C 578	9.8	54.4	19	18	AA033331	Senes primer Exon	C 650	9.8	54.4	23	24	AB058292	Human growth hormo
C 579	9.8	54.4	19	18	AA033331	Oligonucleotide (p	C 651	9.8	54.4	23	24	AB058292	Human growth hormo
C 580	9.8	54.4	19	21	AA061095	PCR primer used fo	C 652	9.8	54.4	24	16	AA080093	Human growth hormo
C 581	9.8	54.4	20	15	AA064102	Human Plk1 promote	C 653	9.8	54.4	24	16	AA080093	Human growth hormo
C 582	9.8	54.4	20	15	AA064102	Mycobacterium xeno	C 654	9.8	54.4	24	17	AA028899	Human ANK gene PCR
583	9.8	54.4	20	18	AA078499	Rat melanocortin r	C 655	9.8	54.4	24	17	AA028899	Human growth hormo
584	9.8	54.4	20	18	AA078499	Cryptosporidium ge	C 656	9.8	54.4	24	18	AA078499	Human growth hormo
585	9.8	54.4	20	18	AA078499	Cryptosporidium ge	C 657	9.8	54.4	24	19	AA078499	Human growth hormo
586	9.8	54.4	20	18	AA078499	Cryptosporidium ge	C 658	9.8	54.4	24	19	AA078499	Human growth hormo
587	9.8	54.4	20	19	AA070000	Cryptosporidium ge	C 659	9.8	54.4	24	20	AA078499	Human growth hormo
C 588	9.8	54.4	20	19	AA070000	Mouse c-jun protel	C 660	9.8	54.4	24	21	AA078499	Human growth hormo
C 589	9.8	54.4	20	19	AA070000	Lactobacillus sp.	C 661	9.8	54.4	24	22	AA078499	Human growth hormo
C 590	9.8	54.4	20	19	AA070000	Lactobacillus sp.	C 662	9.8	54.4	24	22	AA078499	Human growth hormo
C 591	9.8	54.4	20	20	AA070000	Subcellular 16S rRNA	C 663	9.8	54.4	24	22	AA078499	Human growth hormo
C 592	9.8	54.4	20	20	AA070000	Bacterial 16S rRNA	C 664	9.8	54.4	24	24	AB086841	Human synlein pro
C 593	9.8	54.4	20	20	AA070000	PCR primer 8P used	C 665	9.8	54.4	24	24	AB086841	Serine/threonine p
						Oligonucleotide "2	C 666	9.8	54.4	24	24	AB083031	Human X2 checa rep

C 667	9.8	54.4	24	24	ABA98284	Primer 50 for sequ	740	9.6	53.3	20	13	AA031556	Sense primer for t
C 668	9.8	54.4	24	24	ABO00975	Oligonucleotide ad	741	9.6	53.3	20	18	AAT50474	MCSF PCR primer RM
C 669	9.8	54.4	24	24	ABO01417	Oligonucleotide ad	742	9.6	53.3	20	18	AAT60474	MCSF PCR primer RM
C 670	9.8	54.4	24	24	ABO02727	Oligonucleotide ad	743	9.6	53.3	20	18	AAT60476	MCSF PCR primer RM
C 671	9.8	54.4	24	24	ABO05894	Oligonucleotide ad	744	9.6	53.3	20	18	AA260476	MCSF PCR primer RM
C 672	9.8	54.4	24	24	ABO05935	Oligonucleotide ad	745	9.6	53.3	20	20	AA223218	HCV NS5B DNA speci
C 673	9.8	54.4	24	24	ABO06779	Oligonucleotide ad	746	9.6	53.3	20	20	AA231335	CXCR4 gene inhibi
C 674	9.8	54.4	24	24	ABO06820	Oligonucleotide ad	747	9.6	53.3	20	20	AA201951	PCR primer used to
C 675	9.8	54.4	24	24	ABO09342	Oligonucleotide ad	748	9.6	53.3	20	20	AA292522	PCR primer used to
C 676	9.8	54.4	24	24	ABO09383	Oligonucleotide ad	749	9.6	53.3	20	20	AA292556	PCR primer used to
C 677	9.8	54.4	24	24	AB186956	Capture oligonucle	750	9.6	53.3	20	21	AA292556	PCR primer used to
C 678	9.8	54.4	24	24	AB186957	Capture oligonucle	751	9.6	53.3	20	21	AA292556	PCR primer used to
C 679	9.8	54.4	24	24	AA171439	Human excitatory a	752	9.6	53.3	20	21	AA173749	Primer F3c used to
C 680	9.8	54.4	25	17	AA173067	Yeast his3 gene pc	753	9.6	53.3	20	22	AA151213	Human bcl-x antis
C 681	9.8	54.4	25	18	AA153901	Ross River virus A	754	9.6	53.3	20	22	AA151214	Human bcl-x antis
C 682	9.8	54.4	25	19	AAV59414	PCR primer ZC1349	755	9.6	53.3	20	22	AA151214	Hybridisation prob
C 683	9.8	54.4	25	19	AAV59414	PCR primer ZC1349	756	9.6	53.3	20	22	AA151214	Hybridisation prob
C 684	9.8	54.4	25	19	AAV61856	A. contortrix prot	757	9.6	53.3	20	22	AA151214	PCR primer for gene
C 685	9.8	54.4	25	20	AAV58548	Ross River virus A	758	9.6	53.3	20	24	AA151214	PCR primer SEQ ID
C 686	9.8	54.4	25	20	AAV58548	Ross River virus A	759	9.6	53.3	20	24	AA151214	Human SR-CP anti
C 687	9.8	54.4	25	20	AAV58548	Human ZS1G-11 DNA	760	9.6	53.3	20	24	AA151214	Human DB2 anti
C 688	9.8	54.4	25	20	AAV58548	Human ZS1G-11 DNA	761	9.6	53.3	20	24	AA151214	Human MEXK3 CDNA
C 689	9.8	54.4	25	20	AAV58548	PCR primer for hum	762	9.6	53.3	20	24	AA151214	Human MEXK3 CDNA
C 690	9.8	54.4	25	21	AAV58548	FLAG-ZS1G PCR pri	763	9.6	53.3	20	24	AA151214	Mouse HYPL1 locu
C 691	9.8	54.4	25	21	AAV58548	HLA HLA-C gene PCR	764	9.6	53.3	20	24	AA151214	Mouse HYPL1 locu
C 692	9.8	54.4	25	21	AAV58548	PCR primer used to	765	9.6	53.3	20	24	AA151214	Capture oligonucle
C 693	9.8	54.4	25	21	AAV58548	PCR primer used to	766	9.6	53.3	20	24	AA151214	Capture oligonucle
C 694	9.8	54.4	25	21	AAV58548	PCR primer used to	767	9.6	53.3	20	24	AA151214	Capture oligonucle
C 695	9.8	54.4	25	21	AAV58548	PCR primer-1 used	768	9.6	53.3	20	24	AA151214	Capture oligonucle
C 696	9.8	54.4	25	22	AAV58548	PCR primer-1 used	769	9.6	53.3	20	24	AA151214	Capture oligonucle
C 697	9.8	54.4	25	24	AAV58548	Rae gene PCR prime	770	9.6	53.3	20	19	AA151214	Human A2b adeno
C 698	9.8	54.4	25	24	AAV58548	Human GDM/P-1-25-m	771	9.6	53.3	20	20	AAV58548	Human A2b adeno
C 699	9.8	54.4	25	24	AAV58548	Human GDM/P-1-25-m	772	9.6	53.3	20	20	AAV58548	Human A2b adeno
C 700	9.8	54.4	25	24	AAV58548	Human GDM/P-1-25-m	773	9.6	53.3	20	20	AAV58548	Human A2b adeno
C 701	9.8	54.4	25	24	AAV58548	Human GDM/P-1-25-m	774	9.6	53.3	20	21	AAV58548	Human A2b adeno
C 702	9.8	54.4	25	24	AAV58548	Adenovirus 5 tripa	775	9.6	53.3	20	21	AAV58548	Human A2b adeno
C 703	9.6	53.3	16	18	AAV58548	Synthetic PCNA rib	776	9.6	53.3	20	21	AAV58548	Human A2b adeno
C 704	9.6	53.3	16	21	AAV58548	PCNA hairpin riboz	777	9.6	53.3	20	21	AAV58548	Human A2b adeno
C 705	9.6	53.3	16	21	AAV58548	PCNA hairpin riboz	778	9.6	53.3	20	21	AAV58548	Human A2b adeno
C 706	9.6	53.3	16	22	AAV58548	PCNA hairpin/hamme	779	9.6	53.3	20	21	AAV58548	Human A2b adeno
C 707	9.6	53.3	16	22	AAV58548	PCNA hairpin/hamme	780	9.6	53.3	20	21	AAV58548	Human A2b adeno
C 708	9.6	53.3	17	18	AAV58548	Granule bound star	781	9.6	53.3	20	22	AAV58548	Human A2b adeno
C 709	9.6	53.3	17	18	AAV58548	Granule bound star	782	9.6	53.3	20	22	AAV58548	Human A2b adeno
C 710	9.6	53.3	17	19	AAV58548	Human EGF-R target	783	9.6	53.3	20	23	AAV58548	Human A2b adeno
C 711	9.6	53.3	17	19	AAV58548	Potato citrate syn	784	9.6	53.3	20	23	AAV58548	Human A2b adeno
C 712	9.6	53.3	17	19	AAV58548	Potato citrate syn	785	9.6	53.3	20	24	AAV58548	Human A2b adeno
C 713	9.6	53.3	17	20	AAV58548	Fibrinogen recepto	786	9.6	53.3	20	24	AAV58548	Human A2b adeno
C 714	9.6	53.3	17	20	AAV58548	Fibrinogen recepto	787	9.6	53.3	20	24	AAV58548	Human A2b adeno
C 715	9.6	53.3	17	21	AAV58548	Hammerhead ribozym	788	9.6	53.3	20	24	AAV58548	Human A2b adeno
C 716	9.6	53.3	17	21	AAV58548	Hammerhead ribozym	789	9.6	53.3	20	24	AAV58548	Human A2b adeno
C 717	9.6	53.3	17	23	AAV58548	Human NCOG Hamme	790	9.6	53.3	20	16	AAV58548	Human A2b adeno
C 718	9.6	53.3	17	23	AAV58548	Human NCOG Hamme	791	9.6	53.3	20	18	AAV58548	Human A2b adeno
C 719	9.6	53.3	17	24	AAV58548	Human CLOAI gene e	792	9.6	53.3	20	21	AAV58548	Human A2b adeno
C 720	9.6	53.3	17	24	AAV58548	Human GDM/P-1-17-m	793	9.6	53.3	20	22	AAV58548	Human A2b adeno
C 721	9.6	53.3	17	24	AAV58548	Human GDM/P-1-17-m	794	9.6	53.3	20	22	AAV58548	Human A2b adeno
C 722	9.6	53.3	17	24	AAV58548	Human GDM/P-1-17-m	795	9.6	53.3	20	22	AAV58548	Human A2b adeno
C 723	9.6	53.3	17	24	AAV58548	Human ERG hamme	796	9.6	53.3	20	23	AAV58548	Human A2b adeno
C 724	9.6	53.3	17	24	AAV58548	Human ERG hamme	797	9.6	53.3	20	23	AAV58548	Human A2b adeno
C 725	9.6	53.3	17	24	AAV58548	Human ERG hamme	798	9.6	53.3	20	23	AAV58548	Human A2b adeno
C 726	9.6	53.3	17	24	AAV58548	Human ERG hamme	799	9.6	53.3	20	23	AAV58548	Human A2b adeno
C 727	9.6	53.3	18	16	AAV58548	Primer P-1, amplif	800	9.6	53.3	20	22	AAV58548	Human A2b adeno
C 728	9.6	53.3	18	18	AAV58548	Mouse ftk-1 VEGF r	801	9.6	53.3	20	12	AAV58548	Human A2b adeno
C 729	9.6	53.3	18	20	AAV58548	Human AKT-1 phosph	802	9.6	53.3	20	14	AAV58548	Human A2b adeno
C 730	9.6	53.3	18	20	AAV58548	Human Akt-1 mRNA i	803	9.6	53.3	20	18	AAV58548	Human A2b adeno
C 731	9.6	53.3	18	20	AAV58548	Human genome biall	804	9.6	53.3	20	18	AAV58548	Human A2b adeno
C 732	9.6	53.3	18	21	AAV58548	Human biallelic ma	805	9.6	53.3	20	18	AAV58548	Human A2b adeno
C 733	9.6	53.3	19	18	AAV58548	Rat liver derived	806	9.6	53.3	20	19	AAV58548	Human A2b adeno
C 734	9.6	53.3	19	21	AAV58548	Cyclin F ribozyme	807	9.6	53.3	20	19	AAV58548	Human A2b adeno
C 735	9.6	53.3	19	21	AAV58548	Cdc 25 hs ribozyme	808	9.6	53.3	20	20	AAV58548	Human A2b adeno
C 736	9.6	53.3	19	21	AAV58548	PCNA HH ribozyme b	809	9.6	53.3	20	20	AAV58548	Human A2b adeno
C 737	9.6	53.3	19	22	AAV58548	Cyclin F ribozyme	810	9.6	53.3	20	20	AAV58548	Human A2b adeno
C 738	9.6	53.3	19	22	AAV58548	Cdc25 hs ribozyme	811	9.6	53.3	20	20	AAV58548	Human A2b adeno
C 739	9.6	53.3	19	22	AAV58548	PCNA HH ribozyme b	812	9.6	53.3	20	20	AAV58548	Human A2b adeno

C 813	9.6	53.3	24	20	AAx88475	Human MIP-1 beta p
814	9.6	53.3	24	21	AAc80372	Forward primer #14
815	9.6	53.3	24	21	AAz60283	Exon 2 used in t
C 816	9.6	53.3	24	21	AAz44726	Bovine c-Kit bK-1
C 817	9.6	53.3	24	21	AAz44738	Murine and human C
818	9.6	53.3	24	22	AAc85845	Primer 2 to const
819	9.6	53.3	24	22	AAc85811	Primer 8 to const
820	9.6	53.3	24	22	AAc85811	Nicotinamide amin
821	9.6	53.3	24	22	AAc85811	TGAT SPCIS element
822	9.6	53.3	24	24	AAJ39874	Human glycosyl-Hyd
C 823	9.6	53.3	24	24	ABK50798	Acid phosphatase f
824	9.6	53.3	24	24	ABK67701	Transglutaminase 5
825	9.6	53.3	24	24	ABO01511	Oligonucleotide ad
826	9.6	53.3	24	24	ABO06955	Oligonucleotide ad
C 827	9.6	53.3	24	24	ABO06956	Oligonucleotide ad
C 828	9.6	53.3	24	24	ABN93423	Aspergillus oryzae
C 829	9.6	53.3	24	24	ABN96574	Human thyroglobuli
C 830	9.6	53.3	24	24	ABN84200	Capture oligonucle
831	9.6	53.3	24	24	ABN84201	Capture oligonucle
C 832	9.6	53.3	24	24	ABN85942	Capture oligonucle
833	9.6	53.3	24	24	ABN85943	Capture oligonucle
C 834	9.6	53.3	24	24	ABN87388	Capture oligonucle
835	9.6	53.3	24	24	ABN87399	Capture oligonucle
C 836	9.6	53.3	24	24	ABN87399	Capture oligonucle
837	9.6	53.3	24	24	ABN87399	Capture oligonucle
838	9.6	53.3	24	24	ABN90240	Capture oligonucle
C 839	9.6	53.3	24	24	ABN90241	Capture oligonucle
C 840	9.6	53.3	24	24	ABN91388	Capture oligonucle
841	9.6	53.3	24	24	ABN91389	Capture oligonucle
C 842	9.6	53.3	25	19	AAV79740	Purified DNA of si
C 843	9.6	53.3	25	19	AAV79740	ECERO section 3 co
844	9.6	53.3	25	19	AAV79740	ECERO section 3 co
C 845	9.6	53.3	25	19	AAV31336	C-Jun amino acids
846	9.6	53.3	25	20	AAV32700	Probe used to dele
847	9.6	53.3	25	21	AAc80373	Forward primer #14
848	9.6	53.3	25	21	AAc80373	Oligonucleotide pr
C 849	9.6	53.3	25	21	AAz49603	PCR primer p57 for
850	9.6	53.3	25	21	AAz49603	PCR primer p58 for
851	9.6	53.3	25	21	AAz47421	Probe 5 used to co
C 852	9.6	53.3	25	22	AAJ16201	Human uPAR gene 5'
C 853	9.6	53.3	25	24	ABO61280	Human aquaporin 5
854	9.6	53.3	25	24	ABO61333	Human aquaporin 5
855	9.6	53.3	25	24	ABN03589	Human GDM-P-1 25-m
856	9.6	53.3	25	24	ABN03589	Human GDM-P-1 25-m
857	9.6	53.3	25	24	ABN03589	Human GDM-P-1 25-m
C 858	9.6	53.3	25	24	ABN03589	Human GDM-P-1 25-m
C 859	9.6	53.3	25	24	ABN03589	Human GDM-P-1 25-m
C 860	9.6	53.3	25	24	ABN03589	Human GDM-P-1 25-m
861	9.6	53.3	25	24	ABN03589	Human GDM-P-1 25-m
C 862	9.6	53.3	25	24	ABN03589	Human GDM-P-1 25-m
863	9.6	53.3	25	24	ABN03589	Human GDM-P-1 25-m
864	9.6	53.3	25	24	ABN03589	Human GDM-P-1 25-m
865	9.6	53.3	25	24	ABN03589	Human GDM-P-1 25-m
866	9.6	53.3	25	24	ABN03589	Human GDM-P-1 25-m
C 867	9.6	53.3	25	24	ABN03589	Human GDM-P-1 25-m
C 868	9.6	53.3	25	24	ABN03589	Human GDM-P-1 25-m
C 869	9.6	53.3	25	24	ABN03589	Human GDM-P-1 25-m
C 870	9.6	53.3	25	24	ABN03589	Human GDM-P-1 25-m
C 871	9.6	53.3	25	24	ABN03589	Human GDM-P-1 25-m
872	9.6	53.3	25	24	ABN03589	Human GDM-P-1 25-m
873	9.6	53.3	25	24	ABN03589	Human GDM-P-1 25-m
874	9.6	53.3	25	24	ABN03589	Human GDM-P-1 25-m
875	9.6	53.3	25	24	ABN03589	Human GDM-P-1 25-m
876	9.6	53.3	25	24	ABN03589	Human GDM-P-1 25-m
877	9.6	53.3	25	24	ABN03589	Human GDM-P-1 25-m
C 878	9.6	53.3	25	24	ABN03589	Human GDM-P-1 25-m
C 879	9.6	53.3	25	24	ABN03589	Human GDM-P-1 25-m
C 880	9.6	53.3	25	24	ABN03589	Human GDM-P-1 25-m
C 881	9.6	53.3	25	24	ABN03589	Human GDM-P-1 25-m
882	9.6	53.3	25	24	ABN03589	Human GDM-P-1 25-m
C 883	9.6	53.3	25	24	ABN03589	Human GDM-P-1 25-m
C 884	9.6	53.3	25	24	ABN03589	Human GDM-P-1 25-m
C 885	9.6	53.3	25	24	ABN03589	Human GDM-P-1 25-m

C	959	9.4	52.2	20	22	AA545664	Human PAP-1 antis
C	960	9.4	52.2	20	22	AA012146	Rat PPIB antisens
C	961	9.4	52.2	20	22	AA007124	Canine SRP micros
C	962	9.4	52.2	20	22	AA082471	Plagelid vector PC
C	963	9.4	52.2	20	22	AA003564	Oligonucleotide #5
C	964	9.4	52.2	20	22	AA099405	Immunostimulatory
C	965	9.4	52.2	20	22	AA085728	Human PSA promoter
C	966	9.4	52.2	20	24	ABK85221	Rat PPIB antisens
C	967	9.4	52.2	20	24	ABN80862	Human caespase 7 ph
C	968	9.4	52.2	20	24	ABK69536	Rat phosphotyrase
C	969	9.4	52.2	20	24	ABD32144	CTRB3 antigen pep
C	970	9.4	52.2	20	24	ABK37390	Rat PPIB mRNA lev
C	971	9.4	52.2	20	24	AA094742	Rat secreted facto
C	972	9.4	52.2	20	24	AA096822	Human STAT3 antis
C	973	9.4	52.2	20	24	ABK32227	Human vascular end
C	974	9.4	52.2	20	24	ABK32227	Immunostimulatory
C	975	9.4	52.2	20	12	AAQ10735	Oligonucleotide Q1
C	976	9.4	52.2	21	15	AAQ70830	Plasmid construct
C	977	9.4	52.2	21	17	AA022317	Nocardia sp. p
C	978	9.4	52.2	21	17	AA014783	Lacto-N-biosidase
C	979	9.4	52.2	21	17	AA025999	PC-PSA promoter pr
C	980	9.4	52.2	21	17	AA060466	Primer for subclon
C	981	9.4	52.2	21	19	AA032498	Prostate specific
C	982	9.4	52.2	21	19	AA035625	SHOX gene exon 3'
C	983	9.4	52.2	21	19	AA021535	L-oncogene primer
C	984	9.4	52.2	21	19	AA033998	Chicken matrix met
C	985	9.4	52.2	21	19	AA012875	5' PCR primer used
C	986	9.4	52.2	21	21	AA087860	Rho GDI-alpha PCR
C	987	9.4	52.2	21	21	AA090207	Polylysylleucyl (K
C	988	9.4	52.2	21	21	AA090254	Polylysylleucyl (K
C	989	9.4	52.2	21	22	AA019683	Marine NSK-2 cDNA
C	990	9.4	52.2	21	22	AA040493	SNP specific upper
C	991	9.4	52.2	21	22	AA096562	Human gene single
C	992	9.4	52.2	21	22	AA096564	Human gene single
C	993	9.4	52.2	21	24	ABK50545	PCR primer #1 for
C	994	9.4	52.2	21	24	ABK51904	Aspergillus niger
C	995	9.4	52.2	21	24	ABK54041	Rat dipeptidyl pep
C	996	9.4	52.2	21	24	ABK54042	Rab3 GEP related P
C	997	9.4	52.2	21	24	ABK54042	Rab3 GEP related P
C	998	9.4	52.2	21	24	ABK54042	Rab3 GEP related P
C	999	9.4	52.2	21	24	ABK54042	Rab3 GEP related P
C	1000	9.4	52.2	22	18	AA075661	Histidinol selecti

ALIGNMENTS

RESULT 1
ABN99616
ID ABN99616 standard; DNA; 18 BP.

XX	AC	ABN99616;
XX	DT	05-AUG-2002 (first entry)
XX	DE	Fungi probe SEQ ID NO 188.
XX	KW	Fungus; bacteria; quantification; detection; infection; gastroenteritis;
XX	KW	ulcer; asthma; allergy; sinusitis; probe; ss.
XX	OS	Stachybotrys chartarum.
XX	PN	US6387652-B1.
XX	PD	14-MAY-2002.
XX	PF	13-JUN-2000; 2000US-0593012.
XX	PR	15-APR-1998; 98US-081773P.
XX	PR	14-APR-1999; 99US-0290990.
XX	PA	(USSI) US ENVIRONMENTAL PROTECTION AGENCY.

PI	Haugland R, Veepor S;
XX	WPI; 2002-462353/49.
DR	Detection and quantification of specific fungi or bacteria useful e.g.
XX	in medical diagnosis and treatment of fungal and bacterial conditions;
PT	by hybridizing and amplifying DNA using sequences unique to the species
PT	or group of species
PS	Claim 62; Column 97; 55pp; English.
XX	The invention relates to specific fungi or bacteria detected and
CC	quantified in a sample by extracting and recovering DNA from the organism
CC	in the sample and hybridizing and amplifying the DNA sequence using
CC	sequences unique to the species/group of species but common to all
CC	isolates of the species/group of species. The method especially employs
CC	sequences selected from 225 fungal and bacterial primer and probe
CC	sequences (ABN99429-ABN99653) for detection of specified fungi/fungal
CC	groups or specified bacteria. The method enables detection and
CC	quantification of specific fungi or bacteria, or groups of
CC	fungal/bacterial species, useful medically for diagnosis and treatment of
CC	fungi or bacteria associated with health problems such as infections,
CC	gastroenteritis, ulcers, asthma, allergies and sinusitis. It is also
CC	useful to detect and/or quantify microorganisms in the environment e.g.
CC	to establish the risk of adverse health effects (e.g. pulmonary
CC	haemorrhage from levels of Stachybotrys chartarum in air samples in
CC	houses).
XX	Sequence 18 BP; 2 A; 8 C; 6 G; 2 T; 0 other;
SO	Query Match 100.0%; Score 18; DB 24; Length 18;
	Best Local Similarity 100.0%; Pred. No. 31;
	Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 CTGGCCCGGATCCAGGC 18
DB	1 CTGGCCCGGATCCAGGC 18

RESULT 2
ABK29213
ID ABK29213 standard; DNA; 18 BP.

XX	AC	ABK29213;
XX	DT	23-APR-2002 (first entry)
XX	DE	Stachybotrys chartarum probe.
XX	KW	Fungal detection; bacterial detection; probe; primer; ss.
XX	OS	Stachybotrys chartarum.
XX	PN	WO200196612-A2.
XX	PD	20-DEC-2001.
XX	PF	13-JUN-2001; 2001WO-US18892.
XX	PR	13-JUN-2000; 2000US-0593012.
XX	PA	(USSI) US ENVIRONMENTAL PROTECTION AGENCY.
XX	PI	Haugland R, Veepor SJ;
XX	DR	WPI; 2002-098078/13.
XX	PT	Detecting and quantifying fungi and bacteria, involves obtaining a
XX	PT	sequence of the fungus, extracting the DNA from the sample, and
XX	PT	subjecting the DNA to polymerase chain reaction and fluorescent probe
XX	PS	analysis
XX	PS	Claim 62; Page 20; 110pp; English.

XX The invention relates to a method of detecting and quantifying fungi and
 CC bacteria, involving obtaining a sequence of the microorganism to be
 CC detected and quantified, extracting the DNA from the sample, and
 CC subjecting the DNA to polymerase chain reaction (PCR) and fluorescent
 CC probe analysis. The method is useful for identifying and quantifying
 CC specific fungi and bacteria using specific DNA sequences. The specific
 CC DNA sequences are useful for the real time detection of PCR products with
 CC a fluorogenic probe system or other molecular probes like hybridisation.
 CC ABK29026-ABK29474 represent fungal and bacterial PCR primers and probes
 CC used in the method of the invention.

XX Sequence 18 BP, 2 A, 8 C, 6 G, 2 T, 0 other;

Query Match 100.0%; Score 18; DB 24; Length 18;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGCCCGGATCCAGGC 18
 Db 1 GTGGCCCGGATCCAGGC 18

RESULT 3

ABN9534/C
 ID ABN9534 standard; DNA, 17 BP.

AC ABN9534;

DT 05-AUG-2002 (first entry)

DE Fungal probe SEQ ID NO 106.

XX Fungus; bacteria; quantification; detection; infection; gastroenteritis;
 KM ulcers; asthma; allergy; sinusitis; probe; ss.

OS Myrothecium verrucaria.

XX Myrothecium torridum.

PN US6387652-B1.

PD 14-MAY-2002.

PF 13-JUN-2000; 2000US-0593012.

PR 15-APR-1998; 98US-081773P.

XX 14-APR-1999; 99US-0290990.

PA (USST) US ENVIRONMENTAL PROTECTION AGENCY.

PI Haugland R, Vesper S;

DR WPI, 2002-462353/49.

XX The invention relates to a method of detecting and quantifying fungi and
 CC bacteria, involving obtaining a sequence of the microorganism to be
 CC detected and quantified, extracting the DNA from the sample, and
 CC subjecting the DNA to polymerase chain reaction (PCR) and fluorescent
 CC probe analysis. The method is useful for identifying and quantifying
 CC specific fungi and bacteria using specific DNA sequences. The specific
 CC DNA sequences are useful for the real time detection of PCR products with
 CC a fluorogenic probe system or other molecular probes like hybridisation.
 CC ABK29026-ABK29474 represent fungal and bacterial PCR primers and probes
 CC used in the method of the invention.

PS Claim 36; Column 94; 55pp; English.

XX The invention relates to a method of detecting and quantifying fungi and
 CC bacteria, involving obtaining a sequence of the microorganism to be
 CC detected and quantified, extracting the DNA from the sample, and
 CC subjecting the DNA to polymerase chain reaction (PCR) and fluorescent
 CC probe analysis. The method is useful for identifying and quantifying
 CC specific fungi and bacteria using specific DNA sequences. The specific
 CC DNA sequences are useful for the real time detection of PCR products with
 CC a fluorogenic probe system or other molecular probes like hybridisation.
 CC ABK29026-ABK29474 represent fungal and bacterial PCR primers and probes
 CC used in the method of the invention.

CC useful to detect and/or quantify microorganisms in the environment e.g.
 CC to establish the risk of adverse health effects (e.g. pulmonary
 CC hemorrhage from levels of Stachybotrys chartarum in air samples in
 CC houses).

XX Sequence 17 BP, 0 A, 8 C, 6 G, 3 T, 0 other;

Query Match 71.1%; Score 12.8; DB 24; Length 17;
 Best Local Similarity 87.5%; Pred. No. 8.4e+03;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GCGCCCGGATCCAGGC 18
 Db 17 GCGCCCGGATCCAGGC 2

RESULT 4

ABK29131/C
 ID ABK29131 standard; DNA, 17 BP.

AC ABK29131;

DT 23-APR-2002 (first entry)

DE Myrothecium verrucaria/torridum probe.

XX Fungal detection; bacterial detection; probe; primer; ss.

OS Myrothecium verrucaria.

XX Myrothecium torridum.

PN WO200196612-A2.

PD 20-DEC-2001.

PF 13-JUN-2001; 2001WO-US18892.

PR 13-JUN-2000; 2000US-0593012.

PA (USST) US ENVIRONMENTAL PROTECTION AGENCY.

PI Haugland R, Vesper SJ;

DR WPI, 2002-098078/13.

XX Detecting and quantifying fungi and bacteria, involves obtaining a
 CC sequence of the fungus, extracting the DNA from the sample, and
 CC subjecting the DNA to polymerase chain reaction and fluorescent probe
 CC analysis.

PS Claim 36; Page 14; 110pp; English.

XX The invention relates to a method of detecting and quantifying fungi and
 CC bacteria, involving obtaining a sequence of the microorganism to be
 CC detected and quantified, extracting the DNA from the sample, and
 CC subjecting the DNA to polymerase chain reaction (PCR) and fluorescent
 CC probe analysis. The method is useful for identifying and quantifying
 CC specific fungi and bacteria using specific DNA sequences. The specific
 CC DNA sequences are useful for the real time detection of PCR products with
 CC a fluorogenic probe system or other molecular probes like hybridisation.
 CC ABK29026-ABK29474 represent fungal and bacterial PCR primers and probes
 CC used in the method of the invention.

XX Sequence 17 BP, 0 A, 8 C, 6 G, 3 T, 0 other;

Query Match 71.1%; Score 12.8; DB 24; Length 17;
 Best Local Similarity 87.5%; Pred. No. 8.4e+03;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GCGCCCGGATCCAGGC 18
 Db 17 GCGCCCGGATCCAGGC 2

RESULT 5
AAFS1791
ID AAF51791 standard; DNA; 15 BP.
XX
AC AAF51791;
XX
DT 30-MAR-2001 (first entry)
XX
DE IGF-I oligonucleotide #2751.
XX
KM Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KM cytostatic; dermatological; cardiant; vitucide; ophthalmological; keloid;
KM skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KM IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KM growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
KM keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KM hyperneovascular condition; hyperplasia; kidney disease;
KM neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU00693.
XX
PR 21-JUN-1999; 99US-0140345.
XX
PI (MURDOCH CHILDRENS RES INST.
XX
PA Wright CJ, Werther GA, Edmondson SR;
XX
PI Wright CJ, Werther GA, Edmondson SR;
XX
DR WPI; 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by
PT administering UV (ultra-violet) treatment (optional) and an antisense
PT nucleic acid that inhibits or reduces growth factor mediated cell
PT proliferation and/or inflammation -
XX
XX
PS Example 8; Page 78; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects
CC of skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and
CC AAF5153-F5161). The method is useful for ameliorating the effects of
CC psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids,
CC keratosis, neoplasia, scleroderma, wart, benign growths, cancers of the
CC skin, a hyperneovascular condition such as a neovascular condition of the
CC retina, brain or skin, growth factor mediated malignancies, other
CC sclerotic disease, kidney disease, hyperproliferation of the inside of
CC blood vessels or any other hyperplasia.
XX
SQ Sequence 15 BP; 3 A; 5 C; 5 G; 2 T; 0 other;
XX
Query Match 68.9%; Score 12.4; DB 22; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 5 GCCCGATTCAGGC 18
DB 2 GCCCGATTCAGGC 15
XX
RESULT 6
AAFS1792
ID AAF51792 standard; DNA; 15 BP.

XX
AC AAF51792;
XX
DT 30-MAR-2001 (first entry)
XX
DE IGF-I oligonucleotide #2752.
XX
KM Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KM cytostatic; dermatological; cardiant; vitucide; ophthalmological; keloid;
KM skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KM IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KM growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
KM keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KM hyperneovascular condition; hyperplasia; kidney disease;
KM neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU00693.
XX
PR 21-JUN-1999; 99US-0140345.
XX
PI (MURDOCH CHILDRENS RES INST.
XX
PA Wright CJ, Werther GA, Edmondson SR;
XX
PI Wright CJ, Werther GA, Edmondson SR;
XX
DR WPI; 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by
PT administering UV (ultra-violet) treatment (optional) and an antisense
PT nucleic acid that inhibits or reduces growth factor mediated cell
PT proliferation and/or inflammation -
XX
XX
PS Example 8; Page 78; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects
CC of skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and
CC AAF5153-F5161). The method is useful for ameliorating the effects of
CC psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids,
CC keratosis, neoplasia, scleroderma, wart, benign growths, cancers of the
CC skin, a hyperneovascular condition such as a neovascular condition of the
CC retina, brain or skin, growth factor mediated malignancies, other
CC sclerotic disease, kidney disease, hyperproliferation of the inside of
CC blood vessels or any other hyperplasia.
XX
SQ Sequence 15 BP; 2 A; 6 C; 5 G; 2 T; 0 other;
XX
Query Match 68.9%; Score 12.4; DB 22; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 5 GCCCGATTCAGGC 18
DB 1 GCCCGATTCAGGC 14
XX
RESULT 7
AAL42362/c
ID AAL42362 standard; DNA; 24 BP.
XX
AC AAL42362;
XX
DT 28-JUN-2002 (first entry)

XX HBD 4-hydroxytamoxifen-responsive mutant oestrogen receptor PCR primer A.
 DE PCR; primer; ss; fusion protein; mutant oestrogen receptor; mouse;
 XX cytokine receptor; tamoxifen; selective proliferation; gene therapy;
 KW haematopoietic stem cell; hormone binding domain; HBD;
 KW 4-hydroxytamoxifen-responsive mutant oestrogen receptor.
 XX
 OS Mus sp.
 XX
 XX CA2309324-A1.
 PN
 XX 23-NOV-2001.
 PD
 XX 23-MAY-2000; 2000CA-2309324.
 XX
 XX 23-MAY-2000; 2000CA-2309324.
 XX
 XX 23-MAY-2000; 2000CA-2309324.
 XX
 XX (DNAV-) DNA VEC RES INC.
 PA
 XX Ueda Y, Sakata T, Hasegawa M, Ozawa K, Itoh K, Nagashima T;
 PI
 XX WPI, 2002-305122/35.
 DR
 XX
 XX New fusion protein, useful in gene therapy for selective expansion of
 PT transfected cells, comprises mutant estrogen receptor and cytokine
 PT receptor fragment
 XX
 XX Example 2; Page 21; 50pp; English.
 PS
 XX The invention relates to fusion proteins which comprises a mutant
 CC oestrogen receptor and a cytokine receptor that imparts proliferation
 CC activity to cells. The mutant oestrogen receptor does not respond to
 CC oestrogen, but does respond to tamoxifen. The fusion proteins are used to
 CC induce selective proliferation (in vivo or in vitro), of cells
 CC transformed to contain an exogenous gene. The fusion proteins of the
 CC invention are particularly useful in gene therapy where haematopoietic
 CC stem cells are being targeted. Selective proliferation of of cells
 CC through fusion proteins allows effective gene therapy even where gene
 CC transfer efficiency is low. Also, since the fusion proteins can be
 CC expressed in various types of blood cells, the range of cells that can be
 CC targeted is enlarged. The present DNA sequence represents a PCR primer
 CC used in an example of the invention to amplify the coding sequence of the
 CC hormone binding domain (HBD) of the mouse 4-hydroxytamoxifen-responsive
 CC mutant oestrogen receptor.
 CC
 XX
 SO Sequence 24 BP; 5 A; 7 C; 8 G; 4 T; 0 other;
 Query Match 68.9%; Score 12.4; DB 24; Length 24;
 Best Local Similarity 92.9%; Pred. No. 1.3e+04;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 GCGCCCGGATCCAG 16
 DB 14 GTGCCCGGATCCAG 1
 RESULT 8
 ABA96574
 ID ABA96574 standard; DNA, 24 BP.
 XX
 AC ABA96574;
 XX
 DT 19-MAR-2002 (first entry)
 XX
 DE Human thyroglobulin 11 RT-PCR primer, SEQ ID NO:4.
 XX
 XX Human; thyroglobulin 11; recombinant production; gene therapy;
 KW thyroid associated disease; goitre; thyroiditis; hypothyroidism;
 KW hyperthyroidism; struma nodosa; adenomatous goitre;
 KW reverse transcription-PCR; RT-PCR primer; ss.
 XX
 OS Homo sapiens.
 XX

XX
 XX WO200190166-A1.
 PN
 XX 29-NOV-2001.
 PD
 XX 08-MAY-2001; 2001WO-CN00696.
 XX
 XX 09-MAY-2000; 2000CN-0115631.
 XX
 XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
 PA
 XX Mao Y, Xie Y;
 PI
 XX WPI, 2002-106179/14.
 DR
 XX
 XX Human thyroglobulin 11 polynucleotide and polypeptide, useful in
 PT diagnosis and treatment of goiter, thyrotoxicosis, hypothyroidism, and
 PT hyperthyroidism
 XX
 XX Example 2; Page 17; 38pp; Chinese.
 PS
 XX The invention relates to human thyroglobulin 11 (AAM53042), nucleic acids
 CC encoding it (ABA96572), and a method for the recombinant production of
 CC thyroglobulin 11. The protein has a molecular weight of 11 KD. The
 CC present invention additionally discloses an antagonist of thyroglobulin
 CC 11 for therapeutic use, and an antibody which specifically binds to
 CC thyroglobulin 11. Thyroglobulin 11, and nucleotides which encode it may
 CC be used for treating thyroid-associated diseases, such as goitre,
 CC thyroiditis, hypothyroidism, hyperthyroidism, and struma nodosa
 CC (adenomatous goitre). The protein may also be used to screen for
 CC modulators of its activity or for peptide fingerprinting identification.
 CC The polynucleotide can be used as a primer for nucleic acid amplification
 CC reactions or as a probe for hybridisation reactions, or in producing gene
 CC chips or microarrays. Sequences ABA96573-ABA96574 represent reverse
 CC transcription-PCR (RT-PCR) primers used in an exemplification of the
 CC invention to isolate human thyroglobulin 11 cDNA.
 CC
 XX
 SO Sequence 24 BP; 3 A; 11 C; 5 G; 5 T; 0 other;
 Query Match 68.9%; Score 12.4; DB 24; Length 24;
 Best Local Similarity 92.9%; Pred. No. 1.3e+04;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 GCGCGATCCAGGC 18
 DB 5 GCGCGATCCAGGC 18
 RESULT 9
 AAX59160
 ID AAX59160 standard; DNA, 21 BP.
 XX
 AC AAX59160;
 XX
 DT 06-SEP-1999 (first entry)
 XX
 DE Human soluble neuropilin-1 5' PCR primer.
 XX
 XX Neuropilin-1; human; vascular endothelial growth factor receptor;
 KW VEGF165R; inhibitor; metastasis; angiogenesis; inflammation;
 KW arthritis; diabetic retinopathy; cytostatic; antiinflammatory;
 KW antiangiogenic; antidiabetic; ophthalmological; antiarthritic;
 KW PCR; primer; ss.
 XX
 XX Synthetic.
 OS Homo sapiens.
 XX
 XX WO9929858-A1.
 PN
 XX 17-JUN-1999.
 PD
 XX 09-DEC-1998; 98WO-US26138.
 XX

PR 09-SEP-1998; 98US-0099615.
PR 09-DEC-1997; 97US-0069155.
PR 12-DEC-1997; 97US-0069687.
XX
XX (CHIL-) CHILDRENS MEDICAL CENT.
XX
XX Gagnon ML, Klagsbrun M, Soker S;
XX
XX WPI; 1999-394975/33.
XX
XX Soluble human neuropilins and related polynucleotides
XX
XX Example 2; Page 43; 98pp; English.
XX
XX This oligonucleotide was used as 5' primer in the RT-PCR
XX amplification of cDNA (see AAX59153) coding for a truncated,
XX soluble human neuropilin-1 polypeptide (see AY06319). The cDNA
XX was cloned from a PC3 library. Neuropilin-1 is a novel vascular
XX endothelial growth factor (VEGF) receptor that is expressed in
XX endothelial cells and motile metastatic cancer cells. Claimed
XX soluble neuropilin-1 polypeptides are useful for treatment of
XX diseases or disorders associated with VEGF, e.g. metastasis,
XX inappropriate angiogenesis, chronic inflammation, diabetic
XX retinopathy and arthritis. Solid tumors can also be treated.
XX
XX Sequence 21 BP; 2 A; 8 C; 6 G; 5 T; 0 other;
SQ
Query Match 67.8%; Score 12.2; DB 20; Length 21;
Best Local Similarity 82.4%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
CY 2 TGGCGCCGATCCAGGC 18
Db 5 TCTCTCGATCCAGGC 21
RESULT 10
ABK94173/c
ID ABR94173 standard; DNA; 21 BP.
XX
XX ABR94173;
XX
XX 27-AUG-2002 (first entry)
XX
XX Endothelin receptor B (EDNRB) SNP detection PCR primer #15.
XX
XX Endothelin; EDN; endothelin converting enzyme; ECE; endothelin receptor;
XX EDNR; signaling system; cardiovascular disease; coronary heart disease;
XX hypertension; atherosclerosis; angiogenesis; fatty acid metabolism;
XX diabetes; familial hypercholesterolemia; forensic marker;
XX transgenic animal; solid support; cardiovascular regulator; SNP;
XX single nucleotide polymorphism; PCR; primer; ss.
XX
XX Synthetic.
XX
XX WO200224747-A2.
XX
XX 28-MAR-2002.
XX
XX 31-AUG-2001; 2001WO-EP10087.
XX
XX 19-SEP-2000; 2000EP-0120123.
XX
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
XX Brinkmann U, Hoffmeyer S;
XX
XX WPI; 2002-435060/46.
XX
XX Novel polynucleotide of the endothelin/endothelin converting
XX enzyme/receptors of endothelin and endothelin converting enzyme
XX signaling system associated with cardiovascular disease, useful for
XX treating the disease

XX
XX Example 6; Page 59; 190pp; English.
XX
XX The invention describes a polynucleotide (I) of the endothelin
XX (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)
XX signaling system which is associated with a cardiovascular disease. (I),
XX the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I),
XX or (II) is useful for producing cells capable of expressing a molecular
XX variant polypeptide which is associated with a cardiovascular disease.
XX (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing
XX a molecular variant gene comprising (I) is useful for identifying and
XX obtaining a pro-drug or drug capable of modulating the activity of a
XX molecular variant of the EDN/EDNR/ECE signaling system
XX or its gene product, or for identifying and obtaining an inhibitor of
XX the activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE
XX signaling system or its gene product. The isolated proteins and
XX polynucleotides encoding them are useful for preparation of a
XX pharmaceutical composition for treating a cardiovascular disease such as
XX coronary heart disease, hypertension, atherosclerosis, or related to
XX abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial
XX hypercholesterolemia. The gene or a polynucleotide fragment of the
XX EDN/ECE/EDNR signaling system are useful as forensic markers, for
XX creating a transgenic animal and in creation of a solid support
XX comprising polynucleotides, genes, vectors, polypeptides, antibodies or
XX host cells of the invention. This sequence represents a PCR primer used
XX to identify single nucleotide polymorphisms in DNA encoding
XX cardiovascular regulator proteins of the EDN/ECE/EDNR signaling pathway.
XX
XX Sequence 21 BP; 5 A; 3 C; 9 G; 3 T; 1 other;
SQ
Query Match 67.8%; Score 12.2; DB 24; Length 21;
Best Local Similarity 77.8%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
CY 1 CTGCGCCGATCCAGGC 18
Db 20 CTGCGCCAGATCCAGGC 3
RESULT 11
ABK94174
ID ABR94174 standard; DNA; 21 BP.
XX
XX ABR94174;
XX
XX 27-AUG-2002 (first entry)
XX
XX Endothelin receptor B (EDNRB) SNP detection PCR primer #16.
XX
XX Endothelin; EDN; endothelin converting enzyme; ECE; endothelin receptor;
XX EDNR; signaling system; cardiovascular disease; coronary heart disease;
XX hypertension; atherosclerosis; angiogenesis; fatty acid metabolism;
XX diabetes; familial hypercholesterolemia; forensic marker;
XX transgenic animal; solid support; cardiovascular regulator; SNP;
XX single nucleotide polymorphism; PCR; primer; ss.
XX
XX Synthetic.
XX
XX WO200224747-A2.
XX
XX 28-MAR-2002.
XX
XX 31-AUG-2001; 2001WO-EP10087.
XX
XX 19-SEP-2000; 2000EP-0120123.
XX
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
XX Brinkmann U, Hoffmeyer S;
XX
XX WPI; 2002-435060/46.
XX
XX Novel polynucleotide of the endothelin/endothelin converting

PT enzyme/receptors of endothelin and endothelin converting enzyme
PT signaling system associated with cardiovascular disease, useful for
PT treating the disease -

PS Example 6, Page 59, 190pp; English.

XX
CC The invention describes a polynucleotide (I) of the endothelin
CC (EDN)/endothelin converting enzyme (ECE)/receptor of EDN and ECE (EDNR)
CC the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I),
CC or (II) is useful for producing cells capable of expressing a molecular
CC variant polypeptide which is associated with a cardiovascular disease.
CC (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing
CC a molecular variant gene comprising (I) is useful for identifying and
CC obtaining a pro-drug or drug capable of modulating the activity of a
CC molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system
CC or its gene product, or for identifying and obtaining an inhibitor of
CC the activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE
CC signaling system or its gene product. The isolated proteins and
CC polynucleotides encoding them are useful for preparation of a
CC pharmaceutical composition for treating a cardiovascular disease such as
CC coronary heart disease, hypertension, atherosclerosis, or related to
CC abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial
CC hypercholesterolaemia. The gene or a polynucleotide fragment of the
CC EDN/ECE/EDNR signaling system are useful as forensic markers, for
CC creating a transgenic animal and in creation of a solid support
CC comprising polynucleotides, genes, vectors, polypeptides, antibodies or
CC host cells of the invention. This sequence represents a PCR primer used
CC to identify single nucleotide polymorphisms in DNA encoding
CC cardiovascular regulator proteins of the EDN/ECE/EDNR signaling pathway.

SO Sequence 21 BP, 3 A, 9 C, 3 G, 5 T, 1 other;

Query Match 67.8%; Score 12.2; DB 24; Length 21;
Best Local Similarity 77.8%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGGCCCGGATCCAGC 18
DB 2 CTGGCCGAGNATCCAGC 19

RESULT 12

AAK24822/c
ID AAK24822 standard; DNA, 24 BP.

AC AAK24822;

DT 21-JUN-1999 (first entry)

DE Oligonucleotide ZC15035 used in zsig37 DNA amplification.

KW Adipocyte-specific protein; homologue; zsig37; human;
KW fatty acid metabolism; energy balance; nutrition; antimicrobial;
KW neurotransmitter; PCR; primer; ss.

OS Synthetic.

OS Homo sapiens.

PN WO9904000-A1.

PD 28-JAN-1999.

PF 17-JUL-1998; 98MO-US14864.

PR 18-JUL-1997; 97US-0053154.

PA (ZYMO) ZYMOGENETICS INC.

PI Sheppard PO;

PT WPI, 1999-132244/11.

PT New isolated adipocyte complement related polypeptides - used to
PT produce products for modulating energy balance in mammals;
PT protecting endothelial cells from injury or for antimicrobial or
PT neurotransmitter-modulated applications

PS Example 4, Page 118, 128pp; English.

XX
CC Oligonucleotide ZC15035 was used as a primer, together with primer
CC ZC15721 (see AAK24821), in the PCR amplification of an 866 bp
CC fragment of human adipocyte-specific protein homologue zsig37 DNA
CC (see AAK24813). The PCR product was used in the creation of
CC mammalian expression vectors. zsig37 (see also AAW98013) can be used
CC to modulate energy balance in mammals or to protect endothelial
CC cells from injury. It can be used to modulate cellular metabolic
CC reactions including adipogenesis, gluconeogenesis, glycogenolysis,
CC lipogenesis, glucose uptake, protein synthesis, thermogenesis and/or
CC oxygen utilisation. zsig37 may also modulate acetylcholine and/or
CC norepinephrine release, and may find use as a neurotransmitter or
CC as modulator of neurotransmission, as an antimicrobial agent or to
CC modulate nutrient uptake.

SO Sequence 24 BP, 3 A, 6 C, 9 G, 6 T, 0 other;

Query Match 67.8%; Score 12.2; DB 20; Length 24;
Best Local Similarity 82.4%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGGCCCGGATCCAGC 17
DB 20 CCGAGCCCGGATCCAGC 4

RESULT 13

AAA64122/c
ID AAA64122 standard; DNA, 24 BP.

AC AAA64122;

DT 20-DEC-2000 (first entry)

DE PCR primer for the human zsig37 DNA fragment.

KW zsig37; adipocyte complement related protein; haemostasis inhibitor;
KW blood flow; thrombogenic activity; complement activity; angioplasty;
KW collagen-mediated platelet adhesion; vascular reconstruction; aneurysm;
KW coronary artery bypass graft; endarterectomy; microvascular repair;
KW anastomosis; trauma; stroke; ischemia; reperfusion; endarterectomy;
KW intestinal strangulation; cardiopulmonary bypass ischemia; revascularization;
KW myocardial infarction; post-trauma vasospasm; accidental vascular trauma;
KW percutaneous transluminal angioplasty; wound repair; wound healing;
KW PCR primer; ss.

OS Homo sapiens.

PN WO200048625-A2.

PD 24-AUG-2000.

PF 17-FEB-2000; 2000MO-US04161.

PR 19-FEB-1999; 99US-0253604.

PR 22-NOV-1999; 99US-0444794.

PA (ZYMO) ZYMOGENETICS INC.

PI Sheppard PO, Laser GW, Bishop PD,

PT WPI, 2000-565335/52.

PT Use of a human adipocyte complement related protein for promoting blood
PT flow in the vasculature, pacifying damaged collagenous tissues,
PT pacifying the surface of a prostatic biomaterial, and mediating wound
PT repair -

XX Example 4; Page 93; 102pp; English.

PS PCR primers AAA64121-22 were used to amplify zsig37 gene fragment.

CC zsig37 polypeptide an adipocyte complement related protein, and is an

CC inhibitor of haemostasis and immune functions. The zsig37 protein is

CC useful for promoting blood flow in the vasculature, where the polypeptide

CC reduces thrombogenic and complement activity by the inhibition of the

CC complement pathway and inhibiting collagen-mediated platelet adhesion.

CC activation or aggregation. The methods are useful for treating injuries

CC due to, e.g. vascular reconstruction (angioplasty, coronary artery

CC bypass graft, endarterectomy, microvascular repair or anastomosis of a

CC vascular graft), trauma, stroke or aneurysm. The polypeptide is also

CC useful for pacifying damaged collagenous tissues due to injury

CC associated with ischemia and reperfusion (trauma injury ischemia,

CC intestinal strangulation, or injury associated with pre- and

CC post-vascular reconstruction of blood flow), cardiopulmonary bypass ischemia and

CC revascularization, myocardial infarction, or post-trauma vasospasm. In

CC particular, post-trauma vasospasm includes stroke, percutaneous

CC transluminal angioplasty, endarterectomy, accidental vascular trauma or

CC surgical-induced vascular trauma. The polypeptide may also be used for

CC pacifying the surface of a prosthetic biomaterial, where the surface of

CC the prosthetic biomaterial is coated with collagen or collagen

CC fragments, gelatin, fibrin or fibronectin. Finally, the polypeptide is

CC useful for mediating wound repair, where the polypeptide enhances the

CC progression of wound healing.

CC

SO Sequence 24 BP; 3 A; 6 C; 9 G; 6 T; 0 other;

Query Match 67.8%; Score 12.2; DB 21; Length 24;

Best Local Similarity 82.4%; Pred. No. 1.6e+04;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 CTGCCCGCGATTCGAG 17

DB 20 CCGAGCCCGATTCATG 4

RESULT 14

AA519807

ID AA519807 standard; DNA; 15 BP.

AC AA519807;

DT 08-MAY-2002 (first entry)

DE ASO primer #65 to detect human RANGAP1 gene polymorphisms.

KM Human; single nucleotide polymorphism; SNP; RANGAP1; haplotyping

KM chromosome 22q13.2-q13.31; Ran GTPase activating protein 1; genotyping;

KM cancer; irregular cell cycle associated disorder; ASO; primer; ss;

KM allele-specific oligonucleotide.

OS Homo sapiens.

PM W0200179240-A2.

PD 25-OCT-2001.

PF 17-APR-2001; 2001WO-US12455.

PR 17-APR-2000; 2000US-198072P.

PA (GENA-) GENAISSANCE PHARM. INC.

PI Chew A, Choi JY, Koshy B;

XX WPI; 2002-075068/10.

XX Genotyping human Ran GTPase activating protein 1 gene of individual for

PT determining haplotype of individual, involves determining identity of

PT nucleotide pair at specific polymorphic sites for two copies of the

PT gene

XX Claim 15; Page 15; 148pp; English.

CC The present invention relates to novel single nucleotide polymorphisms

CC (SNPs) in the human Ran GTPase activating protein 1 (RANGAP1) gene

CC located on chromosome 22q13.2-q13.31, and methods for haplotyping and/or

CC genotyping the RANGAP1 gene. The methods of the invention make use of

CC allele-specific oligonucleotides (ASOs) as probes and primers and/or

CC primer-extension oligonucleotides for detecting the RANGAP1 gene

CC polymorphisms. The polymorphisms and screened compounds are useful for

CC treatment of diseases associated with RANGAP1 activity, such as

CC cancer and other disorders associated with an irregular cell cycle.

CC AA519743-AA519820 represent ASO primers for detecting human RANGAP1

CC gene polymorphisms.

CC

SO Sequence 15 BP; 0 A; 6 C; 6 G; 2 T; 1 other;

Query Match 66.7%; Score 12; DB 24; Length 15;

Best Local Similarity 85.7%; Pred. No. 2e+04;

Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 3 GCGCCCGGATTCGAG 16

DB 2 GCGCCCGGATTCRG 15

RESULT 15

AAQ40880

ID AAQ40880 standard; DNA; 21 BP.

AC AAQ40880;

DT 29-SEP-1993 (first entry)

DE Apyrase gene reverse primer.

KM Shigella; entero-invasive E.coli; EIEC; virulence;

KM S. flexneri; S. dysenteriae; S. sonnei; S. boydii; ss.

OS Synthetic.

PM GB2261878-A.

PD 02-JUN-1993.

PF 25-NOV-1992; 92GB-0024716.

PR 26-NOV-1991; 91IN-0000874.

PA (ASTR-) ASTRA AB.

PI Ramchandran V, Roy RK, Sankaran K, Subrahmanyam YVB;

XX WPI; 1993-177505/22.

DR ATP di-phospho:hydrolase or apyrase DNA sequence and prods.

PT used for detection, therapy and protection against Shigella and

PT entero-invasive E.coli strains

PS Example; Page 11; 40pp; English.

CC Plasmid DNA from clone PAR25 was used as a template to amplify

CC the apyrase gene, by PCR, using the primers in AAQ40879-80.

CC The apyrase enzyme is associated with the virulence of all species

CC of Shigella (e.g. S. flexneri, S. dysenteriae, S. sonnei, S. boydii)

CC and related entero-invasive E.coli (EIEC) strains. The apyrase

CC nucleotide sequence can be used in the detection of a virulence

CC determinant in pathogenic bacteria.

XX Sequence 21 BP; 3 A; 8 C; 7 G; 3 T; 0 other;

Query Match 66.7%; Score 12; DB 14; Length 21;

Best Local Similarity 100.0%; Pred. No. 2e+04;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCGGATCCAGGC 18
 |||||
 Db 2 CCGGATCCAGGC 13

RESULT 16
 ID AA064130 standard; DNA; 21 BP.
 XX AA064130;
 AC
 XX 10-NOV-1994 (first entry)
 DT
 XX Apyrase gene PCR primer.
 DE
 XX Apyrase; ATP-diphosphohydrolase; virulence; Escherichia coli;
 KM Shigella; probe; hybridization; plasmid PARC25; primer; PCR;
 KW polymerase chain reaction; ss.
 XX Synthetic.
 OS
 XX WO9412211-A.
 PN
 XX 09-JUN-1994.
 PD
 XX 19-NOV-1993; 93WO-SE00996.
 PF
 XX 23-NOV-1992; 92SE-0003506.
 PR
 XX (ASTR) ASTRA AB.
 PA
 XX Ramachandran V, Roy RK, Sankaran K, Subrahmanyam YVBK;
 PI WPI; 1994-199970/24.
 DR
 XX New DNA encoding virulence associated ATP di-phosphohydrolase -
 PT useful as hybridisation probe for specific detection of virulent
 Shigella sp. and entero-invasive E. coli
 XX
 PS Disclosure; Page 26; 40pp; English.
 XX

CC A DNA sequence (AA064128) encoding a virulence-associated apyrase
 CC (ATP-diphosphohydrolase) in Shigella spp. and entero-invasive Escherichia
 CC coli was located in S. flexneri plasmid PARC25. The 20 N-terminal amino
 CC acids of apyrase are given in sequence AARS4083 (positions 1-20 of the
 CC full apyrase sequence, AARS4082). The gene encoding apyrase was
 CC cloned by PCR amplification of PARC25 DNA using the primers given
 CC AA064129-30.
 CC

XX Sequence 21 BP; 3 A; 8 C; 7 G; 3 T; 0 other;
 SQ

Query Match 66.7%; Score 12; DB 15; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2e+04;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCGGATCCAGGC 18
 |||||
 Db 2 CCGGATCCAGGC 13

RESULT 17
 ID AA061767 standard; cDNA; 25 BP.
 XX AA061767;
 AC
 XX 21-OCT-1994 (first entry)
 DT
 XX HEV strain BUR-121 primer D72.
 DE
 XX Hepatitis E virus; HEV; strain SAR-55; open reading frame; ORF; PCR;
 KW

KM antibody; detection; diagnosis; primates; stool suspension; amplify;
 KW polymerase chain reaction; primer; burma; strain BUR-121; ss.
 XX
 OS Synthetic.
 XX
 XX WO9406913-A.
 PN
 XX 31-MAR-1994.
 PD
 XX 17-SEP-1993; 93WO-US008849.
 PF
 XX 18-SEP-1992; 92US-0947263.
 PR
 XX (USSH) US SEC DEPT HEALTH.
 PA
 XX Emerson SU, Purcell RH, Tsarev SA;
 PI WPI; 1994-118462/14.
 DR
 XX Purified hepatitis E strain SAR-55 virus - used to develop prods.
 PT for use in detection, diagnosis, vaccines and therapy of
 PT hepatitis E virus infection
 XX
 XX Example 1; Page 40; 114pp; English.
 XX

CC The sequences given in AA045198-200 and AA061687-777 are primers which
 CC were used in the isolation and amplification of the genomic sequence
 CC of the hepatitis E virus (HEV) strain SAR-55. These primers were
 CC based on sequences derived from the SAR-55 strain and a strain from
 CC Burma (BUR-121). The amplified sequence contains three open reading
 CC frames (ORFs). The proteins encoded by this sequence can be used to
 CC stimulate the production of protective antibodies upon injection into
 CC a mammal that would serve to protect the mammal upon challenge with
 CC wild type HEV. The proteins can be used for detection and diagnosis
 CC of HEV infection. This cDNA was isolated from primates inoculated
 CC with stool suspensions obtained from hepatitis E patients.
 CC

XX Sequence 25 BP; 4 A; 6 C; 10 G; 5 T; 0 other;
 SQ

Query Match 66.7%; Score 12; DB 15; Length 25;
 Best Local Similarity 100.0%; Pred. No. 2e+04;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCGGATCCAGGC 18
 |||||
 Db 20 CCGGATCCAGGC 9

RESULT 18
 ID AAT27478 standard; DNA; 25 BP.
 XX AAT27478;
 AC
 XX 27-NOV-1996 (first entry)
 DT
 XX HEV strain Burma-121 derived forward primer 72 (ORF-1).
 DE
 XX Hepatitis E virus; HEV; SAR-55 strain; enteric transmission;
 KW structural region; antigen; detection; antibody; vaccine;
 KW immunisation; infection; primer; Burma-121;
 KW polymerase chain reaction; PCR; ss.
 XX
 XX Synthetic.
 OS
 XX WO9610580-A2.
 PN
 XX 11-APR-1996.
 PD
 XX 03-OCT-1995; 95WO-US13102.
 PF
 XX 03-OCT-1994; 94US-0316765.
 PR
 XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Emerson SU, Purcell RH, Tearev SA;
 XX
 DR WPI, 1996-209320/21.
 XX
 PT Isolated and purified hepatitis E virus strain SAR-55 DNA - encodes
 PT antigenic protein useful in diagnosis, prophylaxis and treatment of
 PT hepatitis E virus infection
 XX
 PS Example 1, Page 44, 121pp, English.
 XX
 CC The present sequence is a hepatitis E virus (HEV) strain Burma-121
 CC derived primer, used in the isolation of the HEV strain SAR-55
 CC CDNA. The HEV strain SAR-55 was implicated in an enterically
 CC transmitted non-A, non-B hepatitis in Pakistan. The protein encoded
 CC by the structural region of the virus (i.e. ORF-2), which is
 CC capable of forming HEV like particles, is useful for the detection
 CC of HEV antibodies (pref. IgG or IgM) in blood, plasma, sera,
 CC cerebrospinal fluid, tissue, urine or pleural fluid. The protein,
 CC and anti-HEV antibodies generated using the protein, can also be
 CC used in vaccines for immunising an animal against HEV infection.
 CC The protein is identified as a band of greater than 50 kD
 CC following SDS-PAGE of cell lysates of insect cells infected with
 CC a HEV ORF-2 contg. baculovirus, i.e. the claimed recombinant
 CC expression vectors pPIC9-1779, -1780 and -1781.
 XX
 SO Sequence 25 BP; 4 A; 6 C; 10 G; 5 T; 0 other;
 Query Match 66.7%; Score 12; DB 17; Length 25;
 Best Local Similarity 100.0%; Pred. No. 2e+04;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 7 CCGGATCCAGGC 18
 |||||
 20 CCGGATCCAGGC 9
 Db
 RESULT 19
 AAV71688/c
 ID AAV71688 standard; DNA; 25 BP.
 XX
 AC AAV71688;
 XX
 DT 02-FEB-1999 (first entry)
 XX
 DE HEV ORF proteins encoding DNA amplifying primer D 72 B.
 XX
 KM Hepatitis E virus; HEV; SAR-55; diagnostic agent; vaccine; antibody;
 KM passive immunisation; open reading frame; ORF; PCR primer; ss.
 XX
 OS Synthetic.
 OS Hepatitis E virus.
 XX
 PN WO9846761-A1.
 XX
 PD 22-OCT-1998.
 XX
 PF 09-APR-1998; 98WO-US07418.
 XX
 PR 11-APR-1997; 97US-0840316.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Emerson SU, Purcell RH, Robinson RA, Tearev SA;
 XX
 DR WPI, 1998-568733/48.
 XX
 PT New hepatitis E virus DNA from Pakistani strain SAR-55 - used for,
 PT e.g. developing products for diagnosis of, and vaccination against
 PT hepatitis E virus infection
 XX
 PS Example 1, Page 46; 204pp; English.

XX
 CC Sequences AAV71605 to AAV71698 represent primers used for PCR
 CC amplification of the hepatitis E virus (HEV) DNA SAR-55 encoding the open
 CC reading frame (ORF) proteins ORF-1, ORF-2 and ORF-3. A host organism
 CC transformed or transfected with a recombinant expression vector
 CC containing the SAR-55 nucleic acid can be used to produce the HEV
 CC proteins, especially ORF-2 protein. The recombinant HEV proteins can be
 CC used as diagnostic agents and as vaccines for use against HEV infection.
 CC The detection of antibodies specific for HEV can be used for the
 CC diagnosis of infection and diseases caused by HEV, and for monitoring the
 CC progression of such disease. Such methods are also useful for monitoring
 CC the efficacy of therapeutic agents during the course of treatment of HEV
 CC infection and disease in a mammal. The antibodies can be used for
 CC detection or for passive immunisation of mammals.
 XX
 SO Sequence 25 BP; 4 A; 6 C; 10 G; 5 T; 0 other;
 Query Match 66.7%; Score 12; DB 19; Length 25;
 Best Local Similarity 100.0%; Pred. No. 2e+04;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 7 CCGGATCCAGGC 18
 |||||
 20 CCGGATCCAGGC 9
 Db
 RESULT 20
 AA068697/c
 ID AA068697 standard; DNA; 18 BP.
 XX
 AC AA068697;
 XX
 DT 20-FEB-1995 (first entry)
 XX
 DE Bacillus licheniformis alkaline protease N-terminal probe.
 XX
 KM Pullulanase; recombinant production; pullulan; amylopectin;
 KM hydrolysis; alpha-1,6-glycosidic bond; starch saccharification;
 KM alkaline protease; ss.
 XX
 OS Synthetic.
 OS
 PN EP605040-A.
 XX
 PD 06-JUL-1994.
 XX
 PF 20-DEC-1993; 93EP-0203593.
 XX
 PR 28-DEC-1992; 92BE-0001156.
 PR 15-JUL-1993; 93BE-0000744.
 PR 19-NOV-1993; 93BE-0001278.
 XX
 PA (SOLV) SOLVAY SA.
 XX
 PI AMORY A, DeWeer P;
 XX
 DR WPI, 1994-210291/26.
 XX
 PT New pullulanase from Bacillus deramificans - for starch
 PT saccharification etc., with good stability over wide temp. and pH
 PT ranges, also related DNA vectors, transformed cells etc.
 XX
 PS Example 15; Page 20; 61pp; French.
 XX
 CC A probe was constructed which corresponded to the N-terminal part
 CC of the alkaline protease (AP) gene of Bacillus licheniformis S82.
 CC The probe (AA068697) localised the N-terminal part of the gene to a
 CC 5.5kD PstI fragment as part of a procedure for preparing a deletion
 CC plasmid for deleting the AP gene from B. licheniformis S82.
 XX
 SO Sequence 18 BP; 2 A; 6 C; 7 G; 3 T; 0 other;
 Query Match 65.6%; Score 11.8; DB 15; Length 18;

Best Local Similarity 86.7%; Pred. No. 2.5e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGGCGCCGATCCA 15
|||
DB 16 CTGGCGCCAGAGCCA 2

RESULT 21

AA080932/c
ID AA080932 standard; DNA; 18 BP.

AC AA080932;

DT 02-AUG-1995 (first entry)

DE Alkaline protease N-terminus probe.

XX Xylanase; endo-1,4-beta-D-xylanase; wood pulp; pulping;

KM biobleaching; bleaching; Bacillus licheniformis;

KW probe; hybridization; alkaline protease; ss.

XX Synthetic.

PN GB2279955-A.

PD 18-JAN-1995.

PF 15-JUL-1993; 93GB-0014780.

PR 15-JUL-1993; 93GB-0014780.

XX (SOLV) SOLVAY SA.

PA (SOLV) SOLVAY & CIE.

PI Amory A, Andre C, De Buyl E, Detroz R, Lahaye A;

XX Ledoux P;

XX WPI; 1995-039214/06.

PT Purified xylanase from Bacillus pumilus PRL B12 - esp. produced

PT in transformed Bacillus licheniformis, and related DNA, vectors,

PT etc.; used for pre-treatment of wood pulp to reduce chlorine or

PT ozone consumption in subsequent bleaching

PS Example 23; Page 55; 97p; English.

XX The C- and N-terminal portions of the Bacillus licheniformis

CC SE2 alkaline protease gene were cloned by hybridization to

CC the probe given in AA090831-32, respectively.

XX Sequence 18 BP; 2 A; 6 C; 7 G; 3 T; 0 other;

QY Query Match 65.6%; Score 11.8; DB 16; Length 18;

Best Local Similarity 86.7%; Pred. No. 2.5e+04;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 1 CTGGCGCCGATCCA 15
|||
16 CTGGCGCCAGAGCCA 2

XX AAT41772 standard; DNA; 24 BP.

AC AAT41772;

XX 24-JAN-1997 (first entry)

XX Human CDC27 gene 5' PCR primer.

DE Human CDC27 gene 5' PCR primer.

XX CDC27, mitotic destruction complex; cell cycle regulatory protein;

KW CCRP; inhibitor; apoptosis; cell differentiation; primer; PCR;

KM polymerase chain reaction; ss.

XX Synthetic.

XX WO9633286-A1.

XX 24-OCT-1996.

PF 19-APR-1996; 96WO-US05643.

XX 20-APR-1995; 95US-0425299.

XX (HARD) HARVARD COLLEGE.

XX King RW, Kirschner MW, Peters J;

DR WPI; 1996-485790/48.

XX Detecting inhibitors of ubiquitin-mediated proteolysis of CCRPs -

PT used in the treatment of proliferative and/or differentiation

PT diseases, and in modulation of apoptosis

XX Example 1; Page 24; 63p; English.

XX PCR primers (AAT41772 and AAT41773) were used to amplify the coding

CC sequence (AAT41774) for CDC27 (AA00364) from a human cDNA library.

CC The amplified cDNA was cloned into vector pRSET and used to

CC transfect E. coli JM109 for the prodn. of poly(His)-tagged CDC27

CC fusion protein. CDC27 can be used in novel cell-free ubiquitin-

CC conjugating systems for the detection of inhibitors of ubiquitin-

CC mediated proteolysis of cell cycle regulatory proteins.

XX Sequence 24 BP; 3 A; 7 C; 10 G; 4 T; 0 other;

QY Query Match 65.6%; Score 11.8; DB 17; Length 24;

Best Local Similarity 86.7%; Pred. No. 2.4e+04;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 3 GCGCGCGATCCAGG 17
|||
1 GCGCGCGATCCATG 15

XX ABA98282/c

AC ABA98282;

XX 18-JUN-2002 (first entry)

DE Primer 48 for sequencing of pcu.

XX PHBA; para-Hydrobenzoate; liquid crystal polymer; LCP;

KM toluene monooxygenase; TMO; pcu gene; p-creol; PCR primer; ss.

XX Pseudomonas mendocina KR-1.

XX WO200192539-A2.

XX 06-DEC-2001.

XX 22-MAY-2001; 2001WO-US16574.

XX 01-JUN-2000; 2000US-0585174.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX Ben-Bassat A, Cattermole M, Gatenby AA, Gibson KJ;

PI Ramos-Gonzales MI, Ramos JL, Sarielani S;

XX WPI; 2002-171436/22.

XX New nucleic acid fragments encoding bacterial toluene monooxygenase
PT enzyme pathway, useful for isolating genes encoding proteins from the
PT same or other microbial species, and for producing para-hydroxybenzoate
XX
PS Example 1, Page 81, 97pp; English.
XX
CC The invention relates to an isolated nucleic acid fragment encoding a
CC bacterial toluene monooxygenase enzyme pathway. The nucleic acid
CC fragments of the invention may be used to isolate genes encoding
CC proteins from the same or other microbial species. Bacterial strains
CC transformed with the p-cresol utilizing (pcu) genes are useful for
CC producing para-hydroxybenzoate (PHBA) which can be used for
CC synthesizing liquid crystal polymers (LCP). The sequences given in
CC ABA98235-ABA98331 represent primers for; pcu sequencing, cloning of the
CC p. putida pcuA gene, sequencing tmox, cloning pcu for insertion into
CC pMC3, construction of plasmids pPCU1 and 2, mapping the transcript
CC initiation site of tmox, and the identification of pcba and B genes.
XX
SQ Sequence 19 BP; 2 A; 5 C; 7 G; 5 T; 0 other;
Query Match 64.4%; Score 11.6; DB 24; Length 19;
Best Local Similarity 77.8%; Pred. No. 3e+04; 4; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
DB 1 CTGGCGCCGGATCCAGGC 18
18 CAGCACCCTGATCAAGGC 1
RESULT 24
AA226752/c
ID AA226752 standard; DNA; 21 BP.
XX
AC AA226752;
XX
DT 30-NOV-1999 (first entry)
XX
XX Human polymorphic region 941.
XX
XX Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
XX cell viability; loss of heterozygosity; precancerous condition; ASI;
XX allele specific inhibitor; somatic cell; diagnosis; prevention;
XX atherosclerotic plaque; premalignant metastatic lesion; endometriosis;
XX dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
XX graft versus host disease; malignant cell removal; bone marrow; ss.
XX
OS Homo sapiens.
XX
XX MO9841648-A2.
XX
XX 24-SEP-1998.
XX
XX 19-MAR-1998; 98WO-US05419.
XX
XX 20-MAR-1997; 97US-0041057.
XX
XX (VARI-) VARIAGENICS INC.
XX
XX Housman D, Ledley FD, Stanton VP;
XX
XX WPI; 1998-521232/44.
XX
XX Identifying target genes for allele-specific drugs - used for
XX diagnosis, prevention and treatment of, e.g. cancers, atherosclerotic
XX plaque, dysplastic lesions, endometriosis or graft versus host disease
XX
XX Disclosure; Figure 7, 605pp; English.
XX
XX This invention describes a novel method for identifying an inhibitor
XX potentially useful for treatment of cancer, where the inhibitor is
XX active on a gene vital for cell growth or viability, and where the gene

CC is subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC used for preventing the development of cancer in a patient having a
CC precancerous condition, by administering to the patient a first allele
CC specific inhibitor (ASI) targeted to an allele of a first essential gene
CC present in cells of the precancerous condition, where the normal somatic
CC cells of the patient are heterozygous for the first gene, the inhibitor
CC is active on at least one but less than all allelic forms of the gene
CC present in a population and targets only one allelic form present in the
CC normal somatic cells, and the first gene. The products and methods can
CC be used in the diagnosis, prevention and treatment of LOH disorders,
CC e.g. cancers, atherosclerotic plaques, premalignant metastatic or
CC dysplastic lesions, benign tumours, endometriosis, polycystic kidney
CC disease, and graft versus host disease. The method can also be used to
CC remove malignant cells from bone marrow transplants. AA25812-226825
CC represent human polymorphic sites described in the method of the
CC invention.
XX
SQ Sequence 21 BP; 4 A; 8 C; 7 G; 2 T; 0 other;
Query Match 64.4%; Score 11.6; DB 19; Length 21;
Best Local Similarity 77.8%; Pred. No. 3e+04; 4; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
DB 1 CTGGCGCCGGATCCAGGC 18
18 CTGGCGCCGGATTCATGC 1
RESULT 25
AAV41150/c
ID AAV41150 standard; cDNA; 21 BP.
XX
XX AAV41150;
XX
XX 02-OCT-1998 (first entry)
XX
XX CAPL 3' splice site.
XX
XX CAPL; inhibitor; human; calcium-binding protein; S100 family; therapy;
XX metastatic cancer; 3' splice site; ss.
XX
XX Homo sapiens.
XX
XX US5789248-A.
XX
XX 04-AUG-1998.
XX
XX 16-FEB-1996; 96US-0602036.
XX
XX 16-FEB-1996; 96US-0602036.
XX
XX 17-FEB-1995; 95US-0391375.
XX
XX (HYBR-) HYBRIDON INC.
XX (NORA-) NORWEGIAN RADIIUM HOSPITAL RES FOUND.
XX
XX Agrawal S, Engebraaten O, Fodstad O, Hovig E, Maelandmo G;
XX
XX WPI; 1998-446090/38.
XX
XX Oligo:nucleotides inhibiting expression of CAPL mRNA - useful for
XX treating metastatic cancer
XX
XX Disclosure; Column 6; 28pp; English.
XX
XX This sequence represents a 3' splice site from the human CAPL gene, and
XX is targeted by the oligonucleotide of the invention. The oligonucleotide
XX inhibits expression of mRNA encoding CAPL (a calcium-binding protein of
XX the S100 family) and has a sequence complementary to a sequence of the
XX CAPL mRNA. The oligonucleotide may be used for inhibiting expression of
XX CAPL mRNA in a cell-free reaction mixture or in a cell in vitro or for
XX treating metastatic cancer. The oligonucleotide provides a novel method
XX for blocking the metastatic cascade.

50 Sequence 21 BP; 5 A; 3 C; 10 G; 3 T; 0 other;

Query Match 64.4%; Score 11.6; DB 19; Length 21;
Best Local Similarity 77.8%; Pred. No. 3e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGGCCCCGATCCAGGC 18
18 CTGCTCCAGATCTGAC 1

Db

RESULT 26
AAI7717/C
ID AAI7717 standard; DNA; 21 BP.
XX
XX AAI7717;
AC
XX
XX 10-MAY-1999 (first entry)
DT
XX
XX US5877308 Seq ID 23.
DE
XX
XX Human; CAPL; RNA splicing; antisense; metastatic cancer; ss.
KM
XX
XX Synthetic.
OS
XX
XX US5877308-A.
PN
XX
XX 02-MAR-1999.
PD
XX
XX 03-MAY-1996; 96US-0642407.
PT
XX
XX 16-FEB-1996; 96US-0602036.
PR
XX
XX 19-FEB-1995; 95US-0391375.
XX
XX 03-MAY-1996; 96US-0642407.
XX
XX (HYBR-) HYBRIDON INC.
PA
XX
XX (NORA-) NORWEGIAN RADIUM HOSPITAL RES FOUND.
XX
XX Agrawal S; Engebraten O; Fodstad O; Hovig E; Maelandemo G;
PI
XX
XX Von Hofe B;
DR
XX
XX WPI; 1999-189725/16.
XX
XX PT New synthetic oligonucleotides complementary to human CAPL mRNA -
PT useful for inhibiting expression of a100 calcium binding protein for
PT the treatment of metastatic cancer
XX
XX
XX Disclosure; Column 37; 27pp; English.
XX
XX The invention provides synthetic oligonucleotides which are complementary
CC to and inhibit expression of human CAPL mRNA that includes the 3' or 5'
CC splice site or the translational start site. The oligonucleotides prevent
CC translation and splicing of RNA and can be used as antisense or triple-
CC helix forming oligonucleotides to treat metastatic cancer.
XX
XX Sequence 21 BP; 5 A; 3 C; 10 G; 3 T; 0 other;

Query Match 64.4%; Score 11.6; DB 20; Length 21;
Best Local Similarity 77.8%; Pred. No. 3e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGGCCCCGATCCAGGC 18
18 CTGCTCCAGATCTGAC 1

Db

RESULT 27
ABK94171/c
ID ABK94171 standard; DNA; 21 BP.
XX
XX ABK94171;
AC
XX
XX 27-AUG-2002 (first entry)
DT

XX
XX Endothelin receptor B (EDNRB) SNP detection PCR primer #13.
DE
XX
XX Endothelin; EDN; endothelin converting enzyme; ECE; endothelin receptor;
KM EDNR; signaling system; cardiovascular disease; coronary heart disease;
KM hypertension; atherosclerosis; angiogenesis; fatty acid metabolism;
KM diabetes; familial hypercholesterolemia; forensic marker;
KM transgenic animal; solid support; cardiovascular regulator; SNP;
KM single nucleotide polymorphism; PCR; primer; ss.
XX
XX
XX Synthetic.
OS
XX
XX WO200224747-A2.
PN
XX
XX 28-MAR-2002.
PD
XX
XX 31-AUG-2001; 2001WO-EP10087.
PF
XX
XX 19-SEP-2000; 2000EP-0120123.
PR
XX
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
PA
XX
XX Brinkmann U; Hoffmeyer S;
PI
XX
XX WPI; 2002-435060/46.
DR
XX
XX Novel polynucleotide of the endothelin/endothelin converting
PT enzyme/receptors of endothelin and endothelin converting enzyme
PT signaling system associated with cardiovascular disease, useful for
PT treating the disease -
XX
XX
XX Example 6; Page 59; 190pp; English.
PS
XX
XX The invention describes a polynucleotide (I) of the endothelin
CC (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)
CC signaling system which is associated with a cardiovascular disease. (I),
CC the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I)
CC or (II) is useful for producing cells capable of expressing a molecular
CC variant polypeptide which is associated with a cardiovascular disease.
CC (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing
CC a molecular variant gene comprising (I) is useful for identifying and
CC obtaining a pro-drug or drug capable of modulating the activity of a
CC molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system
CC or its gene product, or for identifying and obtaining an inhibitor of
CC the activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE
CC signaling system or its gene product. The isolated proteins and
CC polynucleotides encoding them are useful for preparation of a
CC pharmaceutical composition for treating a cardiovascular disease such as
CC coronary heart disease, hypertension, atherosclerosis, or related to
CC abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial
CC hypercholesterolemia. The gene or a polynucleotide fragment of the
CC EDN/ECE/EDNR signaling system are useful as forensic markers, for
CC creating a transgenic animal and in creation of a solid support
CC comprising polynucleotides, genes, vectors, polypeptides, antibodies or
CC host cells of the invention. This sequence represents a PCR primer used
CC to identify single nucleotide polymorphisms in DNA encoding
CC cardiovascular regulator proteins of the EDN/ECE/EDNR signaling pathway.
XX
XX Sequence 21 BP; 6 A; 3 C; 9 G; 3 T; 0 other;

Query Match 64.4%; Score 11.6; DB 24; Length 21;
Best Local Similarity 77.8%; Pred. No. 3e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGGCCCCGATCCAGGC 18
20 CTGCGCCAGATCCAGC 3

Db

RESULT 28
ABK94172
ID ABK94172 standard; DNA; 21 BP.
XX

XX	ABK94172:
DT	27-AUG-2002 (first entry)
DE	Endothelin receptor B (EDNRB) SNP detection PCR primer #14.
KW	Endothelin; EDN; endothelin converting enzyme; ECE; endothelin receptor;
KM	EDNR; signaling system; cardiovascular disease; coronary heart disease;
KW	hyperextension; atherosclerosis; angiogenesis; fatty acid metabolism;
KM	diabetes; familial hypercholesterolemia; forensic marker;
KW	transgenic animal; solid support; cardiovascular regulator; SNP;
XX	single nucleotide polymorphism; PCR; primer; ss.
OS	Synthetic.
PN	MO200224747-A2.
PD	28-MAR-2002.
PR	31-AUG-2001; 2001WO-EPI0087.
XX	19-SEP-2000; 2000EP-0120123.
PA	(EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
P1	Brinkmann U, Hofmeyer S;
DR	WP1; 2002-435060/46.
PT	Novel polynucleotide of the endothelin/endothelin converting
PT	enzyme/receptors of endothelin and endothelin converting enzyme
PT	signaling system associated with cardiovascular disease, useful for
PT	treating the disease -
PS	Example 6; Page 59; 190pp; English.
XX	The invention describes a polynucleotide (I) of the endothelin
CC	(EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)
CC	signaling system which is associated with a cardiovascular disease. (I),
CC	the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I)
CC	or (II) is useful for producing cells capable of expressing a molecular
CC	variant polypeptide which is associated with a cardiovascular disease.
CC	(II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing
CC	a molecular variant gene comprising (I) is useful for identifying and
CC	obtaining a pro-drug or drug capable of modulating the activity of a
CC	molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system
CC	or its gene product, or for identifying and obtaining an inhibitor of
CC	the activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE
CC	signaling system or its gene product. The isolated proteins and
CC	polynucleotides encoding them are useful for preparation of a
CC	pharmaceutical composition for treating a cardiovascular disease such as
CC	coronary heart disease, hypertension, atherosclerosis, or related to
CC	abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial
CC	hypercholesterolaemia. The gene or a polynucleotide fragment of the
CC	EDN/ECE/EDNR signaling system are useful as forensic markers, for
CC	creating a transgenic animal and in creation of a solid support
CC	comprising polynucleotides, genes, vectors, polypeptides, antibodies or
CC	host cells of the invention. This sequence represents a PCR primer used
CC	to identify single nucleotide polymorphisms in DNA encoding
CC	cardiovascular regulator proteins of the EDN/ECE/EDNR signaling pathway.
XX	
SQ	Sequence 21 BP; 3 A; 9 C; 3 G; 6 T; 0 other;
Query Match	64.4%; Score 11.6; DB 24; Length 21;
Best Local Similarity	77.8%; Pred. No. 3e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0	
OY	1 CTGCGCCCGATCCAGGC 18
DB	2 CTTGCCGACGATCCAGC 19

RESULT 29

ID ABR94175/c
 AC ABR94175 standard; DNA; 21 BP.
 XX
 DT ABR94175;
 XX
 DE 27-AUG-2002 (first entry)
 XX
 EN Endothelin receptor B (EDNRB) SNP detection PCR primer #17.
 KW Endothelin; EDN; endothelin converting enzyme; ECE; endothelin receptor;
 KW EDNR; signaling system; cardiovascular disease; coronary heart disease;
 KW hypertension; atherosclerosis; angiogenesis; fatty acid metabolism;
 KW transgenic; familial hypercholesterolaemia; forensic marker;
 KW diabetic animal; solid support; cardiovascular regulator; SNP;
 KW single nucleotide polymorphism; PCR; primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO200224747-A2.
 PD 28-MAR-2002.
 XX
 PF 31-AUG-2001; 2001WO-EPI0087.
 XX
 PR 19-SEP-2000; 2000EP-0120123.
 XX
 RA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 PI Brinkmann U, Hoffmeyer S;
 DR WPI, 2002-435060/46.
 XX
 PT Novel polynucleotide of the endothelin/endothelin converting
 PT enzyme/receptors of endothelin and endothelin converting enzyme
 PT signaling system associated with cardiovascular disease, useful for
 PT treating the disease -
 XX
 PS Claim 1, Page 59; 190pp; English.
 XX
 AB The invention describes a polynucleotide (I) of the endothelin
 (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)
 CC signaling system which is associated with a cardiovascular disease. (I),
 CC the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I)
 CC or (II) is useful for producing cells capable of expressing a molecular
 CC variant polypeptide which is associated with a cardiovascular disease.
 CC (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing
 CC a molecular variant gene comprising (I) is useful for identifying and
 CC obtaining a pro-drug or drug capable of modulating the activity of a
 CC molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system
 CC or its gene product, or for identifying and obtaining an inhibitor of
 CC the activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE
 CC signaling system or its gene product. The isolated proteins and
 CC polynucleotides encoding them are useful for preparation of a
 CC pharmaceutical composition for treating a cardiovascular disease such as
 CC coronary heart disease, hypertension, atherosclerosis, or related to
 CC abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial
 CC hypercholesterolemia. The gene or a polynucleotide fragment of the
 CC EDN/ECE/EDNR signaling system are useful as forensic markers, for
 CC creating a transgenic animal and in creation of a solid support
 CC comprising polynucleotides, genes, vectors, polypeptides, antibodies or
 CC host cells of the invention. This sequence represents a PCR primer used
 CC to identify single nucleotide polymorphisms in DNA encoding
 CC cardiovascular regulator proteins of the EDN/ECE/EDNR signaling pathway.
 XX
 SQ Sequence 21 BP; 5 A; 3 C; 10 G; 3 T; 0 other;
 QY Query Match 64.4%; Score 11.6; DB 24; Length 21;
 Best Local Similarity 77.8%; Pred. No. 3e+04; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 4;
 DB 20 CTTGCCGACGATCCAGCG 3
 1 CTGGCCCGGATCCAGCG 18
 |||||
 20 CTTGCCGACGATCCAGCG 3

RESULT 30
 ABR94176
 ID ABR94176 standard; DNA; 21 BP.
 AC
 XX ABR94176;
 XX
 DT 27-AUG-2002 (first entry)
 DE Endothelin receptor B (EDNRB) SNP detection PCR primer #18.
 XX
 XX Endothelin; EDN; endothelin converting enzyme; ECE; endothelin receptor;
 KM EDNR; signaling system; cardiovascular disease; coronary heart disease;
 KM hypertension; atherosclerosis; angiogenesis; fatty acid metabolism;
 KM diabetes; familial hypercholesterolemia; forensic marker;
 KM transgenic animal; solid support; cardiovascular regulator; SNP;
 KM single nucleotide polymorphism; PCR; primer; ss.
 XX
 XX Synthetic.
 OS
 XX WO200224747-A2.
 PN
 PD 28-MAR-2002.
 XX
 PP 31-AUG-2001; 2001WO-EP10087.
 XX
 PR 19-SEP-2000; 2000EP-0120123.
 XX
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 XX
 PI Brinkmann U, Hofmeyer S;
 XX
 XX WPI; 2002-435060/46.
 DR
 XX
 PT Novel polynucleotide of the endothelin/endothelin converting
 PT enzyme/receptors of endothelin and endothelin converting enzyme
 PT signaling system associated with cardiovascular disease, useful for
 PT creating the disease -
 PT
 XX
 XX
 XX Claim 1; Page 59; 190pp; English.
 PS
 XX The invention describes a polynucleotide (I) of the endothelin
 CC (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)
 CC signaling system which is associated with a cardiovascular disease. (I)
 CC or (II) is useful for producing cells capable of expressing a molecular
 CC variant polypeptide which is associated with a cardiovascular disease.
 CC (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing
 CC a molecular variant gene comprising (i) is useful for identifying and
 CC obtaining a pro-drug or drug capable of modulating the activity of a
 CC molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system
 CC or its gene product, or for identifying and obtaining an inhibitor of
 CC the activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE
 CC signaling system or its gene product. The isolated proteins and
 CC polynucleotides encoding them are useful for preparation of a
 CC pharmaceutical composition for treating a cardiovascular disease such as
 CC coronary heart disease, hypertension, atherosclerosis, or related to
 CC abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial
 CC hypercholesterolemia. The gene or a polynucleotide fragment of the
 CC EDN/ECE/EDNR signaling system are useful as forensic markers, for
 CC creating a transgenic animal and in creation of a solid support
 CC comprising polynucleotides, genes, vectors, polypeptides, antibodies or
 CC host cells of the invention. This sequence represents a PCR primer used
 CC to identify single nucleotide polymorphisms in DNA encoding
 CC cardiovascular regulator proteins of the EDN/ECE/EDNR signaling pathway.
 CC
 XX Sequence 21 BP; 3 A; 10 C; 3 G; 5 T; 0 other;
 SQ

```

Oy      1 CTGGCCCCGATCCAGGC 18
        ||| | | | | | | | | |
Db       2 CTTGCCCGCATCAGC 19

RESULT 31
AAV41141/c
ID AAV41141 standard; cDNA; 22 BP.
XX
AC AAV41141;
XX
DT 02-OCT-1998 (first entry)
XX
DE CAPL 3' splice site.
XX
KW CAPL; inhibitor; human; calcium-binding protein; S100 family; therapy; metastatic cancer; 3' splice site; ss.
XX
OS Homo sapiens.
XX
PN US5789248-A.
XX
PD 04-AUG-1998.
XX
PP 16-FEB-1996; 96US-0602036.
XX
PR 16-FEB-1996; 96US-0602036.
XX
PR 17-FEB-1995; 95US-0391375.
XX
PA (HYBR-) HYBRIDON INC.
PA (NORA-) NORMEGIAN RADIUM HOSPITAL RES FOUND.
XX
PI Agrawal S, Engebraaten O, Fodstad O, Hovig E, Maelandsmo G;
XX WPT; 1998-446090/38.
XX DR
PT Oligo:nucleotides inhibiting expression of CAPL mRNA - useful for treating metastatic cancer
PS Claim 1; Column 6; 28pp; English.
XX
CC This sequence represents a 3' splice site from the human CAPL gene, and CC is targeted by the oligonucleotide of the invention. The oligonucleotide CC inhibits expression of mRNA encoding CAPL (a calcium-binding protein of the S100 family) and has a sequence complementary to a sequence of the CAPL mRNA. The oligonucleotide may be used for inhibiting expression of CAPL mRNA in a cell-free reaction mixture or in a cell in vitro or for treating metastatic cancer. The oligonucleotide provides a novel method for blocking the metastatic cascade.
CC
CC
CC Sequence 22 BP; 5 A; 3 C; 11 G; 3 T; 0 other;
SO

Query Match          64.4%; Score 11.6; DB 19; Length 22;
Best Local Similarity 77.8%; Pred.No. 3e+04;
Matches   14; Conservative    0; Mismatches    4; Indels    0; Gaps    0;

OY           1 CTGGCCCGGATCCAGGC 18
              ||||| | | | | |
DB            18 CTGTCCCGATCCTGAC 1

RESULT 32
AAV41142/c
ID AAV41142 standard; RNA; 22 BP.
XX
AC AAV41142;
XX
DT 02-OCT-1998 (first entry)
XX
DE CAPL 3' splice site.
XX
KW CAPL; inhibitor; human; calcium-binding protein; S100 family; therapy; metastatic cancer; 3' splice site; ss.
XX
```

XX Homo sapiens.
OS
XX US5789248-A.
PN
XX 04-AUG-1998.
PD
XX
PF 16-FEB-1996; 96US-0602036.
PR
XX 16-FEB-1996; 96US-0602036.
PR 17-FEB-1995; 95US-0391375.
XX
XX (HYBR-) HYBRIDON INC.
PA (NORA-) NORWEGIAN RADIUM HOSPITAL RES FOUND.
XX
XX Agrawal S, Engebraten O, Fodstad O, Hovig E, Maelandsmo G;
PI WPI, 1998-446090/38.
DR
XX Oligonucleotides inhibiting expression of CAPL mRNA - useful for
PT treating metastatic cancer
XX
XX Claim 1, Column 6; 28pp; English.
PS
XX This sequence represents a 3' splice site from the human CAPL gene, and
CC is targeted by the oligonucleotide of the invention. The oligonucleotide
CC inhibits expression of mRNA encoding CAPL (a calcium-binding protein of
CC the S100 family) and has a sequence complementary to a sequence of the
CC CAPL mRNA. The oligonucleotide may be used for inhibiting expression of
CC CAPL mRNA in a cell-free reaction mixture or in a cell in vitro or for
CC treating metastatic cancer. The oligonucleotide provides a novel method
CC for blocking the metastatic cascade.
XX
XX Sequence 22 BP; 5 A; 3 C; 11 G; 3 U; 0 other;
SQ
Query Match 64.4%; Score 11.6; DB 19; Length 22;
Best Local Similarity 77.8%; Pred. No. 3e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CTGGCGCCCGATCCAGGC 18
DB 18 CTGCTCCAGATCTGTAC 1
RESULT 33
AAI17697/C
ID AAI17697 standard; DNA; 22 BP.
XX
XX AAI17697;
AC
XX
XX 10-MAY-1999 (first entry)
DT
XX
XX Antisense oligo for human CAPL.
DE
XX
XX Human; CAPL; RNA splicing; antisense; metastatic cancer; ss.
KW
XX
XX Synthetic.
OS
XX Homo sapiens.
PN
XX US5877308-A.
PN
XX
XX 02-MAR-1999.
PD
XX
XX 03-MAY-1996; 96US-0642407.
PF
XX
XX 16-FEB-1996; 96US-0602036.
PR 19-FEB-1995; 95US-0391375.
PR 03-MAY-1996; 96US-0642407.
XX
XX (HYBR-) HYBRIDON INC.
PA (NORA-) NORWEGIAN RADIUM HOSPITAL RES FOUND.
XX
XX Agrawal S, Engebraten O, Fodstad O, Hovig E, Maelandsmo G;
PI

PI Von Hofe E;
XX
XX WPI, 1999-189725/16.
DR
XX
XX New synthetic oligonucleotides complementary to human CAPL mRNA -
PT useful for inhibiting expression of s100 calcium binding protein for
PT the treatment of metastatic cancer
XX
XX Claim 2; Columns 27; 27pp; English.
PS
XX The invention provides synthetic oligonucleotides which are complementary
CC to and inhibit expression of human CAPL mRNA that includes the 3' or 5'
CC splice site or the translational start site. The oligonucleotides prevent
CC translation and splicing of RNA and can be used as antisense or triple-
CC helix forming oligonucleotides to treat metastatic cancer.
XX
XX Sequence 22 BP; 5 A; 3 C; 11 G; 3 T; 0 other;
SQ
Query Match 64.4%; Score 11.6; DB 20; Length 22;
Best Local Similarity 77.8%; Pred. No. 3e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CTGGCGCCCGATCCAGGC 18
DB 18 CTGCTCCAGATCTGTAC 1
RESULT 34
AAI17698/C
ID AAI17698 standard; RNA; 22 BP.
XX
XX AAI17698;
AC
XX
XX 10-MAY-1999 (first entry)
DT
XX
XX Antisense oligo for human CAPL.
DE
XX
XX Human; CAPL; RNA splicing; antisense; metastatic cancer; ss.
KW
XX
XX Synthetic.
OS
XX Homo sapiens.
PN
XX US5877308-A.
PN
XX
XX 02-MAR-1999.
PD
XX
XX 03-MAY-1996; 96US-0642407.
PF
XX
XX 16-FEB-1996; 96US-0602036.
PR 19-FEB-1995; 95US-0391375.
PR 03-MAY-1996; 96US-0642407.
XX
XX (HYBR-) HYBRIDON INC.
PA (NORA-) NORWEGIAN RADIUM HOSPITAL RES FOUND.
XX
XX Agrawal S, Engebraten O, Fodstad O, Hovig E, Maelandsmo G;
PI Von Hofe E;
XX
XX WPI, 1999-189725/16.
DR
XX
XX New synthetic oligonucleotides complementary to human CAPL mRNA -
PT useful for inhibiting expression of s100 calcium binding protein for
PT the treatment of metastatic cancer
XX
XX Claim 2; Columns 27; 27pp; English.
PS
XX The invention provides synthetic oligonucleotides which are complementary
CC to and inhibit expression of human CAPL mRNA that includes the 3' or 5'
CC splice site or the translational start site. The oligonucleotides prevent
CC translation and splicing of RNA and can be used as antisense or triple-
CC helix forming oligonucleotides to treat metastatic cancer.
XX
XX Sequence 22 BP; 5 A; 3 C; 11 G; 3 U; 0 other;
SQ

Query Match 64.4%; Score 11.6; DB 20; Length 22;
Best Local Similarity 77.8%; Pred. No. 3e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Db 1 CTGCGCCCGATCCAGGC 18
18 CTGCTCCCGATCCTGAC 1

RESULT 35
AAC58261 standard; DNA; 22 BP.
AAC58261;
29-JAN-2001 (first entry)
Human PRO212 hybridisation probe SEQ ID NO:80.
Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
proliferation; tumourigenesis; identification; cancer; PCR primer;
hybridisation; probe; cytostatic; neurotropic; neuroprotective;
antiinflammatory; immunosuppressive; immunostimulant; angiogenic;
leukaemia; lymphoid malignancy; neuronal disorder; glial disorder;
astrocytal disorder; hypothalamic disorder; glandular disorder;
macrophagal disorder; epithelial disorder; stromal disorder;
blastocoeic disorder; inflammatory disorder; angiogenic;
immunologic disorder; ss.
Homo sapiens.
MO200053755-A2.
14-SEP-2000.
06-JAN-2000; 2000MO-US00376.
08-MAR-1999; 99MO-US05028.
02-JUN-1999; 99MO-US12252.
23-JUN-1999; 99US-0141037.
07-JUL-1999; 99US-0143048.
26-JUL-1999; 99US-0145698.
30-NOV-1999; 99MO-US28313.
20-DEC-1999; 99MO-US30911.
05-JAN-2000; 2000MO-US00219.
(GETH) GENENTECH INC.
Aehkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;
Watnabe CK, Wood WI,
WPI; 2000-572270/53.
Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
treatment, diagnosis and prevention of cancer -
Example 23; Page 133; 286pp; English.

The present invention describes an isolated antibody that binds to
one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO345,
PRO619, PRO717, PRO809, PRO848, PRO849, PRO1005, PRO1009,
PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184,
PRO1187, PRO1281, PRO23, PRO33, PRO834, PRO1317, PRO1710, PRO2094,
PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell
growth. The PRO polypeptides and nucleotides are useful in the
treatment, diagnosis and prevention of cancer. The antibodies and other
anti-tumour compounds may be used to treat various conditions, including
those characterised by overexpression and/or activation of the amplified
PRO genes. Exemplary conditions or disorders to be treated with such
antibodies and other compounds include benign or malignant tumours
(e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,
colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic

CC carcinomas, sarcomas, glioblastomas, and various head and neck tumours),
CC leukaemias and lymphoid malignancies, other disorders such as neuronal,
CC gliol, astrocytal, hypothalamic and other glandular, macrophagal,
CC epithelial, stromal and blastocoeic disorders, and inflammatory,
CC angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR
CC primers and hybridisation probes used in the isolation of the human PRO
CC sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human
CC PRO polynucleotide and protein sequences given in the exemplification of
CC the present invention.

Sequence 22 BP; 2 A; 10 C; 5 G; 5 T; 0 other;
Query Match 64.4%; Score 11.6; DB 21; Length 22;
Best Local Similarity 77.8%; Pred. No. 3e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Db 1 CTGCGCCCGATCCAGGC 18
3 CTGTCACATGATCCTGAC 20

RESULT 36
AAH78624/C
ID AAH78624 standard; DNA; 23 BP.
AAH78624;
10-DEC-2001 (first entry)
PCR primer RFC780(9) for amplification of human RFC gene exon 3.
Human; reduced folate carrier gene; RFC gene; cancer;
antifolate chemotherapy; folate metabolism; PCR primer; ss.
Homo sapiens.
MO200165994-A2.
13-SEP-2001.
06-MAR-2001; 2001MO-IL00212.
06-MAR-2000; 2000US-0519673.
(TECR) TECHNION RES & DEV POUND LTD.
Assaraf Y, Dvori S;
WPI; 2001-589905/66.
Assessing responsiveness of a cancer patient to antifolate-containing
chemotherapy, comprising searching for mutation or mutations in a gene
associated with folate metabolism or uptake in cells derived from the
patient -
Example; Page 59; 122pp; English.

PCR primers AAH78624-25 were used to amplify exon 3 of the human
reduced folate carrier (RFC) gene. Detection of mutations associated
with the RFC gene are used to assess the responsiveness of a cancer
patient to antifolate chemotherapy. The RFC gene is associated with
folate metabolism. The method is useful for assessing the responsiveness
of a cancer patient to antifolate chemotherapy.

Sequence 23 BP; 4 A; 8 C; 8 G; 3 T; 0 other;
Query Match 64.4%; Score 11.6; DB 22; Length 23;
Best Local Similarity 77.8%; Pred. No. 3e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Db 1 CTGCGCCCGATCCAGGC 18
20 CTGCGCCCGATCCATGC 3

```

RESULT 37
AAFS1790
ID AAFS1790 standard; DNA; 15 BP.
XX
XX
AC AAFS1790;
XX
XX 30-MAR-2001 (first entry)
XX
XX IGF-1 oligonucleotide #2750.
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cyostatic; dermatological; cardiac; virucide; ophthalmological; keloid;
XX skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX growth factor mediated cell proliferation; ichthyosis; seborrhoea; ruba;
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX hyperneovascular condition; hyperplasia; kidney disease;
XX neovascular condition of the retina; ss.
XX
XX Homo sapiens.
XX
XX MO200078341-A1.
XX
XX 28-DEC-2000.
XX
XX 21-JUN-2000; 2000MO-AU00693.
XX
XX 21-JUN-1999; 99US-0140345.
XX
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX
XX Wright CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX
XX Ameliorating the effects of a disorder, e.g. psoriasis, by
XX administering UV (ultra-violet) treatment (optional) and an antisense
XX nucleic acid that inhibits or reduces growth factor mediated cell
XX proliferation and/or inflammation -
XX
XX Example 8; Page 78; 201pp; English.
XX
XX The present invention relates to a method for ameliorating the effects
XX of skin disorders. The method comprises contacting the skin with an
XX antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX inhibiting or reducing growth factor mediated cell proliferation,
XX inflammation and/or other disorders. The present sequence is an
XX oligonucleotide which can be used to design the antisense
XX oligonucleotides of the present invention (see AAF45151 and
XX AAF45153-F45161). The method is useful for ameliorating the effects of
XX psoriasis, ichthyosis, pityriasis, ruba, pilaris, seborrhoea, keloids,
XX keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the
XX skin, a hyperneovascular condition such as a neovascular condition of the
XX retina, brain or skin, growth factor-mediated malignancies, other
XX sclerotic disease, kidney disease, hyperproliferation of the inside of
XX blood vessels or any other hyperplasia.
XX
XX Sequence 15 BP; 3 A; 5 C; 5 G; 2 T; 0 other;
XX
XX Query Match 63.3%; Score 11.4; DB 22; Length 15;
XX Best Local Similarity 92.3%; Pred. No. 3.8e+04;
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 5 CCGCGATCCAGG 17
Db 3 CCGCGATTCAGG 15

```

RESULT 38
AAFS1793

```

ID AAFS1793 standard; DNA; 15 BP.
XX
XX AAFS1793;
XX
XX 30-MAR-2001 (first entry)
XX
XX IGF-1 oligonucleotide #2753.
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cyostatic; dermatological; cardiac; virucide; ophthalmological; keloid;
XX skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX growth factor mediated cell proliferation; ichthyosis; seborrhoea; ruba;
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX hyperneovascular condition; hyperplasia; kidney disease;
XX neovascular condition of the retina; ss.
XX
XX Homo sapiens.
XX
XX MO200078341-A1.
XX
XX 28-DEC-2000.
XX
XX 21-JUN-2000; 2000MO-AU00693.
XX
XX 21-JUN-1999; 99US-0140345.
XX
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX
XX Wright CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX
XX Ameliorating the effects of a disorder, e.g. psoriasis, by
XX administering UV (ultra-violet) treatment (optional) and an antisense
XX nucleic acid that inhibits or reduces growth factor mediated cell
XX proliferation and/or inflammation -
XX
XX Example 8; Page 78; 201pp; English.
XX
XX The present invention relates to a method for ameliorating the effects
XX of skin disorders. The method comprises contacting the skin with an
XX antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX inhibiting or reducing growth factor mediated cell proliferation,
XX inflammation and/or other disorders. The present sequence is an
XX oligonucleotide which can be used to design the antisense
XX oligonucleotides of the present invention (see AAF45151 and
XX AAF45153-F45161). The method is useful for ameliorating the effects of
XX psoriasis, ichthyosis, pityriasis, ruba, pilaris, seborrhoea, keloids,
XX keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the
XX skin, a hyperneovascular condition such as a neovascular condition of the
XX retina, brain or skin, growth factor-mediated malignancies, other
XX sclerotic disease, kidney disease, hyperproliferation of the inside of
XX blood vessels or any other hyperplasia.
XX
XX Sequence 15 BP; 3 A; 6 C; 4 G; 2 T; 0 other;
XX
XX Query Match 63.3%; Score 11.4; DB 22; Length 15;
XX Best Local Similarity 92.3%; Pred. No. 3.8e+04;
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 6 CCGCGATCCAGG 18
Db 1 CCGCGATTCAGG 13

```

RESULT 39
AAV24277/C
ID AAV24277 standard; DNA; 19 BP.
XX
XX AAV24277;
XX

DT 03-SEP-1998 (first entry)
 XX Chimeric antibody against hPTRP human L chain PCR primer MBCLVRL.
 DE Chimeric antibody against hPTRP human L chain PCR primer MBCLVRL.
 XX Chimeric antibody against hPTRP human L chain PCR primer MBCLVRL.
 KW L chain; H chain; hypercalcaemia; cancer; malignant lymphoma; CDR;
 KW hypophosphataemia; pathogen; vitamin D resistance; V region; C region;
 KW humanised; PCR primer ss.
 XX Synthetic.
 OS Homo sapiens.
 XX MO981338-A1.
 PN 02-APR-1998.
 XX 24-SEP-1997; 97WO-JP03382.
 PF 24-JUL-1997; 97JP-0214168.
 PR 26-SEP-1996; 96JP-0255196.
 XX (CHUS) CHUGAI SEIYAKU KK.
 PA Sato K, Wakahara Y, Yabuta N;
 PI WPI; 1998-230640/20.
 DR New chimeric antibodies against human parathormone related
 XX peptide(s) - useful for, e.g. treatment of hypercalcaemia and other
 PT disorders caused by malignant neoplasm(s)
 XX Example 3, Page 107, 182pp; Japanese.
 PS New antibodies have been developed which are specific for human
 CC parathormone related peptides (hPTRP). The antibodies comprise chimeric
 CC L and/or H chains, where the C region is of human and L region of mouse,
 CC origin. The present sequence represents a PCR primer used in an example
 CC of the present invention. Host cells, transformed with vectors
 CC containing DNA encoding antibodies of the invention, can be used to
 CC produce the antibodies. The antibodies may be used to treat
 CC hypercalcaemia, especially that due to a malignancy, e.g. cancers of
 CC pancreas, lung, throat, larynx, tongue, gum, oesophagus, stomach, liver,
 CC breast, kidney, bladder, womb or prostate or malignant lymphoma. They
 CC may also be used for treatment of hypophosphataemia such as that due to
 CC pathogens or to vitamin D resistance.
 CC Sequence 19 BP; 2 A; 6 C; 6 G; 5 T; 0 other;
 SQ
 Query Match 63.3%; Score 11.4; DB 19; Length 19;
 Best Local Similarity 92.3%; Pred. No. 3.8e+04;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 GCCCGATCCAG 17
 DB 13 GCCCGATCCAG 1
 RESULT 40
 ID AAX00122/C
 XX AAX00122 standard; DNA; 19 BP.
 AC AAX00122;
 XX 14-APR-1999 (first entry)
 DT Human antibody PCR primer MBCLVRL.
 DE Human antibody PCR primer MBCLVRL.
 KW Human; parathyroid hormone related protein; PTHrP; cachexia; cancer;
 KW inhibitor; humanised; PCR primer; ss.
 XX Synthetic.
 OS Homo sapiens.
 XX

PN MO9851329-A1.
 XX 19-NOV-1998.
 PD 13-MAY-1998; 98WO-JP02116.
 XX 18-JUL-1997; 97JP-0194445.
 XX 15-MAY-1997; 97JP-0125505.
 PR (CHUS) CHUGAI SEIYAKU KK.
 PA Ishii K, Sato K, Tunesari T;
 PI WPI; 1999-070101/06.
 DR Inhibitors of binding of parathyroid hormone related peptide to its
 XX receptor - useful for, e.g. treatment of cachexia arising from
 PT cancer or other diseases
 XX Example 4; Page 68; 125pp; Japanese.
 PS The present invention describes compositions for the treatment of
 CC cachexia containing a substance which inhibits the binding of a
 CC parathyroid hormone related peptide (PTHrP) to its receptor, as an
 CC active component. This substance may be an antagonist to the receptor,
 CC or an antibody (preferably monoclonal) or antibody fragment,
 CC recognising PTHrP. The antibody is preferably humanised or chimeric.
 CC The present invention also describes a humanised antibody prepared
 CC by hybridoma 23-57-137-1 (FERM BP-5631). The composition is used for
 CC the treatment of cachexia arising in connection with diseases such as
 CC cancer, thereby improving the quality of life of the patient. The
 CC present sequence represents a PCR primer used in an example from the
 CC present invention.
 CC Sequence 19 BP; 2 A; 6 C; 6 G; 5 T; 0 other;
 SQ
 Query Match 63.3%; Score 11.4; DB 20; Length 19;
 Best Local Similarity 92.3%; Pred. No. 3.8e+04;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 GCCCGATCCAG 17
 DB 13 GCCCGATCCAG 1
 Search completed: June 7, 2003, 08:30:51
 Job time : 162.255 secs

C 66	10.8	63.5	21	6	E36963	E36963 Human telom	C 139	9.8	57.6	17	6	AX262745	AX262745 Sequence
C 67	10.8	63.5	23	6	AR090572	AR090572 Sequence	C 140	9.8	57.6	17	6	AX262748	AX262748 Sequence
C 68	10.8	63.5	23	6	AR197607	AR197607 Sequence	C 141	9.8	57.6	17	6	AX262749	AX262749 Sequence
C 69	10.8	63.5	23	6	AX458827	AX458827 Sequence	C 142	9.8	57.6	18	6	AR098815	AR098815 Sequence
C 70	10.8	63.5	24	6	AX049485	AX049485 Sequence	C 143	9.8	57.6	18	6	AR110538	AR110538 Sequence
C 71	10.6	62.4	20	6	AR116457	AR116457 Sequence	C 144	9.8	57.6	18	6	AR110541	AR110541 Sequence
C 72	10.6	62.4	21	6	AR070874	AR070874 Sequence	C 145	9.8	57.6	18	6	AR110543	AR110543 Sequence
C 73	10.6	62.4	22	6	AR053409	AR053409 Sequence	C 146	9.8	57.6	18	6	AR110545	AR110545 Sequence
C 74	10.6	62.4	22	6	E11228	E11228 PCR primer.	C 147	9.8	57.6	18	6	AR148407	AR148407 Sequence
C 75	10.6	62.4	24	6	AX291927	AX291927 Sequence	C 148	9.8	57.6	18	6	AR151758	AR151758 Sequence
C 76	10.6	62.4	24	6	BD003120	BD003120 Method fo	C 149	9.8	57.6	18	6	AR151761	AR151761 Sequence
C 77	10.6	62.4	25	6	AB2665	AB2665 Sequence 10	C 150	9.8	57.6	18	6	AR151763	AR151763 Sequence
C 78	10.4	61.2	19	6	AX106965	AX106965 Sequence	C 151	9.8	57.6	18	6	AR151765	AR151765 Sequence
C 79	10.4	61.2	20	6	AR022549	AR022549 Sequence	C 152	9.8	57.6	18	6	AR151768	AR151768 Sequence
C 80	10.4	61.2	20	6	AR099519	AR099519 Sequence	C 153	9.8	57.6	18	6	AR151770	AR151770 Sequence
C 81	10.4	61.2	20	6	AR099522	AR099522 Sequence	C 154	9.8	57.6	19	6	E34000	E34000 Sequence
C 82	10.4	61.2	20	6	AR124957	AR124957 Sequence	C 155	9.8	57.6	19	6	AR067855	AR067855 Sequence
C 83	10.4	61.2	20	6	AR178800	AR178800 Sequence	C 156	9.8	57.6	19	6	AR168087	AR168087 Sequence
C 84	10.4	61.2	20	6	AR178901	AR178901 Sequence	C 157	9.8	57.6	19	6	AX113345	AX113345 Sequence
C 85	10.4	61.2	20	6	AR10250	AR10250 Sequence	C 158	9.8	57.6	19	6	E08853	E08853 Sequence
C 86	10.4	61.2	20	6	AX139268	AX139268 Sequence	C 159	9.8	57.6	19	6	E09082	E09082 Sequence
C 87	10.4	61.2	20	6	AX095608	AX095608 Sequence	C 160	9.8	57.6	19	6	E09196	E09196 Sequence
C 88	10.4	61.2	21	6	AX395471	AX395471 Sequence	C 161	9.8	57.6	19	6	E09966	E09966 Sequence
C 89	10.4	61.2	21	6	AR201613	AR201613 Sequence	C 162	9.8	57.6	20	6	A65610	A65610 Sequence
C 90	10.4	61.2	24	6	AR100690	AR100690 Sequence	C 163	9.8	57.6	20	6	AR099538	AR099538 Sequence
C 91	10.2	60.0	18	6	AR202731	AR202731 Sequence	C 164	9.8	57.6	20	6	AR125542	AR125542 Sequence
C 92	10.2	60.0	18	6	AR202731	AR202731 Sequence	C 165	9.8	57.6	20	6	AR163993	AR163993 Sequence
C 93	10.2	60.0	20	6	AB3990	AB3990 Sequence 11	C 166	9.8	57.6	20	6	AR178819	AR178819 Sequence
C 94	10.2	60.0	20	6	AR160782	AR160782 Sequence	C 167	9.8	57.6	20	6	AR195428	AR195428 Sequence
C 95	10.2	60.0	20	11	DOGHOX7A	L77310 Canis fam1	C 168	9.8	57.6	20	6	AX019881	AX019881 Sequence
C 96	10.2	60.0	21	6	A62036	A62036 Sequence 22	C 169	9.8	57.6	20	6	AX032776	AX032776 Sequence
C 97	10.2	60.0	21	6	AB3980	AB3980 Sequence 1	C 170	9.8	57.6	20	6	AX07181	AX07181 Sequence
C 98	10.2	60.0	21	6	AR043702	AR043702 Sequence	C 171	9.8	57.6	20	6	AX486784	AX486784 Sequence
C 99	10.2	60.0	21	6	AR043703	AR043703 Sequence	C 172	9.8	57.6	20	6	E05990	E05990 Sequence
C 100	10.2	60.0	21	6	AR177698	AR177698 Sequence	C 173	9.8	57.6	20	6	I15638	I15638 Sequence
C 101	10.2	60.0	23	6	AX067767	AX067767 Sequence	C 174	9.8	57.6	20	6	I21016	I21016 Sequence
C 102	10.2	60.0	24	6	A25687	A25687 GB4 primer.	C 175	9.8	57.6	20	6	I22135	I22135 Sequence
C 103	10.2	60.0	24	6	A25688	A25688 GB3 primer.	C 176	9.8	57.6	21	6	AX004675	AX004675 Sequence
C 104	10.2	60.0	24	6	AR174143	AR174143 Sequence	C 177	9.8	57.6	21	6	AX06806	AX06806 Sequence
C 105	10.2	60.0	24	6	AR174156	AR174156 Sequence	C 178	9.8	57.6	22	6	A61188	A61188 Sequence
C 106	10.2	60.0	24	6	AX444556	AX444556 Sequence	C 179	9.8	57.6	22	6	AR011651	AR011651 Sequence
C 107	10.2	60.0	25	6	I19015	I19015 Sequence 4	C 180	9.8	57.6	22	6	AR038955	AR038955 Sequence
C 108	10.2	58.8	17	6	AR210204	AR210204 Sequence	C 181	9.8	57.6	22	6	AR086389	AR086389 Sequence
C 109	10.2	58.8	17	6	AR210214	AR210214 Sequence	C 182	9.8	57.6	22	6	AR091310	AR091310 Sequence
C 110	10.2	58.8	17	6	AR210226	AR210226 Sequence	C 183	9.8	57.6	22	6	AR099846	AR099846 Sequence
C 111	10.2	58.8	17	6	AR210239	AR210239 Sequence	C 184	9.8	57.6	22	6	AR116918	AR116918 Sequence
C 112	10.2	58.8	17	6	AR210245	AR210245 Sequence	C 185	9.8	57.6	22	6	AR122376	AR122376 Sequence
C 113	10.2	58.8	17	6	AX325481	AX325481 Sequence	C 186	9.8	57.6	22	6	AR123408	AR123408 Sequence
C 114	10.2	58.8	17	6	AX325482	AX325482 Sequence	C 187	9.8	57.6	22	6	AR137691	AR137691 Sequence
C 115	10.2	58.8	17	6	AX325513	AX325513 Sequence	C 188	9.8	57.6	22	6	AR144239	AR144239 Sequence
C 116	10.2	58.8	17	6	AX325514	AX325514 Sequence	C 189	9.8	57.6	22	6	AR156158	AR156158 Sequence
C 117	10.2	58.8	17	6	AX402632	AX402632 Sequence	C 190	9.8	57.6	22	6	AR182535	AR182535 Sequence
C 118	10.2	58.8	17	6	AX402642	AX402642 Sequence	C 191	9.8	57.6	22	6	AR209921	AR209921 Sequence
C 119	10.2	58.8	17	6	AX402654	AX402654 Sequence	C 192	9.8	57.6	22	6	AX04853	AX04853 Sequence
C 120	10.2	58.8	17	6	AX402667	AX402667 Sequence	C 193	9.8	57.6	22	6	I19763	I19763 Sequence
C 121	10.2	58.8	17	6	AX402671	AX402671 Sequence	C 194	9.8	57.6	23	6	AX085392	AX085392 Sequence
C 122	10.2	58.8	17	6	AX402765	AX402765 Sequence	C 195	9.8	57.6	23	6	AF501864	AF501864 Sequence
C 123	10.2	58.8	17	6	AX402827	AX402827 Sequence	C 196	9.8	57.6	24	6	AR084538	AR084538 Sequence
C 124	10.2	58.8	17	6	AX402833	AX402833 Sequence	C 197	9.8	57.6	24	6	AX291275	AX291275 Sequence
C 125	10.2	58.8	17	6	AX402846	AX402846 Sequence	C 198	9.8	57.6	24	6	AX444987	AX444987 Sequence
C 126	10.2	58.8	19	6	AR1430853	AR1430853 Sequence	C 199	9.8	57.6	24	6	AX445056	AX445056 Sequence
C 127	10.2	58.8	19	6	AR143399	AR143399 Sequence	C 200	9.8	57.6	24	6	AX446595	AX446595 Sequence
C 128	10.2	58.8	20	6	AX297463	AX297463 Sequence	C 201	9.8	57.6	25	6	AR150685	AR150685 Sequence
C 129	10.2	58.8	21	6	A23590	A23590 CE gene mut	C 202	9.8	57.6	25	6	AX146521	AX146521 Sequence
C 130	10.2	58.8	21	6	AR210110	AR210110 Sequence	C 203	9.8	57.6	25	6	AX146525	AX146525 Sequence
C 131	10.2	58.8	21	6	AX095303	AX095303 Sequence	C 204	9.8	57.6	25	6	AX343026	AX343026 Sequence
C 132	10.2	58.8	21	6	AX402538	AX402538 Sequence	C 205	9.8	57.6	25	6	E16234	E16234 Sequence
C 133	10.2	58.8	21	6	AX402753	AX402753 Sequence	C 206	9.8	57.6	25	6	E28318	E28318 Sequence
C 134	10.2	58.8	24	6	AX292541	AX292541 Sequence	C 207	9.6	56.5	17	6	AX068305	AX068305 Sequence
C 135	10.2	58.8	24	6	AX292830	AX292830 Sequence	C 208	9.6	56.5	17	6	AX215566	AX215566 Sequence
C 136	10.2	58.8	24	6	AX447327	AX447327 Sequence	C 209	9.6	56.5	17	6	AX216169	AX216169 Sequence
C 137	9.8	57.6	16	6	AX167198	AX167198 Sequence	C 210	9.6	56.5	18	12	AB069250	AB069250 Sequence
C 138	9.8	57.6	17	6	AX262744	AX262744 Sequence	C 211	9.6	56.5	20	6	A70746	A70746 Sequence

C 212	9.6	56.5	20	6	A792310	A792310 Sequence 67	C 285	9.4	55.3	21	6	A62037	A62037 Sequence 23
C 214	9.6	56.5	20	6	AX294055	AX294055 Sequence	C 286	9.4	55.3	21	6	A82588	A82588 Sequence 62
C 215	9.6	56.5	20	6	AX304781	AX304781 Sequence	C 287	9.4	55.3	21	6	AR043692	AR043692 Sequence
C 216	9.6	56.5	20	6	BD003460	BD003460 A gene re	C 288	9.4	55.3	21	6	AR043693	AR043693 Sequence
C 217	9.6	56.5	20	6	E16974	E16974 PCR primer	C 289	9.4	55.3	21	6	AR052430	AR052430 Sequence
C 218	9.6	56.5	21	6	E36640	E36640 DNA and pla	C 290	9.4	55.3	21	6	AR052418	AR052418 Sequence
C 219	9.6	56.5	21	6	AR008056	AR008056 Sequence	C 291	9.4	55.3	21	6	AR027458	AR027458 Sequence
C 220	9.6	56.5	21	6	AX189554	AX189554 Sequence	C 292	9.4	55.3	21	6	AX060726	AX060726 Sequence
C 221	9.6	56.5	21	6	AX487177	AX487177 Sequence	C 293	9.4	55.3	21	6	AX060905	AX060905 Sequence
C 222	9.6	56.5	22	6	I26601	I26601 Sequence 16	C 294	9.4	55.3	21	6	AX092790	AX092790 Sequence
C 223	9.6	56.5	22	6	AR048539	AR048539 Sequence	C 295	9.4	55.3	21	6	AX095984	AX095984 Sequence
C 224	9.6	56.5	22	6	AR075928	AR075928 Sequence	C 296	9.4	55.3	21	6	AX154487	AX154487 Sequence
C 225	9.6	56.5	23	6	AX098393	AX098393 Sequence	C 297	9.4	55.3	22	6	E08381	E08381 PCR primer
C 226	9.6	56.5	23	6	E26379	E26379 Neutralized	C 298	9.4	55.3	22	6	AR029571	AR029571 Sequence
C 227	9.6	56.5	24	6	A44861	A44861 Sequence 2	C 299	9.4	55.3	22	6	AR098524	AR098524 Sequence
C 228	9.6	56.5	24	6	A50950	A50950 Sequence 29	C 300	9.4	55.3	22	6	AR104810	AR104810 Sequence
C 229	9.6	56.5	24	6	A57557	A57557 Sequence 49	C 301	9.4	55.3	22	6	AX441455	AX441455 Sequence
C 230	9.6	56.5	24	6	AR012373	AR012373 Sequence	C 302	9.4	55.3	22	6	AX453951	AX453951 Sequence
C 231	9.6	56.5	24	6	AR052545	AR052545 Sequence	C 303	9.4	55.3	22	6	E08673	E08673 Sequence pr
C 232	9.6	56.5	24	6	AR052991	AR052991 Sequence	C 304	9.4	55.3	22	6	E08674	E08674 Sequence pr
C 233	9.6	56.5	24	6	AR072787	AR072787 Sequence	C 305	9.4	55.3	22	6	I32033	I32033 Sequence 44
C 234	9.6	56.5	24	6	AR134685	AR134685 Sequence	C 306	9.4	55.3	22	6	I32717	I32717 Sequence 44
C 235	9.6	56.5	24	6	AR134691	AR134691 Sequence	C 307	9.4	55.3	22	6	I41484	I41484 Sequence 86
C 236	9.6	56.5	24	6	AR207687	AR207687 Sequence	C 308	9.4	55.3	22	6	I64763	I64763 Sequence 18
C 237	9.6	56.5	24	6	AX205068	AX205068 Sequence	C 309	9.4	55.3	23	6	AX110640	AX110640 Sequence
C 238	9.6	56.5	24	6	AX289422	AX289422 Sequence	C 310	9.4	55.3	23	6	A02544	A02544 Nucleotide
C 239	9.6	56.5	24	6	AX443562	AX443562 Sequence	C 311	9.4	55.3	24	6	AX151751	AX151751 Sequence
C 240	9.6	56.5	24	6	AX445033	AX445033 Sequence	C 312	9.4	55.3	24	6	AX288913	AX288913 Sequence
C 241	9.6	56.5	24	6	AX445520	AX445520 Sequence	C 313	9.4	55.3	24	6	AX291255	AX291255 Sequence
C 242	9.6	56.5	24	6	AX445557	AX445557 Sequence	C 314	9.4	55.3	24	6	AX420107	AX420107 Sequence
C 243	9.6	56.5	24	6	AX446522	AX446522 Sequence	C 315	9.4	55.3	24	6	AX446471	AX446471 Sequence
C 244	9.6	56.5	24	6	AX446741	AX446741 Sequence	C 316	9.4	55.3	24	6	AX446421	AX446421 Sequence
C 245	9.6	56.5	24	6	AX447271	AX447271 Sequence	C 317	9.4	55.3	25	6	AR165421	AR165421 Sequence
C 246	9.6	56.5	24	6	AX447275	AX447275 Sequence	C 318	9.4	55.3	25	6	AR184026	AR184026 Sequence
C 247	9.6	56.5	25	6	E38389	E38389 Transcription	C 319	9.4	55.3	25	6	AX117684	AX117684 Sequence
C 248	9.6	56.5	25	6	AX043212	AX043212 Sequence	C 320	9.4	55.3	25	6	I59883	I59883 Sequence 10
C 249	9.6	56.5	25	6	AX354444	AX354444 Sequence	C 321	9.4	55.3	25	6	I68664	I68664 Sequence 29
C 250	9.6	56.5	25	6	BD005985	BD005985 Sequence	C 322	9.4	55.3	25	6	I68741	I68741 Sequence 10
C 251	9.6	56.5	25	6	BD005992	BD005992 Sequence	C 323	9.4	55.3	25	6	I61582	I61582 Sequence 13
C 252	9.4	55.3	14	6	E16661	E16661 PCR primer	C 324	9.2	54.1	15	6	I61771	I61771 Sequence 32
C 253	9.4	55.3	14	6	A95417	A95417 Sequence 8	C 325	9.2	54.1	15	6	AX281895	AX281895 Sequence
C 254	9.4	55.3	14	6	AX006861	AX006861 Sequence	C 326	9.2	54.1	15	6	AX28060	AX28060 Sequence
C 255	9.4	55.3	14	6	E38194	E38194 Expression	C 327	9.2	54.1	16	6	I31704	I31704 Sequence 12
C 256	9.4	55.3	14	9	HSDMBR41	HSDMBR41 Sequence	C 328	9.2	54.1	16	6	I62230	I62230 Sequence 78
C 257	9.4	55.3	15	6	AR033541	AR033541 Sequence	C 329	9.2	54.1	16	6	AR046812	AR046812 Sequence
C 258	9.4	55.3	15	6	AR113363	AR113363 Sequence	C 330	9.2	54.1	17	6	AR186235	AR186235 Sequence
C 259	9.4	55.3	15	6	AX028319	AX028319 Sequence	C 331	9.2	54.1	17	6	AX265435	AX265435 Sequence
C 260	9.4	55.3	16	6	I57770	I57770 Sequence 30	C 332	9.2	54.1	17	6	AX265436	AX265436 Sequence
C 261	9.4	55.3	16	6	A65527	A65527 Sequence 23	C 333	9.2	54.1	17	6	AX325777	AX325777 Sequence
C 262	9.4	55.3	16	6	A65528	A65528 Sequence 24	C 334	9.2	54.1	17	6	AX325778	AX325778 Sequence
C 263	9.4	55.3	16	6	A65529	A65529 Sequence 25	C 335	9.2	54.1	17	6	AX325813	AX325813 Sequence
C 264	9.4	55.3	17	6	A65530	A65530 Sequence 26	C 336	9.2	54.1	17	6	AX325814	AX325814 Sequence
C 265	9.4	55.3	17	6	AR036945	AR036945 Sequence	C 337	9.2	54.1	17	6	AX325837	AX325837 Sequence
C 266	9.4	55.3	17	6	AR097280	AR097280 Sequence	C 338	9.2	54.1	17	6	I46295	I46295 Sequence 27
C 267	9.4	55.3	18	6	A12953	A12953 Nucleotide	C 339	9.2	54.1	17	6	I53864	I53864 Sequence 16
C 268	9.4	55.3	18	6	AR073377	AR073377 Sequence	C 340	9.2	54.1	17	6	I55130	I55130 Sequence 7
C 269	9.4	55.3	18	6	AR092844	AR092844 Sequence	C 341	9.2	54.1	17	6	I55143	I55143 Sequence 20
C 270	9.4	55.3	18	6	AR162294	AR162294 Sequence	C 342	9.2	54.1	18	6	AR043153	AR043153 Sequence
C 271	9.4	55.3	18	6	AX395468	AX395468 Sequence	C 343	9.2	54.1	18	6	AR074653	AR074653 Sequence
C 272	9.4	55.3	18	6	BD001151	BD001151 Method an	C 344	9.2	54.1	18	6	AX192837	AX192837 Sequence
C 273	9.4	55.3	18	6	BD001580	BD001580 Method an	C 345	9.2	54.1	18	6	AX359695	AX359695 Sequence
C 274	9.4	55.3	19	6	AX130985	AX130985 Sequence	C 346	9.2	54.1	18	6	I32093	I32093 Sequence 37
C 275	9.4	55.3	19	6	AX130986	AX130986 Sequence	C 347	9.2	54.1	19	6	A39750	A39750 Sequence 18
C 276	9.4	55.3	20	6	AR163994	AR163994 Sequence	C 348	9.2	54.1	19	6	AR069641	AR069641 Sequence
C 277	9.4	55.3	20	6	AX104331	AX104331 Sequence	C 349	9.2	54.1	19	6	AR181487	AR181487 Sequence
C 278	9.4	55.3	20	6	AX104665	AX104665 Sequence	C 350	9.2	54.1	19	6	AX035666	AX035666 Sequence
C 279	9.4	55.3	20	6	AX286797	AX286797 Sequence	C 351	9.2	54.1	19	6	AX333163	AX333163 Sequence
C 280	9.4	55.3	20	6	AX293546	AX293546 Sequence	C 352	9.2	54.1	19	6		
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C 284	9.4	55.3	20	6	E07661	E07661 Primer. 9/1	C 356	9.2	54.1	19	6		
							C 357	9.2	54.1	19	6		

C 358	9.2	54.1	19	6	AX363008	Sequence	C 431	9.2	54.1	24	6	AR014502	AR014502 Sequence
C 359	9.2	54.1	19	6	I12792	Sequence 90	432	9.2	54.1	24	6	AR043949	AR043949 Sequence
C 360	9.2	54.1	19	6	I31669	Sequence 20	433	9.2	54.1	24	6	AR049765	AR049765 Sequence
C 361	9.2	54.1	20	6	A27570	Synthetic V	434	9.2	54.1	24	6	AR059319	AR059319 Sequence
C 362	9.2	54.1	20	6	A41627	Sequence 36	435	9.2	54.1	24	6	AR064308	AR064308 Sequence
C 363	9.2	54.1	20	6	A95689	Sequence 36	436	9.2	54.1	24	6	AR073482	AR073482 Sequence
C 364	9.2	54.1	20	6	A95731	Sequence 36	437	9.2	54.1	24	6	AR140041	AR140041 Sequence
C 365	9.2	54.1	20	6	A95773	Sequence 36	438	9.2	54.1	24	6	AR149659	AR149659 Sequence
C 366	9.2	54.1	20	6	A95815	Sequence 36	439	9.2	54.1	24	6	AX022076	AX022076 Sequence
C 367	9.2	54.1	20	6	AR011624	Sequence	440	9.2	54.1	24	6	AX034803	AX034803 Sequence
C 368	9.2	54.1	20	6	AR095585	Sequence	441	9.2	54.1	24	6	AX068393	AX068393 Sequence
C 369	9.2	54.1	20	6	AR116306	Sequence	442	9.2	54.1	24	6	AX110631	AX110631 Sequence
C 370	9.2	54.1	20	6	AR129668	Sequence	443	9.2	54.1	24	6	AX288795	AX288795 Sequence
C 371	9.2	54.1	20	6	AR206657	Sequence	444	9.2	54.1	24	6	AX289167	AX289167 Sequence
C 372	9.2	54.1	20	6	AX024024	Sequence	445	9.2	54.1	24	6	AX289369	AX289369 Sequence
C 373	9.2	54.1	20	6	AX024026	Sequence	446	9.2	54.1	24	6	AX289476	AX289476 Sequence
C 374	9.2	54.1	20	6	AX078028	Sequence	447	9.2	54.1	24	6	AX289926	AX289926 Sequence
C 375	9.2	54.1	20	6	AX110091	Sequence	448	9.2	54.1	24	6	AX289987	AX289987 Sequence
C 376	9.2	54.1	20	6	AX180914	Sequence	449	9.2	54.1	24	6	AX290002	AX290002 Sequence
C 377	9.2	54.1	20	6	AX180935	Sequence	450	9.2	54.1	24	6	AX290145	AX290145 Sequence
C 378	9.2	54.1	20	6	AX180938	Sequence	451	9.2	54.1	24	6	AX290561	AX290561 Sequence
C 379	9.2	54.1	20	6	AX293428	Sequence	452	9.2	54.1	24	6	AX291385	AX291385 Sequence
C 380	9.2	54.1	20	6	AX294002	Sequence	453	9.2	54.1	24	6	AX291960	AX291960 Sequence
C 381	9.2	54.1	20	6	AX294559	Sequence	454	9.2	54.1	24	6	AX292670	AX292670 Sequence
C 382	9.2	54.1	20	6	AX294620	Sequence	455	9.2	54.1	24	6	AX427972	AX427972 Sequence
C 383	9.2	54.1	20	6	AX294635	Sequence	456	9.2	54.1	24	6	AX443563	AX443563 Sequence
C 384	9.2	54.1	20	6	AX295194	Sequence	457	9.2	54.1	24	6	AX444394	AX444394 Sequence
C 385	9.2	54.1	20	6	AX296018	Sequence	458	9.2	54.1	24	6	AX444452	AX444452 Sequence
C 386	9.2	54.1	20	6	AX296650	Sequence	459	9.2	54.1	24	6	AX445298	AX445298 Sequence
C 387	9.2	54.1	20	6	AX296693	Sequence	460	9.2	54.1	24	6	AX445654	AX445654 Sequence
C 388	9.2	54.1	20	6	AX297303	Sequence	461	9.2	54.1	24	6	E13471	E13471 PCR primer
C 389	9.2	54.1	20	6	AX297703	Sequence	462	9.2	54.1	24	6	E14778	E14778 PCR primer
C 390	9.2	54.1	20	6	AX298400	Sequence	463	9.2	54.1	24	6	I64744	I64744 Sequence 40
C 391	9.2	54.1	20	6	AX323496	Sequence	464	9.2	54.1	24	6	I93353	I93353 Sequence 23
C 392	9.2	54.1	20	6	AX488467	Sequence	465	9.2	54.1	24	6	AR003742	AR003742 Sequence
C 393	9.2	54.1	20	6	AX488474	Sequence	466	9.2	54.1	24	6	HSAR010620	HSAR010620 Homo sapi
C 394	9.2	54.1	20	6	E03199	Sequence	467	9.2	54.1	25	6	AR010078	AR010078 Sequence
C 395	9.2	54.1	20	6	E03465	Sequence	468	9.2	54.1	25	6	AR055284	AR055284 Sequence
C 396	9.2	54.1	20	6	E03483	Sequence	469	9.2	54.1	25	6	AR067218	AR067218 Sequence
C 397	9.2	54.1	20	6	E09681	Sequence	470	9.2	54.1	25	6	AR141213	AR141213 Sequence
C 398	9.2	54.1	20	6	I12791	Sequence 89	471	9.2	54.1	25	6	AR141450	AR141450 Sequence
C 399	9.2	54.1	20	6	I44662	Sequence 20	472	9.2	54.1	25	6	AR198475	AR198475 Sequence
C 400	9.2	54.1	21	6	A04389	Sequence	473	9.2	54.1	25	6	AR198476	AR198476 Sequence
C 401	9.2	54.1	21	6	A04404	Oligonucleo	474	9.2	54.1	25	6	AX041987	AX041987 Sequence
C 402	9.2	54.1	21	6	AR070170	Sequence	475	9.2	54.1	25	6	AX042741	AX042741 Sequence
C 403	9.2	54.1	21	6	AR101968	Sequence	476	9.2	54.1	25	6	AX042821	AX042821 Sequence
C 404	9.2	54.1	21	6	AR120065	Sequence	477	9.2	54.1	25	6	AX043053	AX043053 Sequence
C 405	9.2	54.1	21	6	AX026695	Sequence	478	9.2	54.1	25	6	AX043503	AX043503 Sequence
C 406	9.2	54.1	21	6	AX099870	Sequence	479	9.2	54.1	25	6	AX447547	AX447547 Sequence
C 407	9.2	54.1	21	6	AX137890	Sequence	480	9.2	54.1	25	6	AX468828	AX468828 Sequence
C 408	9.2	54.1	21	6	AX453963	Sequence	481	9.2	54.1	25	6	E07091	E07091 Probe for H
C 409	9.2	54.1	21	6	I13861	Sequence 69	482	9.2	54.1	25	6	I11922	I11922 Sequence 32
C 410	9.2	54.1	21	6	I21374	Sequence 2	483	9.2	54.1	25	6	I140495	I140495 Sequence 32
C 411	9.2	54.1	22	10	MUSTCGXAU	Mouse T-cell	484	9.2	52.9	10	6	AX152950	AX152950 Sequence
C 412	9.2	54.1	22	6	A05406	Synthetic C	485	9.2	52.9	10	6	AX301579	AX301579 Sequence
C 413	9.2	54.1	22	6	A09613	Oligonucleo	486	9.2	52.9	16	6	AR035144	AR035144 Sequence
C 414	9.2	54.1	22	6	A59549	Sequence 2	487	9.2	52.9	16	6	AX471987	AX471987 Sequence
C 415	9.2	54.1	22	6	A82431	Sequence 19	488	9.2	52.9	17	6	AR046594	AR046594 Sequence
C 416	9.2	54.1	22	6	AR050946	Sequence	489	9.2	52.9	17	6	AX149100	AX149100 Sequence
C 417	9.2	54.1	22	6	AR128112	Sequence	490	9.2	52.9	17	6	AX132547	AX132547 Sequence
C 418	9.2	54.1	22	6	AR139493	Sequence	491	9.2	52.9	17	6	AX325478	AX325478 Sequence
C 419	9.2	54.1	22	6	AR139555	Sequence	492	9.2	52.9	17	6	AX325509	AX325509 Sequence
C 420	9.2	54.1	22	6	AX241171	Sequence	493	9.2	52.9	17	6	AX325510	AX325510 Sequence
C 421	9.2	54.1	22	6	AX486723	Sequence	494	9.2	52.9	17	6	AX391478	AX391478 Sequence
C 422	9.2	54.1	22	6	I34829	Sequence 22	495	9.2	52.9	17	6	AX394765	AX394765 Sequence
C 423	9.2	54.1	22	6	I51747	Sequence 15	496	9.2	52.9	17	6	AX394796	AX394796 Sequence
C 424	9.2	54.1	23	6	A39752	Sequence 20	497	9.2	52.9	17	6	AX475780	AX475780 Sequence
C 425	9.2	54.1	23	6	A86795	Sequence 6	498	9.2	52.9	17	6	I53645	I53645 Sequence 13
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C 427	9.2	54.1	23	6	AR166577	Sequence	500	9.2	52.9	18	6	A70809	A70809 Sequence 13
C 428	9.2	54.1	23	6	AX029245	Sequence	501	9.2	52.9	18	6	A79293	A79293 Sequence 13
C 429	9.2	54.1	23	6	AX039721	Sequence	502	9.2	52.9	18	6	A79293	A79293 Sequence 13
C 430	9.2	54.1	23	6	I31671	Sequence 22	503	9.2	52.9	18	6	A79718	A79718 Sequence 14

C 504	9	52.9	18	6	AR112300	AR113300 Sequence	C 577	9	52.9	24	6	AX288473	AX288473 Sequence
C 505	9	52.9	18	6	AR203563	AR203563 Sequence	C 578	9	52.9	24	6	AX288561	AX288561 Sequence
C 506	9	52.9	18	6	AX428585	AX428585 Sequence	C 579	9	52.9	24	6	AX289357	AX289357 Sequence
C 507	9	52.9	18	6	BD003523	BD003523 A gene re	C 580	9	52.9	24	6	AX289603	AX289603 Sequence
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C 509	9	52.9	19	6	A61201	A61201 Sequence 38	C 582	9	52.9	24	6	AX290438	AX290438 Sequence
C 510	9	52.9	19	6	AR076583	AR076583 Sequence	C 583	9	52.9	24	6	AX290642	AX290642 Sequence
C 511	9	52.9	19	6	AR076585	AR076585 Sequence	C 584	9	52.9	24	6	AX290937	AX290937 Sequence
C 512	9	52.9	19	6	AX359802	AX359802 Sequence	C 585	9	52.9	24	6	AX291263	AX291263 Sequence
C 513	9	52.9	19	6	AX472012	AX472012 Sequence	C 586	9	52.9	24	6	AX292188	AX292188 Sequence
C 514	9	52.9	20	6	A58995	A58995 Sequence 3	C 587	9	52.9	24	6	AX342202	AX342202 Sequence
C 515	9	52.9	20	6	AR023994	AR023994 Sequence	C 588	9	52.9	24	6	AX343612	AX343612 Sequence
C 516	9	52.9	20	6	AR089470	AR089470 Sequence	C 589	9	52.9	24	6	AX444222	AX444222 Sequence
C 517	9	52.9	20	6	AR116524	AR116524 Sequence	C 590	9	52.9	24	6	AX444724	AX444724 Sequence
C 518	9	52.9	20	6	AR167955	AR167955 Sequence	C 591	9	52.9	24	6	AX445018	AX445018 Sequence
C 519	9	52.9	20	6	AX066405	AX066405 Sequence	C 592	9	52.9	24	6	AX445187	AX445187 Sequence
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C 522	9	52.9	20	6	AX148927	AX148927 Sequence	C 595	9	52.9	24	6	AX445877	AX445877 Sequence
C 523	9	52.9	20	6	AX148928	AX148928 Sequence	C 596	9	52.9	24	6	AX445912	AX445912 Sequence
C 524	9	52.9	20	6	AX293106	AX293106 Sequence	C 597	9	52.9	24	6	AX445950	AX445950 Sequence
C 525	9	52.9	20	6	AX293194	AX293194 Sequence	C 598	9	52.9	24	6	AX446476	AX446476 Sequence
C 526	9	52.9	20	6	AX293990	AX293990 Sequence	C 599	9	52.9	24	6	AX447473	AX447473 Sequence
C 527	9	52.9	20	6	AX294236	AX294236 Sequence	C 600	9	52.9	24	6	AX488489	AX488489 Sequence
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C 529	9	52.9	20	6	AX295071	AX295071 Sequence	C 602	9	52.9	24	6	BD011176	BD011176 Human tel
C 530	9	52.9	20	6	AX295570	AX295570 Sequence	C 603	9	52.9	24	6	E36925	E36925 Human telom
C 531	9	52.9	20	6	AX295886	AX295886 Sequence	C 604	9	52.9	24	6	I30971	I30971 Sequence 3
C 532	9	52.9	20	6	AX296821	AX296821 Sequence	C 605	9	52.9	24	6	I30975	I30975 Sequence 7
C 533	9	52.9	20	6	AX297174	AX297174 Sequence	C 606	9	52.9	24	6	I30978	I30978 Sequence 10
C 534	9	52.9	20	6	AX298864	AX298864 Sequence	C 607	9	52.9	24	6	I30981	I30981 Sequence 13
C 535	9	52.9	20	6	AX356929	AX356929 Sequence	C 608	9	52.9	24	6	I30987	I30987 Sequence 19
C 536	9	52.9	20	6	AX351246	AX351246 Sequence	C 609	9	52.9	24	6	I30987	I30987 Sequence 19
C 537	9	52.9	20	6	E36214	E36214 Japanese cl	C 610	9	52.9	24	10	MUSTCGXAP	M59524 Mouse T-cell
C 538	9	52.9	20	6	E36214	E36214 Japanese cl	C 611	9	52.9	24	13	AX031455	AX031455 Sequence
C 539	9	52.9	20	6	E36877	E36877 Chimeric an	C 612	9	52.9	24	13	AX031462	AX031462 Sequence
C 540	9	52.9	20	6	E36877	E36877 Chimeric an	C 613	9	52.9	24	13	AX031465	AX031465 Sequence
C 541	9	52.9	20	12	AB069027	AB069027 Synthetic	C 614	9	52.9	24	13	AX031471	AX031471 Sequence
C 542	9	52.9	21	6	AR031457	AR031457 Sequence	C 615	9	52.9	25	6	A57005	A57005 Sequence 5
C 543	9	52.9	21	6	AR112754	AR112754 Sequence	C 616	9	52.9	25	6	AR084194	AR084194 Sequence
C 544	9	52.9	21	6	AR118869	AR118869 Sequence	C 617	9	52.9	25	6	AR085004	AR085004 Sequence
C 545	9	52.9	21	6	AR162648	AR162648 Sequence	C 618	9	52.9	25	6	AR090657	AR090657 Sequence
C 546	9	52.9	21	6	AX006711	AX006711 Sequence	C 619	9	52.9	25	6	AR141420	AR141420 Sequence
C 547	9	52.9	21	6	AX094960	AX094960 Sequence	C 620	9	52.9	25	6	AR197692	AR197692 Sequence
C 548	9	52.9	21	6	AX095231	AX095231 Sequence	C 621	9	52.9	25	6	AX077734	AX077734 Sequence
C 549	9	52.9	21	6	AX095841	AX095841 Sequence	C 622	9	52.9	25	6	AX133809	AX133809 Sequence
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C 553	9	52.9	22	6	A08339	A08339 Oligonucleo	C 626	9	52.9	25	6	AX278991	AX278991 Sequence
C 554	9	52.9	22	6	AR179906	AR179906 Sequence	C 627	9	52.9	25	6	AX279123	AX279123 Sequence
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C 556	9	52.9	22	6	I46957	I46957 Sequence 50	C 629	9	52.9	25	6	AX448188	AX448188 Sequence
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C 558	9	52.9	23	6	AR043240	AR043240 Sequence	C 631	9	52.9	25	6	AX476758	AX476758 Sequence
C 559	9	52.9	23	6	AR074895	AR074895 Sequence	C 632	9	52.9	25	6	AX476759	AX476759 Sequence
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C 561	9	52.9	23	6	AR197776	AR197776 Sequence	C 634	9	52.9	25	6	AX476761	AX476761 Sequence
C 562	9	52.9	23	6	AX082174	AX082174 Sequence	C 635	9	52.9	25	6	AX476762	AX476762 Sequence
C 563	9	52.9	23	6	I82091	I82091 Sequence 28	C 636	9	52.9	25	6	AX476763	AX476763 Sequence
C 564	9	52.9	24	6	A62489	A62489 Sequence 4	C 637	9	52.9	25	6	AX476764	AX476764 Sequence
C 565	9	52.9	24	6	AR035632	AR035632 Sequence	C 638	9	52.9	25	6	AX476765	AX476765 Sequence
C 566	9	52.9	24	6	AR091182	AR091182 Sequence	C 639	9	52.9	25	6	E12501	E12501 Primer. 4/1
C 567	9	52.9	24	6	AR174261	AR174261 Sequence	C 640	9	52.9	25	6	E15861	E15861 PCR primer
C 568	9	52.9	24	6	AR198217	AR198217 Sequence	C 641	9	52.9	25	6	E31897	E31897 Method for
C 569	9	52.9	24	6	AR208336	AR208336 Sequence	C 642	9	52.9	25	6	E34109	E34109 Protein par
C 570	9	52.9	24	6	AX031345	AX031345 Sequence	C 643	9	52.9	25	12	SYNANVAN	ME0083 Avian neovl
C 571	9	52.9	24	6	AX031349	AX031349 Sequence	C 644	9	51.8	12	6	A46084	A46084 Sequence 9
C 572	9	52.9	24	6	AX031352	AX031352 Sequence	C 645	9	51.8	12	6	AR027677	AR027677 Sequence
C 573	9	52.9	24	6	AX031355	AX031355 Sequence	C 646	9	51.8	13	6	A89148	A89148 Sequence 12
C 574	9	52.9	24	6	AX031361	AX031361 Sequence	C 647	9	51.8	14	6	AR148601	AR148601 Sequence
C 575	9	52.9	24	6	AX060697	AX060697 Sequence	C 648	9	51.8	14	6	AX358009	AX358009 Sequence
C 576	9	52.9	24	6	AX288378	AX288378 Sequence	C 649	9	51.8	14	6	I46934	I46934 Sequence 27

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662	8.8	51.8	16	6	AF480515	AF480515 Homo sapi	735	8.8	51.8	20	6	E07135	E07135 Primer: 9/1
663	8.8	51.8	16	9	AF480515	AF480515 Homo sapi	736	8.8	51.8	20	6	E08654	E08654 PCR primer
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666	8.8	51.8	17	6	A66943	A66943 Sequence 11	739	8.8	51.8	20	6	E17268	E17268 Primer: 7/1
667	8.8	51.8	17	6	A67043	A67043 Sequence 21	740	8.8	51.8	20	6	E38874	E38874 Chimeric an
668	8.8	51.8	17	6	A67045	A67045 Sequence 21	741	8.8	51.8	20	6	E49528	E49528 Antisense o
669	8.8	51.8	17	6	AX325781	AX325781 Sequence	742	8.8	51.8	20	6	E49528	E49528 Antisense o
670	8.8	51.8	17	6	AX325782	AX325782 Sequence	743	8.8	51.8	20	6	E115430	E115430 Sequence 5
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672	8.8	51.8	17	6	AX325818	AX325818 Sequence	745	8.8	51.8	20	6	E125858	E125858 Sequence 18
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674	8.8	51.8	17	6	AX325842	AX325842 Sequence	747	8.8	51.8	20	6	E143495	E143495 Sequence 2
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678	8.8	51.8	18	6	A61308	A61308 Sequence 45	751	8.8	51.8	21	6	A07666	A07666 Oligonucleo
679	8.8	51.8	18	6	A67046	A67046 Sequence 21	752	8.8	51.8	21	6	A30577	A30577 Synthetic m
680	8.8	51.8	18	6	AR034582	AR034582 Sequence	753	8.8	51.8	21	6	AR022540	AR022540 Sequence
681	8.8	51.8	18	6	AR036933	AR036933 Sequence	754	8.8	51.8	21	6	AR099913	AR099913 Sequence
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692	8.8	51.8	18	6	AX269666	AX269666 Sequence	765	8.8	51.8	21	6	AX486897	AX486897 Sequence
693	8.8	51.8	18	6	AX326551	AX326551 Sequence	766	8.8	51.8	21	6	E65332	E65332 Sequence 11
694	8.8	51.8	18	6	AX375732	AX375732 Sequence	767	8.8	51.8	22	6	A61184	A61184 Sequence 21
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697	8.8	51.8	19	6	AX000014	AX000014 Sequence	770	8.8	51.8	22	6	AR072349	AR072349 Sequence
698	8.8	51.8	19	6	AX113134	AX113134 Sequence	771	8.8	51.8	22	6	AR079339	AR079339 Sequence
699	8.8	51.8	19	6	AX113144	AX113144 Sequence	772	8.8	51.8	22	6	AR091305	AR091305 Sequence
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701	8.8	51.8	20	6	A26505	A26505 PROBE-10K o	774	8.8	51.8	22	6	AR123403	AR123403 Sequence
702	8.8	51.8	20	6	A27552	A27552 Synthetic V	775	8.8	51.8	22	6	AR123407	AR123407 Sequence
703	8.8	51.8	20	6	A42583	A42583 Sequence 10	776	8.8	51.8	22	6	AR137686	AR137686 Sequence
704	8.8	51.8	20	6	A61373	A61373 Sequence 13	777	8.8	51.8	22	6	AR137686	AR137686 Sequence
705	8.8	51.8	20	6	A72430	A72430 Sequence 17	778	8.8	51.8	22	6	AR137690	AR137690 Sequence
706	8.8	51.8	20	6	A80140	A80140 Sequence 17	779	8.8	51.8	22	6	AR153784	AR153784 Sequence
707	8.8	51.8	20	6	A84809	A84809 Sequence 4	780	8.8	51.8	22	6	AR156147	AR156147 Sequence
708	8.8	51.8	20	6	A88772	A88772 Sequence 92	781	8.8	51.8	22	6	AX076901	AX076901 Sequence
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710	8.8	51.8	20	6	AR035579	AR035579 Sequence	783	8.8	51.8	22	6	AX147937	AX147937 Sequence
711	8.8	51.8	20	6	AR035644	AR035644 Sequence	784	8.8	51.8	22	6	AX188743	AX188743 Sequence
712	8.8	51.8	20	6	AR060630	AR060630 Sequence	785	8.8	51.8	22	6	AX201336	AX201336 Sequence
713	8.8	51.8	20	6	AR067069	AR067069 Sequence	786	8.8	51.8	22	6	AX230276	AX230276 Sequence
714	8.8	51.8	20	6	AR073949	AR073949 Sequence	787	8.8	51.8	22	6	AX342710	AX342710 Sequence
715	8.8	51.8	20	6	AR080641	AR080641 Sequence	788	8.8	51.8	22	6	AX358017	AX358017 Sequence
716	8.8	51.8	20	6	AR117670	AR117670 Sequence	789	8.8	51.8	22	6	BD011744	BD011744 795, a no
717	8.8	51.8	20	6	AR160722	AR160722 Sequence	790	8.8	51.8	22	6	E121377	E121377 Sequence 5
718	8.8	51.8	20	6	AR163960	AR163960 Sequence	791	8.8	51.8	22	6	E126460	E126460 Sequence 15
719	8.8	51.8	20	6	AR172974	AR172974 Sequence	792	8.8	51.8	22	9	AF480527	AF480527 Homo sapi
720	8.8	51.8	20	6	AR175939	AR175939 Sequence	793	8.8	51.8	22	9	HS4421744	HS4421744 Homo sapi
721	8.8	51.8	20	6	AX007260	AX007260 Sequence	794	8.8	51.8	22	9	HS4421745	HS4421745 Homo sapi
722	8.8	51.8	20	6	AX018940	AX018940 Sequence	795	8.8	51.8	22	10	MMU459715	MMU459715 Mus muscu

796	8.8	51.8	22	23	Bd007696																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										
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942 8.6 50.6 21 6 AR11126 Sequence
943 8.6 50.6 21 6 AR123012 Sequence
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945 8.6 50.6 21 6 AR160932 Sequence
946 8.6 50.6 21 6 AX004426 Sequence
947 8.6 50.6 21 6 AX022063 Sequence
948 8.6 50.6 21 6 AX096704 Sequence
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950 8.6 50.6 21 6 AX097307 Sequence
951 8.6 50.6 21 6 AX375726 Sequence
952 8.6 50.6 21 6 AX375727 Sequence
953 8.6 50.6 21 6 E21986
954 8.6 50.6 21 6 E26005
955 8.6 50.6 21 6 E29435
956 8.6 50.6 21 6 I75042
957 8.6 50.6 21 6 I93340
958 8.6 50.6 21 8 PTRRND04
959 8.6 50.6 22 6 A09899
960 8.6 50.6 22 6 A47993
961 8.6 50.6 22 6 A86783
962 8.6 50.6 22 6 AR019664
963 8.6 50.6 22 6 AR030176
964 8.6 50.6 22 6 AR080244
965 8.6 50.6 22 6 AR093695
966 8.6 50.6 22 6 AR128062
967 8.6 50.6 22 6 AR177038
968 8.6 50.6 22 6 AR181077
969 8.6 50.6 22 6 AR210070
970 8.6 50.6 22 6 AX011595
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974 8.6 50.6 22 6 AX098591
975 8.6 50.6 22 6 AX191001
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977 8.6 50.6 22 6 AX375728
978 8.6 50.6 22 6 E06853
979 8.6 50.6 22 6 I12812
980 8.6 50.6 22 6 I30875
981 8.6 50.6 22 6 I30876
982 8.6 50.6 22 6 I46334
983 8.6 50.6 22 6 I46335
984 8.6 50.6 22 6 I88037
985 8.6 50.6 23 6 A80535
986 8.6 50.6 23 6 AR026776
987 8.6 50.6 23 6 AR049202
988 8.6 50.6 23 6 AR065460
989 8.6 50.6 23 6 AR069859
990 8.6 50.6 23 6 AX023932
991 8.6 50.6 23 6 AX046193
992 8.6 50.6 23 6 AX076940
993 8.6 50.6 23 6 AX253407
994 8.6 50.6 23 6 AX278690
995 8.6 50.6 23 6 AX403785
996 8.6 50.6 23 6 AX468808
997 8.6 50.6 23 6 E33021
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999 8.6 50.6 24 6 AR000509
1000 8.6 50.6 24 6 AR059918

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ALIGNMENTS

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RESULT 1
LOCUS AX402771/c 22 bp DNA linear PAT 07-JUN-2002
DEFINITION Sequence 255 from Patent WO0196612.
ACCESSION AX402771
VERSION AX402771.1 GI:21387762
KEYWORDS Aspergillus sclerotiorum.
SOURCE Aspergillus sclerotiorum.
ORGANISM Aspergillus sclerotiorum

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REFERENCE
AUTHORS Haugland,R. and Vesper,S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: WO 0196612-A 255 20-DEC-2001;
UNITED STATES ENVIRONMENTAL PROTECTION AGENCY (US)
FEATURES
SOURCE 1. .22
/organism="Aspergillus sclerotiorum"
/db_xref="taxon:138282"
BASE COUNT 7 a 8 c 6 g 1 t
ORIGIN
Query Match 82.4%; Score 14; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 GTTGCTTCGGCGG 14
14 GTTGCTTCGGCGG 1

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RESULT 2
LOCUS AX402778/c 22 bp DNA linear PAT 07-JUN-2002
DEFINITION Sequence 262 from Patent WO0196612.
ACCESSION AX402778
VERSION AX402778.1 GI:21387769
KEYWORDS Aspergillus wentii.
SOURCE Aspergillus wentii.
ORGANISM Aspergillus wentii.
REFERENCE
AUTHORS Haugland,R. and Vesper,S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: WO 0196612-A 262 20-DEC-2001;
UNITED STATES ENVIRONMENTAL PROTECTION AGENCY (US)
FEATURES
SOURCE 1. .22
/organism="Aspergillus wentii"
/db_xref="taxon:5066"
BASE COUNT 7 a 8 c 6 g 1 t
ORIGIN
Query Match 82.4%; Score 14; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 GTTGCTTCGGCGG 14
14 GTTGCTTCGGCGG 1

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RESULT 3
LOCUS AX402921/c 22 bp DNA linear PAT 07-JUN-2002
DEFINITION Sequence 405 from Patent WO0196612.
ACCESSION AX402921
VERSION AX402921.1 GI:21387912
KEYWORDS Aspergillus auricomus.
SOURCE Aspergillus auricomus.
ORGANISM Aspergillus auricomus
REFERENCE
AUTHORS Haugland,R. and Vesper,S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: WO 0196612-A 405 20-DEC-2001;
UNITED STATES ENVIRONMENTAL PROTECTION AGENCY (US)
FEATURES
SOURCE 1. .22
Location/Qualifiers

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BASE COUNT /organism="Aspergillus auricomus"
ORIGIN 7 a 8 c 6 g 1 t

Query Match 82.4%; Score 14; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGGG 14
14 GTTGCTTCGGCGGG 1

RESULT 4
AX402757 16 bp DNA linear PAT 07-JUN-2002
LOCUS Sequence 241 from Patent WO0196612.
ACCESSION AX402757
VERSION AX402757.1 GI:21387748
KEYWORDS
SOURCE Aspergillus flavipes.
ORGANISM Aspergillus flavipes.
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
TITLE Haugland, R. and Vesper, S.
JOURNAL Method of identifying and quantifying specific fungi and bacteria
PATENT: WO 0196612-A 241 20-DEC-2001;
UNITED STATES ENVIRONMENTAL PROTECTION AGENCY (US)
FEATURES
source Location/Qualifiers
1.16
/organism="Aspergillus flavipes"
/db_xref="taxon:41900"

BASE COUNT 0 a 6 c 6 g 4 t
ORIGIN

Query Match 76.5%; Score 13; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTGCTTCGGCGGG 14
1 TTGCTTCGGCGGG 13

RESULT 5
AX402760 16 bp DNA linear PAT 07-JUN-2002
LOCUS Sequence 244 from Patent WO0196612.
ACCESSION AX402760
VERSION AX402760.1 GI:21387751
KEYWORDS
SOURCE Fennellia nivea.
ORGANISM Fennellia nivea.
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
TITLE Haugland, R. and Vesper, S.
JOURNAL Method of identifying and quantifying specific fungi and bacteria
PATENT: WO 0196612-A 244 20-DEC-2001;
UNITED STATES ENVIRONMENTAL PROTECTION AGENCY (US)
FEATURES
source Location/Qualifiers
1.16
/organism="Fennellia nivea"
/db_xref="taxon:41281"

BASE COUNT 0 a 6 c 6 g 4 t
ORIGIN

Query Match 76.5%; Score 13; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTGCTTCGGCGGG 14
1 TTGCTTCGGCGGG 13

RESULT 6
AX402744 23 bp DNA linear PAT 07-JUN-2002
LOCUS Sequence 228 from Patent WO0196612.
ACCESSION AX402744
VERSION AX402744.1 GI:21387735
KEYWORDS
SOURCE Aspergillus caespitosus.
ORGANISM Aspergillus caespitosus.
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
TITLE Haugland, R. and Vesper, S.
JOURNAL Method of identifying and quantifying specific fungi and bacteria
PATENT: WO 0196612-A 228 20-DEC-2001;
UNITED STATES ENVIRONMENTAL PROTECTION AGENCY (US)
FEATURES
source Location/Qualifiers
1.23
/organism="Aspergillus caespitosus"
/db_xref="taxon:176165"

BASE COUNT 3 a 7 c 8 g 5 t
ORIGIN

Query Match 75.3%; Score 12.8; DB 6; Length 23;
Best Local Similarity 87.5%; Pred. No. 2.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGGAA 16
5 GTTGCTTCGGCGGAGA 20

RESULT 7
AX402775 23 bp DNA linear PAT 07-JUN-2002
LOCUS Sequence 259 from Patent WO0196612.
ACCESSION AX402775
VERSION AX402775.1 GI:21387766
KEYWORDS
SOURCE Aspergillus unguis.
ORGANISM Aspergillus unguis.
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
TITLE Haugland, R. and Vesper, S.
JOURNAL Method of identifying and quantifying specific fungi and bacteria
PATENT: WO 0196612-A 259 20-DEC-2001;
UNITED STATES ENVIRONMENTAL PROTECTION AGENCY (US)
FEATURES
source Location/Qualifiers
1.23
/organism="Aspergillus unguis"
/db_xref="taxon:40381"

BASE COUNT 3 a 7 c 8 g 5 t
ORIGIN

Query Match 75.3%; Score 12.8; DB 6; Length 23;
Best Local Similarity 87.5%; Pred. No. 2.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGGAA 16
5 GTTGCTTCGGCGGAGA 20

RESULT 8
AR210283 15 bp DNA linear PAT 20-JUN-2002
LOCUS Sequence 195 from patent US 6387652.

ACCESSION AR210283
VERSION AR210283.1 GI:21512474
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Haugland,R. and Vesper,S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: US 6387652-A 195 14-MAY-2002;
FEATURES
source
1.15
/organism="unknown"
BASE COUNT 1 a 4 c 6 g 4 t
ORIGIN

Query Match 72.9%; Score 12.4; DB 6; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.9e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTGCTTCGGCGGGA 15
1 TTGCTTCGGCGGGA 14

RESULT 9
AX402711 15 bp DNA linear PAT 07-JUN-2002
LOCUS Sequence 195 from Patent WO0196612.
ACCESSION AX402711
VERSION AX402711.1 GI:21387702
KEYWORDS
SOURCE Trichoderma harzianum.
ORGANISM Trichoderma harzianum.
REFERENCE 1 (bases 1 to 15)
AUTHORS Haugland,R. and Vesper,S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: WO 0196612-A 195 20-DEC-2001;
FEATURES
source
1.15
/organism="Trichoderma harzianum"
/db_xref="taxon:5544"
BASE COUNT 1 a 4 c 6 g 4 t
ORIGIN

Query Match 72.9%; Score 12.4; DB 6; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.9e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTGCTTCGGCGGGA 15
1 TTGCTTCGGCGGGA 14

RESULT 10
AX402941 16 bp DNA linear PAT 07-JUN-2002
LOCUS Sequence 425 from Patent WO0196612.
ACCESSION AX402941
VERSION AX402941.1 GI:21387932
KEYWORDS
SOURCE Penicillium expansum.
ORGANISM Penicillium expansum.
REFERENCE 1 (bases 1 to 21)
AUTHORS Haugland,R. and Vesper,S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: WO 0196612-A 425 20-DEC-2001;
FEATURES
source
1.21
/organism="Penicillium expansum"
/db_xref="taxon:27334"
BASE COUNT 3 a 7 c 5 g 1 t
ORIGIN

Query Match 72.9%; Score 12.4; DB 6; Length 16;
Best Local Similarity 92.9%; Pred. No. 4e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGG 14
8 GTTGCTTCGGCGG 21

RESULT 11
AR210279 21 bp DNA linear PAT 20-JUN-2002
LOCUS Sequence 191 from patent US 6387652.
ACCESSION AR210279
VERSION AR210279.1 GI:21512469
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Haugland,R. and Vesper,S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: US 6387652-A 191 14-MAY-2002;
FEATURES
source
1.21
/organism="unknown"
BASE COUNT 3 a 7 c 7 g 4 t
ORIGIN

Query Match 72.9%; Score 12.4; DB 6; Length 21;
Best Local Similarity 92.9%; Pred. No. 4e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGG 14
8 GTTGCTTCGGCGG 21

RESULT 12
AR210282 21 bp DNA linear PAT 20-JUN-2002
LOCUS Sequence 194 from patent US 6387652.
ACCESSION AR210282
VERSION AR210282.1 GI:21512472
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Haugland,R. and Vesper,S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: US 6387652-A 194 14-MAY-2002;
FEATURES
source
1.21
/organism="unknown"
BASE COUNT 3 a 7 c 7 g 4 t
ORIGIN

Query Match 72.9%; Score 12.4; DB 6; Length 21;
Best Local Similarity 92.9%; Pred. No. 4e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGG 14
8 GTTGCTTCGGCGG 21

FEATURES
source
1.16
/organism="Penicillium expansum"
/db_xref="taxon:27334"
BASE COUNT 3 a 7 c 5 g 1 t
ORIGIN

Query Match 72.9%; Score 12.4; DB 6; Length 16;
Best Local Similarity 92.9%; Pred. No. 3.9e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGG 14
15 GTTGCTTCGGCGG 2

RESULT 11
AR210279 21 bp DNA linear PAT 20-JUN-2002
LOCUS Sequence 191 from patent US 6387652.
ACCESSION AR210279
VERSION AR210279.1 GI:21512469
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Haugland,R. and Vesper,S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: US 6387652-A 191 14-MAY-2002;
FEATURES
source
1.21
/organism="unknown"
BASE COUNT 3 a 7 c 7 g 4 t
ORIGIN

Query Match 72.9%; Score 12.4; DB 6; Length 21;
Best Local Similarity 92.9%; Pred. No. 4e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGG 14
8 GTTGCTTCGGCGG 21

RESULT 12
AR210282 21 bp DNA linear PAT 20-JUN-2002
LOCUS Sequence 194 from patent US 6387652.
ACCESSION AR210282
VERSION AR210282.1 GI:21512472
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Haugland,R. and Vesper,S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: US 6387652-A 194 14-MAY-2002;
FEATURES
source
1.21
/organism="unknown"
BASE COUNT 3 a 7 c 7 g 4 t
ORIGIN

Query Match 72.9%; Score 12.4; DB 6; Length 21;
Best Local Similarity 92.9%; Pred. No. 4e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGG 14
8 GTTGCTTCGGCGG 21

RESULT 13
AR210291 21 bp DNA linear PAT 20-JUN-2002
LOCUS Sequence 203 from patent US 6387652.
DEFINITION AR210291.1 GI:21512484
ACCESSION AR210291.1
VERSION AR210291.1
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE
1 (bases 1 to 21)
AUTHORS Haugland, R. and Vesper, S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: US 6387652-A 203 14-MAY-2002;
FEATURES
source
1..21
/organism="unknown"
BASE COUNT 3 a 7 c 7 g 4 t
ORIGIN

Query Match 72.9%; Score 12.4; DB 6; Length 21;
Best Local Similarity 92.9%; Pred. No. 4e+04; 1; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTGCTCGGGCGG 14
|||||
8 GTTGCTCGGGCGG 21

RESULT 14
AX402707 21 bp DNA linear PAT 07-JUN-2002
LOCUS Sequence 191 from Patent WO0196612.
DEFINITION AX402707
ACCESSION AX402707
VERSION AX402707.1 GI:21387698
KEYWORDS
SOURCE Trichoderma asperellum.
ORGANISM Trichoderma asperellum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; microsporitic Hypocreales; Trichoderma.
REFERENCE
1 Haugland, R. and Vesper, S.
AUTHORS Method of identifying and quantifying specific fungi and bacteria
TITLE Patent: WO 0196612-A 191 20-DEC-2001;
JOURNAL UNITED STATES ENVIRONMENTAL PROTECTION AGENCY (US)
FEATURES
source
1..21
/organism="Trichoderma asperellum"
/db_xref="taxon:101201"
BASE COUNT 3 a 7 c 7 g 4 t
ORIGIN

Query Match 72.9%; Score 12.4; DB 6; Length 21;
Best Local Similarity 92.9%; Pred. No. 4e+04; 1; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTGCTCGGGCGG 14
|||||
8 GTTGCTCGGGCGG 21

RESULT 15
AX402710 21 bp DNA linear PAT 07-JUN-2002
LOCUS Sequence 194 from Patent WO0196612.
DEFINITION AX402710
ACCESSION AX402710
VERSION AX402710.1 GI:21387701
KEYWORDS
SOURCE Trichoderma asperellum.
ORGANISM Trichoderma asperellum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; microsporitic Hypocreales; Trichoderma.

REFERENCE 1
AUTHORS Haugland, R. and Vesper, S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: WO 0196612-A 194 20-DEC-2001;
FEATURES
source
1..21
/organism="Trichoderma asperellum"
/db_xref="taxon:101201"
BASE COUNT 3 a 7 c 7 g 4 t
ORIGIN

Query Match 72.9%; Score 12.4; DB 6; Length 21;
Best Local Similarity 92.9%; Pred. No. 4e+04; 1; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTGCTCGGGCGG 14
|||||
8 GTTGCTCGGGCGG 21

RESULT 16
AX402719 21 bp DNA linear PAT 07-JUN-2002
LOCUS Sequence 203 from Patent WO0196612.
DEFINITION AX402719
ACCESSION AX402719
VERSION AX402719.1 GI:21387710
KEYWORDS
SOURCE Trichoderma viride.
ORGANISM Trichoderma viride
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; microsporitic Hypocreales; Trichoderma.
REFERENCE
1 Haugland, R. and Vesper, S.
AUTHORS Method of identifying and quantifying specific fungi and bacteria
TITLE Patent: WO 0196612-A 203 20-DEC-2001;
JOURNAL UNITED STATES ENVIRONMENTAL PROTECTION AGENCY (US)
FEATURES
source
1..21
/organism="Trichoderma viride"
/db_xref="taxon:5547"
BASE COUNT 3 a 7 c 7 g 4 t
ORIGIN

Query Match 72.9%; Score 12.4; DB 6; Length 21;
Best Local Similarity 92.9%; Pred. No. 4e+04; 1; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTGCTCGGGCGG 14
|||||
8 GTTGCTCGGGCGG 21

RESULT 17
AR210119 22 bp DNA linear PAT 20-JUN-2002
LOCUS Sequence 31 from patent US 6387652.
DEFINITION AR210119
ACCESSION AR210119
VERSION AR210119.1 GI:21512267
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE
1 (bases 1 to 22)
AUTHORS Haugland, R. and Vesper, S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: US 6387652-A 31 14-MAY-2002;
FEATURES
source
1..22
/organism="unknown"
BASE COUNT 2 a 8 c 6 g 6 t
ORIGIN

Query Match 72.9%; Score 12.4; DB 6; Length 22;
Best Local Similarity 92.9%; Pred. No. 4e+04; 1; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGG 14
Db 6 GTTGCTTCGGCGG 19

RESULT 18
AX402547 22 bp DNA linear PAT 07-JUN-2002
LOCUS Sequence 31 from Patent W00196612.
DEFINITION AX402547
ACCESSION AX402547.1 GI:21387538
VERSION
KEYWORDS
SOURCE Aspergillus ochraceus.
ORGANISM Aspergillus ochraceus
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
AUTHORS Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
TITLE Haugland, R. and Vesper, S.
JOURNAL Method of identifying and quantifying specific fungi and bacteria
Patent: WO 0196612-A 31 20-DEC-2001;
FEATURES UNITED STATES ENVIRONMENTAL PROTECTION AGENCY (US)
LOCATION/Qualifiers
SOURCE 1. .22
/organism="Aspergillus ochraceus"
/db_xref="taxon:40380"

BASE COUNT 2 a 8 c 6 g 6 t

Query Match 72.9%; Score 12.4; DB 6; Length 22;
Best Local Similarity 92.9%; Pred. No. 4e+04; 1; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGG 14
Db 6 GTTGCTTCGGCGG 19

RESULT 19
AR043140 20 bp DNA linear PAT 29-SEP-1999
LOCUS AR043140
DEFINITION Sequence 24 from patent US 5814453.
ACCESSION AR043140
VERSION AR043140.1 GI:5964148
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Beck, J. Joseph.
TITLE Detection of fungal pathogens using the polymerase chain reaction
JOURNAL Patent: US 5814453-A 24 29-SEP-1998;
FEATURES Location/Qualifiers
SOURCE 1. .20
/organism="unknown"

BASE COUNT 1 a 5 c 9 g 5 t

Query Match 71.8%; Score 12.2; DB 6; Length 20;
Best Local Similarity 82.4%; Pred. No. 5.2e+04; 3; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGG 17
Db 1 GTTGCTTCGGCGG 17

RESULT 20
AR074640 20 bp DNA linear PAT 28-AUG-2000
LOCUS AR074640

DEFINITION Sequence 24 from patent US 5955274.
ACCESSION AR074640
VERSION AR074640.1 GI:10001393
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Ligson, J.M. and Beck, J.J.
TITLE Detection of fungal pathogens using the polymerase chain reaction
JOURNAL Patent: US 5955274-A 24 21-SEP-1999;
FEATURES Location/Qualifiers
SOURCE 1. .20
/organism="unknown"

BASE COUNT 1 a 5 c 9 g 5 t

Query Match 71.8%; Score 12.2; DB 6; Length 20;
Best Local Similarity 82.4%; Pred. No. 5.2e+04; 3; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGG 17
Db 1 GTTGCTTCGGCGG 17

RESULT 21
I12080 20 bp DNA linear PAT 06-FEB-1997
LOCUS I12080
DEFINITION Sequence 24 from patent US 5585238.
ACCESSION I12080
VERSION I12080.1 GI:1822871
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Ligson, J.M. and Beck, J.J.
TITLE Detection of fungal pathogens using the polymerase chain reaction
JOURNAL Patent: US 5585238-A 24 17-DEC-1996;
FEATURES Location/Qualifiers
SOURCE 1. .20
/organism="unknown"

BASE COUNT 1 a 5 c 9 g 5 t

Query Match 71.8%; Score 12.2; DB 6; Length 20;
Best Local Similarity 82.4%; Pred. No. 5.2e+04; 3; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGG 17
Db 1 GTTGCTTCGGCGG 17

RESULT 22
AX286541 24 bp DNA linear PAT 21-NOV-2001
LOCUS AX286541
DEFINITION Sequence 15 from Patent W00181423.
ACCESSION AX286541
VERSION AX286541.1 GI:117048644
KEYWORDS
SOURCE Synthetic construct.
ORGANISM Synthetic construct
REFERENCE 1
AUTHORS Terneess, P., Kleist, C., Opelz, G., Wejschof, M., Arnold-Schild, D.,
TITLE Antibodies against native gp96, production and use thereof
JOURNAL Patent: WO 0181423-A 15 01-NOV-2001;
FEATURES Dr..Fenning Biomed GmbH (DE)
LOCATION/Qualifiers
SOURCE 1. .24

/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Zufallssequenz, codiert für CDR3 einer schweren Kette eines Antikorpers, Herstellung siehe Messim et al, 1994"

BASE COUNT

3 a 4 c 8 g 9 t

Query Match 71.8%; Score 12.2; DB 6; Length 24;
Best Local Similarity 82.4%; Pred. No. 5.2e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 GTTGCTTCGGCGGAC 17
6 GTTGCTTCGGCGGAC 22

Db

RESULT 23
LOCUS AR210208 17 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 120 from patent US 6387652.
ACCESSION AR210208 GI:21512380
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Haugland, R. and Vesper, S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: US 6387652-A 120 14-MAY-2002;
FEATURES
Location/Qualifiers
1..17
/organism="unknown"

BASE COUNT 1 a 5 c 5 g 6 t
ORIGIN
Query Match 70.6%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.8e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTTGCTTCGGCG 12
5 GTTGCTTCGGCG 16

Db

RESULT 24
LOCUS AX402636 17 bp DNA linear PAT 07-JUN-2002
DEFINITION Sequence 120 from Patent WO0196612.
ACCESSION AX402636
VERSION AX402636.1 GI:21387627
KEYWORDS
SOURCE Penicillium brevicompactum.
ORGANISM Penicillium brevicompactum.
REFERENCE 1 (bases 1 to 17)
AUTHORS Haugland, R. and Vesper, S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: WO 0196612-A 120 20-DEC-2001;
UNITED STATES ENVIRONMENTAL PROTECTION AGENCY (US)
FEATURES
Location/Qualifiers
1..17
/organism="Penicillium brevicompactum"
/db_xref="taxon:5074"

BASE COUNT 1 a 5 c 5 g 6 t
ORIGIN

Query Match 70.6%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.8e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTTGCTTCGGCG 12
5 GTTGCTTCGGCG 16

Db

RESULT 25
LOCUS AX150222 19 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 18 from Patent WO0132919.
ACCESSION AX150222
VERSION AX150222.1 GI:14348242
KEYWORDS
SOURCE soybean.
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosoid 1; Fabales; Fabaceae; Papilionoideae; Phaseolae; Glycine.

REFERENCE 1 (bases 1 to 19)
AUTHORS Vollenhofer, S., Mansfeld, M. and Kroach, H.
TITLE Group of novel primer pairs for PCR amplification, primer pairs, gene probes and method for detecting technically genetically modified plant material
JOURNAL Patent: WO 0132919-A 18 10-MAY-2001;
Oesterreichisches Forschungszentrum Seibersdorf Ges.m.b.H (AT)
FEATURES
Location/Qualifiers
1..19
/organism="Glycine max"
/db_xref="taxon:3847"
/note="SojaLektin-Gen Lb1"

BASE COUNT 3 a 5 c 5 g 6 t
ORIGIN

Query Match 69.4%; Score 11.8; DB 6; Length 19;
Best Local Similarity 86.7%; Pred. No. 8.9e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

3 TGCTTCGGCGGAC 17
1 TGCTTCGGCGGAC 15

Db

RESULT 26
LOCUS AR125569 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 70 from patent US 6177273.
ACCESSION AR125569
VERSION AR125569.1 GI:14111631
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett, C. Frank. and Cowsett, L.M.
TITLE Antisense modulation of integrin-linked kinase expression
JOURNAL Patent: US 6177273-A 70 23-JAN-2001;
FEATURES
Location/Qualifiers
1..20
/organism="unknown"

BASE COUNT 6 a 8 c 3 g 3 t
ORIGIN

Query Match 69.4%; Score 11.8; DB 6; Length 20;
Best Local Similarity 86.7%; Pred. No. 8.9e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

3 TGCTTCGGCGGAC 17
18 TGCTTCGGCGGAC 4

Db

RESULT 27
AX294487/c

LOCUS AX294487 20 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 6249 from Patent WO0179548.
ACCESSION AX294487
VERSION AX294487.1 GI:17056170
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Barany, F., Zivvi, M., Gerry, N.P., Favis, R. and Kliman, R.
TITLE Method of designing addressable array for detection of nucleic acid
JOURNAL Sequence differences using ligase detection reaction
Patent: WO 0179548-A 6249 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES
source
1. 20
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"
BASE COUNT 7 a 6 c 5 g 2 t
ORIGIN
Query Match 69.4%; Score 11.8; DB 6; Length 20;
Best Local Similarity 86.7%; Pred. No. 8.9e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 2 TTGCTTCGGCGGAA 16
DB 20 TTGCTTCGGCGTCA 6
RESULT 26
LOCUS AX289854 24 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 1616 from Patent WO0179548.
ACCESSION AX289854
VERSION AX289854.1 GI:17051537
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Barany, F., Zivvi, M., Gerry, N.P., Favis, R. and Kliman, R.
TITLE Method of designing addressable array for detection of nucleic acid
JOURNAL Sequence differences using ligase detection reaction
Patent: WO 0179548-A 1616 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES
source
1. 24
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"
BASE COUNT 7 a 7 c 7 g 3 t
ORIGIN
Query Match 69.4%; Score 11.8; DB 6; Length 24;
Best Local Similarity 86.7%; Pred. No. 9e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 2 TTGCTTCGGCGGAA 16
DB 20 TTGCTTCGGCTCA 6
RESULT 29
LOCUS AX100490 25 bp DNA linear PAT 10-APR-2001
DEFINITION Sequence 4 from Patent WO0121783.
ACCESSION AX100490
VERSION AX100490.1 GI:13619504
KEYWORDS
SOURCE
ORGANISM
Zea mays.
Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 25)
AUTHORS Jiao, S., Habben, J.E. and Niu, X.
TITLE Seed-preferred promoter from maize.
JOURNAL Patent: WO 0121783-A 4 29-MAR-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
source
1. 25
/organism="Zea mays"
/db_xref="taxon:4577"
BASE COUNT 5 a 8 c 6 g 6 t
ORIGIN
Query Match 69.4%; Score 11.8; DB 6; Length 25;
Best Local Similarity 86.7%; Pred. No. 9e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 2 TTGCTTCGGCGGAA 16
DB 15 TTGCTTCGGCGCA 1
RESULT 30
LOCUS AR043173 16 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 57 from patent US 5814453.
ACCESSION AR043173
VERSION AR043173.1 GI:5964181
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 16)
AUTHORS Beck, J. Joseph.
TITLE Detection of fungal pathogens using the polymerase chain reaction
JOURNAL Patent: US 5814453-A 57 29-SEP-1998;
FEATURES
source
1. 16
/organism="unknown"
BASE COUNT 1 a 4 c 6 g 5 t
ORIGIN
Query Match 67.1%; Score 11.4; DB 6; Length 16;
Best Local Similarity 92.3%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 GTTGCTTCGGCGG 13
DB 4 GTTGCTTCGGCGG 16
RESULT 31
LOCUS AR043180 16 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 64 from patent US 5814453.
ACCESSION AR043180
VERSION AR043180.1 GI:5964188
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 16)
AUTHORS Beck, J. Joseph.
TITLE Detection of fungal pathogens using the polymerase chain reaction
JOURNAL Patent: US 5814453-A 64 29-SEP-1998;
FEATURES
source
1. 16
/organism="unknown"
BASE COUNT 1 a 5 c 6 g 4 t
ORIGIN

Query Match 67.1%; Score 11.4; DB 6; Length 16;
Best Local Similarity 92.3%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGG 13
|||||
1 GTTGCTTCGGCGG 13

Db 1 GTTGCTTCGGCGG 13

RESULT 32
LOCUS AR074673 16 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 57 from patent US 5955274.
ACCESSION AR074673
VERSION AR074673.1 GI:10001426
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Ijgon,J.M. and Beck,J.J.
TITLE Detection of fungal pathogens using the polymerase chain reaction
JOURNAL Patent: US 5955274-A 57 21-SEP-1999;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"

BASE COUNT 1 a 4 c 6 g 5 t

Query Match 67.1%; Score 11.4; DB 6; Length 16;
Best Local Similarity 92.3%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGG 13
|||||
4 GTTGCTTCGGCGG 16

Db 4 GTTGCTTCGGCGG 16

RESULT 33
LOCUS AR074680 16 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 64 from patent US 5955274.
ACCESSION AR074680
VERSION AR074680.1 GI:10001433
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Ijgon,J.M. and Beck,J.J.
TITLE Detection of fungal pathogens using the polymerase chain reaction
JOURNAL Patent: US 5955274-A 64 21-SEP-1999;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"

BASE COUNT 1 a 5 c 6 g 4 t

Query Match 67.1%; Score 11.4; DB 6; Length 16;
Best Local Similarity 92.3%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGG 13
|||||
1 GTTGCTTCGGCGG 13

Db 1 GTTGCTTCGGCGG 13

RESULT 34
LOCUS AR210286 16 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 198 from patent US 6387652.
ACCESSION AR210286
VERSION AR210286.1 GI:21512477

KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Haugland,R. and Vesper,S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: US 6387652-A 198 14-MAY-2002;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"

BASE COUNT 1 a 5 c 6 g 4 t

Query Match 67.1%; Score 11.4; DB 6; Length 16;
Best Local Similarity 92.3%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGCTTCGGCGGA 15
|||||
1 TGCTTCGGCGGA 13

Db 1 TGCTTCGGCGGA 13

RESULT 35
LOCUS AX402714 16 bp DNA linear PAT 07-JUN-2002
DEFINITION Sequence 198 from Patent WO0196612.
ACCESSION AX402714
VERSION AX402714.1 GI:21387705
KEYWORDS
SOURCE Trichoderma longibrachiatum.
ORGANISM Trichoderma longibrachiatum.
REFERENCE 1
AUTHORS Haugland,R. and Vesper,S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: WO 0196612-A 198 20-DEC-2001;
FEATURES Location/Qualifiers
source 1..16
/organism="Trichoderma longibrachiatum"
/db_xref="taxon:5548"

BASE COUNT 1 a 5 c 6 g 4 t

Query Match 67.1%; Score 11.4; DB 6; Length 16;
Best Local Similarity 92.3%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGCTTCGGCGGA 15
|||||
1 TGCTTCGGCGGA 13

Db 1 TGCTTCGGCGGA 13

RESULT 36
LOCUS I62258 16 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 812 from patent US 5658780.
ACCESSION I62258
VERSION I62258.1 GI:2480206
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Stinchcomb,D.T., Draper,K.G. and McSwiggan,J.
TITLE Rel a targeted ribozymes
JOURNAL Patent: US 5658780-A 812 19-AUG-1997;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"

BASE COUNT 7 a 5 c 4 g 0 t

ORIGIN

Query Match 67.1%; Score 11.4; DB 6; Length 16;
Best Local Similarity 92.3%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCTTCGGCGG 13
Db 16 GTTCTTCGGCGG 4

RESULT 37
LOCUS AR110539 18 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 19 from patent US 6114601.
ACCESSION AR110539
VERSION AR110539.1 GI:12826915
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 18)
AUTHORS Kikuchi,Y., Kiyokawa,S., Shimada,Y., Ohbayashi,M., Shimada,R. and Okinaka,Y.
TITLE Plant genes encoding flavonoid-3', 5'-hydroxylase
JOURNAL Patent: US 6114601-A 19 05-SEP-2000;
FEATURES
source 1..18
/organism="unknown"

BASE COUNT 4 a 7 c 4 g 1 t 2 others
ORIGIN

Query Match 67.1%; Score 11.4; DB 6; Length 18;
Best Local Similarity 80.0%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 TGGCTTCGGCGGAC 17
Db 18 TGGCTTCGGCGGATC 4

RESULT 38
LOCUS AR151759 18 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 19 from patent US 6232109.
ACCESSION AR151759
VERSION AR151759.1 GI:15117809
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 18)
AUTHORS Kikuchi,Y., Kiyokawa,S., Shimada,Y., Ohbayashi,M., Shimada,R. and Okinaka,Y.
TITLE Plant genes
JOURNAL Patent: US 6232109-A 19 15-MAY-2001;
FEATURES
source 1..18
/organism="unknown"

BASE COUNT 4 a 7 c 4 g 1 t 2 others
ORIGIN

Query Match 67.1%; Score 11.4; DB 6; Length 18;
Best Local Similarity 80.0%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 TGGCTTCGGCGGAC 17
Db 18 TGGCTTCGGCGGATC 4

RESULT 39
LOCUS AR022121 21 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 1 from patent US 5792611.
ACCESSION AR022121
VERSION AR022121.1 GI:3976183
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 21)
AUTHORS Hamelin,R.C.
TITLE Detection of plant pathogenic fungi
JOURNAL Patent: US 5792611-A 1 11-AUG-1998;
FEATURES
source 1..21
/organism="unknown"

BASE COUNT 0 a 6 c 8 g 7 t
ORIGIN

Query Match 67.1%; Score 11.4; DB 6; Length 21;
Best Local Similarity 92.3%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCTTCGGCGG 13
Db 3 GTTCTTCGGCGG 15

RESULT 40
LOCUS AX057972 21 bp DNA linear PAT 17-JAN-2001
DEFINITION Sequence 32 from Patent WO0075333.
ACCESSION AX057972
VERSION AX057972.1 GI:12310590
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 21)
AUTHORS Goshorn,S.C., Graves,S.S., Schultz,J.E., Lin,Y., Sanderson,J.A. and Reno,J.M.
TITLE Streptavidin expressed gene fusions and methods of use thereof
JOURNAL Patent: WO 0075333-A 32 14-DEC-2000;
FEATURES
source 1..21
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="oligonucleotide primer"

BASE COUNT 2 a 6 c 9 g 4 t
ORIGIN

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Best Local Similarity 92.3%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCTTCGGCGG 13
Db 7 GTTCTTCGGCGG 19

Search completed: June 7, 2003, 08:50:45
Job time : 400.673 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 7, 2003, 07:20:34 ; Search time 434.909 Seconds

(without alignments)
1338.340 Million cell updates/sec

Title: US-10-080-959A-2

Perfect score: 20

Sequence: 1 ttctgcgttcgcacacagag 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 521186

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1000 summaries

Database :

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1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pac:*
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8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
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12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pac:*
24: em_ph:*
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27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rtd:*
36: em_htg_mam:*
37: em_htg_vrc:*
38: em_sy:*
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40: em_htgo_mus:*
41: em_htgo_other:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	15	75.0	25 6 AR210275	AR210275 Sequence
2	15	75.0	25 6 AX402703	AX402703 Sequence
3	14.4	72.0	25 6 AX164511	AX164511 Sequence
4	13.8	69.0	20 6 AR122463	AR122463 Sequence
5	13.4	67.0	17 6 BD000958	BD000958 Method an
6	13.4	67.0	17 6 BD001387	BD001387 Method an
7	12.8	64.0	24 6 AX288902	AX288902 Sequence
8	12.8	64.0	25 6 AX150973	AX150973 Sequence
9	12.6	63.0	20 6 AX353540	AX353540 Sequence
10	12.6	63.0	21 6 AX039884	AX039884 Sequence
11	12.2	61.0	17 6 AX217169	AX217169 Sequence
12	12.2	61.0	17 6 AX422057	AX422057 Sequence
13	12.2	61.0	20 4 DOGP41402	DOGP41402 Sequence
14	12.2	61.0	22 6 AR003705	AR003705 Sequence
15	12.2	61.0	24 6 AR210196	AR210196 Sequence
16	12.2	61.0	24 6 AX402624	AX402624 Sequence
17	12	60.0	17 6 AR040151	AR040151 Sequence
18	12	60.0	21 6 AR166679	AR166679 Sequence
19	12	60.0	23 6 AX268543	AX268543 Sequence
20	11.8	59.0	17 6 AX216558	AX216558 Sequence
21	11.8	59.0	20 6 AX059295	AX059295 Sequence
22	11.8	59.0	22 6 AX467734	AX467734 Sequence
23	11.8	59.0	24 6 AX291474	AX291474 Sequence
24	11.6	58.0	21 6 AR088260	AR088260 Sequence
25	11.6	58.0	21 6 I13019	I13019 Sequence 4
26	11.6	58.0	21 6 I34228	I34228 Sequence 4
27	11.6	58.0	21 12 AB068925	AB068925 Synthetic
28	11.6	58.0	24 6 AX445793	AX445793 Sequence
29	11.6	58.0	25 6 AX116728	AX116728 Sequence
30	11.4	57.0	21 6 AX001122	AX001122 Sequence
31	11.4	57.0	21 6 AX153566	AX153566 Sequence
32	11.4	57.0	24 6 AX32924	AX32924 Synthetic P
33	11.4	57.0	24 6 AX175376	AX175376 Sequence
34	11.4	57.0	25 6 AR090389	AR090389 Sequence
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36	11.4	57.0	25 6 BD006741	BD006741 Novel pol
37	11.2	56.0	17 6 AX215063	AX215063 Sequence
38	11.2	56.0	17 6 AX422987	AX422987 Sequence
39	11.2	56.0	19 6 AX119996	AX119996 Sequence
40	11.2	56.0	19 6 I25829	I25829 Sequence 9
41	11.2	56.0	19 6 I50992	I50992 Sequence 7
42	11.2	56.0	20 6 AX020042	AX020042 Sequence
43	11.2	56.0	20 6 AX020117	AX020117 Sequence
44	11.2	56.0	20 6 AX296539	AX296539 Sequence
45	11.2	56.0	21 6 I30543	I30543 Sequence 6
46	11.2	56.0	24 6 AX231906	AX231906 Sequence
47	11.2	56.0	25 6 AX150972	AX150972 Sequence
48	11	55.0	20 6 AX249751	AX249751 Sequence
49	11	55.0	20 6 AX250104	AX250104 Sequence
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51	11	55.0	20 6 AX406775	AX406775 Sequence
52	11	55.0	20 6 I50807	I50807 Sequence 1
53	11	55.0	20 12 AB068086	AB068086 Synthetic
54	11	55.0	21 6 AR129440	AR129440 Sequence
55	11	55.0	22 6 AR099850	AR099850 Sequence
56	11	55.0	22 6 AX402193	AX402193 Sequence
57	11	55.0	23 6 AR048502	AR048502 Sequence
58	11	55.0	23 6 AR088530	AR088530 Sequence
59	11	55.0	23 6 AX003422	AX003422 Sequence
60	11	55.0	23 6 BD011748	BD011748 795, a no
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62	11	55.0	24 6 AR000483	AR000483 Sequence
63	11	55.0	24 6 AX289702	AX289702 Sequence
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65	11	55.0	25 6 AX043429	AX043429 Sequence

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67	10.8	54.0	15	6	AR113564	AR113564 Sequence
68	10.8	54.0	17	6	AX215924	AX215924 Sequence
69	10.8	54.0	17	6	AX422988	AX422988 Sequence
70	10.8	54.0	20	6	AR061755	AR061755 Sequence
71	10.8	54.0	20	6	AR061996	AR061996 Sequence
72	10.8	54.0	20	6	AR067304	AR067304 Sequence
73	10.8	54.0	20	6	AR203381	AR203381 Sequence
74	10.8	54.0	20	6	AR206230	AR206230 Sequence
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77	10.8	54.0	20	6	BD002116	BD002116 Method an
78	10.8	54.0	20	6	BD002159	BD002159 Method an
79	10.8	54.0	20	6	E39136	E39136 Improved PC
80	10.8	54.0	20	12	AB069624	AB069624 Synthetic
81	10.8	54.0	21	6	AX096504	AX096504 Sequence
82	10.8	54.0	21	6	AX486782	AX486782 Sequence
83	10.8	54.0	21	6	E14067	E14067 Sequence 8
84	10.8	54.0	22	6	E31656	E31656 Method for
85	10.8	54.0	22	6	E119934	E119934 Sequence 31
86	10.8	54.0	23	6	AR150454	AR150454 Sequence
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88	10.8	54.0	24	6	AX291090	AX291090 Sequence
89	10.8	54.0	24	6	AX288558	AX288558 Sequence
90	10.8	54.0	24	6	AX291090	AX291090 Sequence
91	10.8	54.0	24	6	AX354440	AX354440 Sequence
92	10.8	54.0	24	6	AX445927	AX445927 Sequence
93	10.8	54.0	25	6	AR026643	AR026643 Sequence
94	10.6	53.0	18	6	AR051187	AR051187 Sequence
95	10.6	53.0	18	6	AR095853	AR095853 Sequence
96	10.6	53.0	18	6	E125331	E125331 Sequence 11
97	10.6	53.0	19	6	AX132156	AX132156 Sequence
98	10.6	53.0	19	6	AX132157	AX132157 Sequence
99	10.6	53.0	20	6	AR067020	AR067020 Sequence
100	10.6	53.0	20	6	AR159419	AR159419 Sequence
101	10.6	53.0	20	6	AR159421	AR159421 Sequence
102	10.6	53.0	20	6	AR159422	AR159422 Sequence
103	10.6	53.0	20	6	AR156671	AR156671 Sequence
104	10.6	53.0	20	6	AR166671	AR166671 Sequence
105	10.6	53.0	20	6	AX488335	AX488335 Sequence
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119	10.4	52.0	15	6	AR113565	AR113565 Sequence
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121	10.4	52.0	18	6	AX175528	AX175528 Sequence
122	10.4	52.0	19	6	E172023	E172023 Sequence 59
123	10.4	52.0	19	6	AX130125	AX130125 Sequence
124	10.4	52.0	19	6	AX130125	AX130125 Sequence
125	10.4	52.0	19	6	AX201282	AX201282 Sequence
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134	10.4	52.0	20	6	AX008469	AX008469 Sequence
135	10.4	52.0	20	6	AX297460	AX297460 Sequence
136	10.4	52.0	20	6	AX470207	AX470207 Sequence
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138	10.4	52.0	20	6	AX470275	AX470275 Sequence
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140	10.4	52.0	21	6	A11444	A11444 Nucleotide
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149	10.4	52.0	23	6	AR177003	AR177003 Sequence
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154	10.4	52.0	23	8	AF501817	AF501817 Arabidops
155	10.4	52.0	24	6	A20329	A20329 oligonucleo
156	10.4	52.0	24	6	A30124	A30124 Probe E. 7/
157	10.4	52.0	24	6	A61975	A61975 Sequence 5
158	10.4	52.0	24	6	AX292827	AX292827 Sequence
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161	10.4	52.0	24	6	E37777	E37777 Process for
162	10.4	52.0	25	6	A04036	A04036 Synthetic o
163	10.4	52.0	25	6	A11445	A11445 Nucleotide
164	10.4	52.0	25	6	AR073583	AR073583 Sequence
165	10.4	52.0	25	6	AR073586	AR073586 Sequence
166	10.4	52.0	25	6	AR173780	AR173780 Sequence
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179	10.2	51.0	15	6	AR204785	AR204785 Sequence
180	10.2	51.0	15	6	E17174	E17174 Pseudomonas
181	10.2	51.0	15	6	E130549	E130549 Sequence 12
182	10.2	51.0	17	6	AR057662	AR057662 Sequence
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189	10.2	51.0	17	6	AR190536	AR190536 Sequence
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199	10.2	51.0	19	6	AX130217	AX130217 Sequence
200	10.2	51.0	19	6	AX132155	AX132155 Sequence
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202	10.2	51.0	19	6	AX319459	AX319459 Sequence
203	10.2	51.0	19	6	E134832	E134832 Sequence 25
204	10.2	51.0	20	6	A94714	A94714 Oligonucleo
205	10.2	51.0	20	6	AR021350	AR021350 Sequence
206	10.2	51.0	20	6	AR036086	AR036086 Sequence
207	10.2	51.0	20	6	AR054240	AR054240 Sequence
208	10.2	51.0	20	6	AR062684	AR062684 Sequence
209	10.2	51.0	20	6	AR100318	AR100318 Sequence
210	10.2	51.0	20	6	AR104787	AR104787 Sequence
211	10.2	51.0	20	6	AR104787	AR104787 Sequence

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C 213	10.2	51.0	20	6	AR108791	AR108791 Sequence	C 286	10	50.0	18	12	AB069550	AB069550 Synthetic
C 214	10.2	51.0	20	6	AR120021	AR120021 Sequence	287	10	50.0	19	6	AB2118	AB2118 Sequence 38
C 215	10.2	51.0	20	6	AR120117	AR120117 Sequence	288	10	50.0	19	6	AX001189	AX001189 Sequence
C 216	10.2	51.0	20	6	AR123271	AR123271 Sequence	289	10	50.0	19	6	AX131404	AX131404 Sequence
C 217	10.2	51.0	20	6	AR124879	AR124879 Sequence	290	10	50.0	19	6	AX132366	AX132366 Sequence
C 218	10.2	51.0	20	6	AR124880	AR124880 Sequence	C 291	10	50.0	19	6	AX404210	AX404210 Sequence
C 219	10.2	51.0	20	6	AR141077	AR141077 Sequence	C 292	10	50.0	19	6	E07044	E07044 Partial seq
C 220	10.2	51.0	20	6	AR141973	AR141973 Sequence	293	10	50.0	19	6	E07068	E07068 Probe for H
C 221	10.2	51.0	20	6	AR153734	AR153734 Sequence	294	10	50.0	20	6	A48125	A48125 Sequence 19
C 222	10.2	51.0	20	6	AR164159	AR164159 Sequence	295	10	50.0	20	6	AR124981	AR124981 Sequence
C 223	10.2	51.0	20	6	AR164170	AR164170 Sequence	296	10	50.0	20	6	AR144312	AR144312 Sequence
C 224	10.2	51.0	20	6	AR165317	AR165317 Sequence	297	10	50.0	20	6	AR177170	AR177170 Sequence
C 225	10.2	51.0	20	6	AR165318	AR165318 Sequence	C 298	10	50.0	20	6	AR207157	AR207157 Sequence
C 226	10.2	51.0	20	6	AR179598	AR179598 Sequence	299	10	50.0	20	6	AX191133	AX191133 Sequence
C 227	10.2	51.0	20	6	AR179601	AR179601 Sequence	C 300	10	50.0	20	6	AX204816	AX204816 Sequence
C 228	10.2	51.0	20	6	AR179602	AR179602 Sequence	301	10	50.0	20	6	AX293511	AX293511 Sequence
C 229	10.2	51.0	20	6	AR179603	AR179603 Sequence	C 302	10	50.0	20	6	AX293842	AX293842 Sequence
C 230	10.2	51.0	20	6	AR179604	AR179604 Sequence	303	10	50.0	20	6	AX295479	AX295479 Sequence
C 231	10.2	51.0	20	6	AR179605	AR179605 Sequence	304	10	50.0	20	6	AX418782	AX418782 Sequence
C 232	10.2	51.0	20	6	AR179606	AR179606 Sequence	305	10	50.0	20	6	AX477721	AX477721 Sequence
C 233	10.2	51.0	20	6	AR179608	AR179608 Sequence	306	10	50.0	20	6	BD011112	BD011112 Human tel
C 234	10.2	51.0	20	6	AR179609	AR179609 Sequence	307	10	50.0	20	6	BD011113	BD011113 Human tel
C 235	10.2	51.0	20	6	AR202054	AR202054 Sequence	308	10	50.0	20	6	E36861	E36861 Human telom
C 236	10.2	51.0	20	6	AR203433	AR203433 Sequence	309	10	50.0	20	6	E36862	E36862 Human telom
C 237	10.2	51.0	20	6	AR212339	AR212339 Sequence	C 310	10	50.0	21	6	AX097110	AX097110 Sequence
C 238	10.2	51.0	20	6	AX164498	AX164498 Sequence	C 311	10	50.0	21	6	AX356931	AX356931 Sequence
C 239	10.2	51.0	20	6	AX295248	AX295248 Sequence	C 312	10	50.0	21	6	E14731	E14731 Japanese He
C 240	10.2	51.0	20	6	AX297028	AX297028 Sequence	C 313	10	50.0	22	6	AX443510	AX443510 Sequence
C 241	10.2	51.0	20	6	I13817	I13817 Sequence	C 314	10	50.0	23	6	E59870	E59870 Method for
C 242	10.2	51.0	20	6	I20686	I20686 Sequence	C 315	10	50.0	24	6	AR078736	AR078736 Sequence
C 243	10.2	51.0	20	6	I27034	I27034 Sequence	C 316	10	50.0	24	6	AR164356	AR164356 Sequence
C 244	10.2	51.0	20	6	I33451	I33451 Sequence	C 317	10	50.0	24	6	AR205899	AR205899 Sequence
C 245	10.2	51.0	21	6	AB6795	AB6795 Sequence	318	10	50.0	24	6	AX07871	AX07871 Sequence
C 246	10.2	51.0	21	6	AR094479	AR094479 Sequence	319	10	50.0	24	6	AX288878	AX288878 Sequence
C 247	10.2	51.0	21	6	AR139687	AR139687 Sequence	C 320	10	50.0	24	6	AX289205	AX289205 Sequence
C 248	10.2	51.0	21	6	AX000973	AX000973 Sequence	C 321	10	50.0	24	6	AX289403	AX289403 Sequence
C 249	10.2	51.0	21	6	AX063587	AX063587 Sequence	C 322	10	50.0	24	6	AX290680	AX290680 Sequence
C 250	10.2	51.0	21	6	AX092721	AX092721 Sequence	C 323	10	50.0	24	6	AX290846	AX290846 Sequence
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C 254	10.2	51.0	21	6	I50991	I50991 Sequence	C 327	10	50.0	25	6	AX043124	AX043124 Sequence
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C 256	10.2	51.0	22	6	AB0977	AB0977 Sequence	329	10	50.0	25	6	AX104989	AX104989 Sequence
C 257	10.2	51.0	22	6	AB062627	AB062627 Sequence	C 330	10	50.0	25	6	AX197191	AX197191 Sequence
C 258	10.2	51.0	22	6	AR068108	AR068108 Sequence	C 331	10	50.0	25	6	AX300144	AX300144 Sequence
C 259	10.2	51.0	22	6	AR104730	AR104730 Sequence	332	10	50.0	25	6	I12305	I12305 Sequence 10
C 260	10.2	51.0	22	6	AR105552	AR105552 Sequence	333	10	50.0	25	6	I15635	I15635 Sequence 2
C 261	10.2	51.0	22	6	AR110392	AR110392 Sequence	334	10	50.0	25	6	I17008	I17008 Sequence 19
C 262	10.2	51.0	22	6	AR123214	AR123214 Sequence	C 335	10	50.0	25	6	I26909	I26909 Sequence 2
C 263	10.2	51.0	22	6	I20629	I20629 Sequence	336	10	50.0	25	6	I41242	I41242 Sequence 10
C 264	10.2	51.0	22	6	I30040	I30040 Sequence	337	10	50.0	25	6	A10665	A10665 Oligonucleo
C 265	10.2	51.0	22	6	I33322	I33322 Sequence	338	9.8	49.0	15	6	I38981	I38981 Sequence 19
C 266	10.2	51.0	23	6	AX350150	AX350150 Sequence	C 339	9.8	49.0	17	6	AR045399	AR045399 Sequence
C 267	10.2	51.0	23	6	AX350158	AX350158 Sequence	340	9.8	49.0	17	6	AR046401	AR046401 Sequence
C 268	10.2	51.0	23	6	AX477191	AX477191 Sequence	C 341	9.8	49.0	17	6	AR158519	AR158519 Sequence
C 269	10.2	51.0	24	6	AR087513	AR087513 Sequence	C 342	9.8	49.0	17	6	AR158520	AR158520 Sequence
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C 272	10.2	51.0	24	6	AX288760	AX288760 Sequence	C 345	9.8	49.0	17	6	AX036822	AX036822 Sequence
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C 274	10.2	51.0	24	6	AX292066	AX292066 Sequence	347	9.8	49.0	17	6	AX215925	AX215925 Sequence
C 275	10.2	51.0	24	6	AX292395	AX292395 Sequence	348	9.8	49.0	17	6	AX263240	AX263240 Sequence
C 276	10.2	51.0	24	6	AX444433	AX444433 Sequence	C 349	9.8	49.0	17	6	AX263241	AX263241 Sequence
C 277	10.2	51.0	24	6	AX446883	AX446883 Sequence	350	9.8	49.0	17	6	AX423058	AX423058 Sequence
C 278	10.2	51.0	25	6	AX448004	AX448004 Sequence	351	9.8	49.0	17	6	AX423059	AX423059 Sequence
C 279	10.2	51.0	25	6	AX448165	AX448165 Sequence	352	9.8	49.0	17	6	AX423204	AX423204 Sequence
C 280	10.2	51.0	25	6	AX459671	AX459671 Sequence	C 353	9.8	49.0	17	6	AX423204	AX423204 Sequence
C 281	10.2	51.0	25	6	AR040149	AR040149 Sequence	354	9.8	49.0	17	6	I39766	I39766 Sequence 39
C 282	10.2	51.0	25	6	AR084049	AR084049 Sequence	355	9.8	49.0	17	6	I53451	I53451 Sequence 11
C 283	10.2	51.0	25	6	AR085643	AR085643 Sequence	356	9.8	49.0	17	6	I53453	I53453 Sequence 11
C 284	10.2	51.0	25	6	AX116938	AX116938 Sequence	C 357	9.8	49.0	18	6	A10606	A10606 Oligonucleo

C 358	9.8	49.0	18	6	AR029252	AR029252 Sequence	431	9.8	49.0	24	6	AR165342	AR165342 Sequence
C 359	9.8	49.0	18	6	AR130032	AR130032 Sequence	432	9.8	49.0	24	6	AR181434	AR181434 Sequence
C 360	9.8	49.0	18	6	AR154096	AR154096 Sequence	433	9.8	49.0	24	6	AR184235	AR184235 Sequence
C 361	9.8	49.0	18	6	AR181705	AR181705 Sequence	434	9.8	49.0	24	6	AR184356	AR184356 Sequence
C 362	9.8	49.0	18	6	125833	125833 Sequence	435	9.8	49.0	24	6	AX001372	AX001372 Sequence
C 363	9.8	49.0	19	6	A65726	A65726 Sequence 7	436	9.8	49.0	24	6	AX098595	AX098595 Sequence
C 364	9.8	49.0	19	6	AR030980	AR030980 Sequence	437	9.8	49.0	24	6	AX117479	AX117479 Sequence
C 365	9.8	49.0	19	6	AR108825	AR108825 Sequence	438	9.8	49.0	24	6	AX127944	AX127944 Sequence
C 366	9.8	49.0	19	6	AR205774	AR205774 Sequence	439	9.8	49.0	24	6	AX288319	AX288319 Sequence
C 367	9.8	49.0	19	6	AX129121	AX129121 Sequence	440	9.8	49.0	24	6	AX289000	AX289000 Sequence
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C 370	9.8	49.0	19	6	AX130734	AX130734 Sequence	443	9.8	49.0	24	6	AX289606	AX289606 Sequence
C 371	9.8	49.0	19	6	AX150992	AX150992 Sequence	444	9.8	49.0	24	6	AX289718	AX289718 Sequence
C 372	9.8	49.0	19	6	AX352870	AX352870 Sequence	445	9.8	49.0	24	6	AX289729	AX289729 Sequence
C 373	9.8	49.0	19	6	AX362715	AX362715 Sequence	446	9.8	49.0	24	6	AX289889	AX289889 Sequence
C 374	9.8	49.0	20	6	AR032109	AR032109 Sequence	447	9.8	49.0	24	6	AX290401	AX290401 Sequence
C 375	9.8	49.0	20	6	AR066942	AR066942 Sequence	448	9.8	49.0	24	6	AX291499	AX291499 Sequence
C 376	9.8	49.0	20	6	AR130833	AR130833 Sequence	449	9.8	49.0	24	6	AX443611	AX443611 Sequence
C 377	9.8	49.0	20	6	AR160181	AR160181 Sequence	450	9.8	49.0	24	6	AX443862	AX443862 Sequence
C 378	9.8	49.0	20	6	AR175691	AR175691 Sequence	451	9.8	49.0	24	6	AX443876	AX443876 Sequence
C 379	9.8	49.0	20	6	AR195267	AR195267 Sequence	452	9.8	49.0	24	6	AX444632	AX444632 Sequence
C 380	9.8	49.0	20	6	AX106918	AX106918 Sequence	453	9.8	49.0	24	6	BD000301	BD000301 CDNA comp
C 381	9.8	49.0	20	6	AX292852	AX292852 Sequence	454	9.8	49.0	25	6	A39731	A39731 Sequence 5
C 382	9.8	49.0	20	6	AX293941	AX293941 Sequence	455	9.8	49.0	25	6	AR199715	AR199715 Sequence
C 383	9.8	49.0	20	6	AX294239	AX294239 Sequence	456	9.8	49.0	25	6	AX115734	AX115734 Sequence
C 384	9.8	49.0	20	6	AX294451	AX294451 Sequence	457	9.8	49.0	25	6	AX115792	AX115792 Sequence
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C 386	9.8	49.0	20	6	AX296255	AX296255 Sequence	459	9.8	49.0	25	6	AX447593	AX447593 Sequence
C 387	9.8	49.0	20	6	AX296827	AX296827 Sequence	460	9.8	49.0	25	6	AX447840	AX447840 Sequence
C 388	9.8	49.0	20	6	AX298329	AX298329 Sequence	461	9.8	49.0	25	6	AX447853	AX447853 Sequence
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C 390	9.8	49.0	20	6	AX363218	AX363218 Sequence	463	9.8	49.0	25	6	S50120507	S50120507 Sequence
C 391	9.8	49.0	20	6	AX363219	AX363219 Sequence	464	9.8	49.0	25	6	AR186005	AR186005 Sequence
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C 394	9.8	49.0	20	6	134025	134025 Sequence 12	467	9.8	49.0	25	6	AR191755	AR191755 Sequence
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C 396	9.8	49.0	20	6	192469	192469 Sequence 5	469	9.8	49.0	25	6	AR191812	AR191812 Sequence
C 397	9.8	49.0	20	6	A22400	A22400 Oligonucleo	470	9.8	49.0	25	6	A58986	A58986 Sequence 3
C 398	9.8	49.0	21	6	A24312	A24312 SK69 consen	471	9.8	49.0	25	6	AR027575	AR027575 Sequence
C 399	9.8	49.0	21	6	A24312	A24312 SK69 primer	472	9.8	49.0	25	6	AR100435	AR100435 Sequence
C 400	9.8	49.0	21	6	A45448	A45448 Sequence 11	473	9.8	49.0	25	6	AR100436	AR100436 Sequence
C 401	9.8	49.0	21	6	AR007374	AR007374 Sequence	474	9.8	49.0	25	6	AR100437	AR100437 Sequence
C 402	9.8	49.0	21	6	AR061253	AR061253 Sequence	475	9.8	49.0	25	6	AR139775	AR139775 Sequence
C 403	9.8	49.0	21	6	AR112849	AR112849 Sequence	476	9.8	49.0	25	6	AR150090	AR150090 Sequence
C 404	9.8	49.0	21	6	AR120034	AR120034 Sequence	477	9.8	49.0	25	6	AR150091	AR150091 Sequence
C 405	9.8	49.0	21	6	AR138841	AR138841 Sequence	478	9.8	49.0	25	6	AR150092	AR150092 Sequence
C 406	9.8	49.0	21	6	AR138841	AR138841 Sequence	479	9.8	49.0	25	6	AR208453	AR208453 Sequence
C 407	9.8	49.0	21	6	AX039561	AX039561 Sequence	480	9.8	49.0	25	6	AX5413	AX5413 Sequence
C 408	9.8	49.0	21	6	AX093784	AX093784 Sequence	481	9.8	49.0	25	6	AR098946	AR098946 Sequence
C 409	9.8	49.0	21	6	AX201794	AX201794 Sequence	482	9.8	49.0	25	6	AX130758	AX130758 Sequence
C 410	9.8	49.0	21	6	AX201804	AX201804 Sequence	483	9.8	49.0	25	6	AX352860	AX352860 Sequence
C 411	9.8	49.0	21	6	AX203424	AX203424 Sequence	484	9.8	49.0	25	6	AX352880	AX352880 Sequence
C 412	9.8	49.0	21	6	AX203441	AX203441 Sequence	485	9.8	49.0	25	6	AX362705	AX362705 Sequence
C 413	9.8	49.0	21	6	E04323	E04323 Oligonucleo	486	9.8	49.0	25	6	AX362725	AX362725 Sequence
C 414	9.8	49.0	21	6	E04329	E04329 Oligonucleo	487	9.8	49.0	25	6	179786	179786 Sequence 82
C 415	9.8	49.0	21	6	E11672	E11672 PCR primer.	488	9.8	49.0	25	6	AR072511	AR072511 Sequence
C 416	9.8	49.0	21	6	113830	113830 Sequence 38	489	9.8	49.0	25	6	AR100416	AR100416 Sequence
C 417	9.8	49.0	21	6	159585	159585 Sequence 41	490	9.8	49.0	25	6	AR100417	AR100417 Sequence
C 418	9.8	49.0	21	14	PPHSPrILRB	M64813 Human papil	491	9.8	49.0	25	6	AR100418	AR100418 Sequence
C 419	9.8	49.0	22	6	AX249957	AX249957 Sequence	492	9.8	49.0	25	6	AR100419	AR100419 Sequence
C 420	9.8	49.0	22	6	E07843	E07843 Probe for n	493	9.8	49.0	25	6	AR100420	AR100420 Sequence
C 421	9.8	49.0	22	6	E31639	E31639 Method for	494	9.8	49.0	25	6	AR150071	AR150071 Sequence
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C 424	9.8	49.0	23	6	AR029614	AR029614 Sequence	497	9.8	49.0	25	6	AR150074	AR150074 Sequence
C 425	9.8	49.0	23	6	AR096943	AR096943 Sequence	498	9.8	49.0	25	6	AR150075	AR150075 Sequence
C 426	9.8	49.0	23	6	AR176229	AR176229 Sequence	499	9.8	49.0	25	6	AR159418	AR159418 Sequence
C 427	9.8	49.0	23	6	AX003201	AX003201 Sequence	500	9.8	49.0	25	6	AR159423	AR159423 Sequence
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C 429	9.8	49.0	24	6	AR059439	AR059439 Sequence	502	9.8	49.0	25	6		
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C 504	9.6	48.0	20	6	AR179749	Sequence	577	9.4	47.0	18	6	AR156047	Sequence
C 505	9.6	48.0	20	6	AX137426	Sequence	578	9.4	47.0	18	6	AX076879	Sequence
C 506	9.6	48.0	20	6	AX201466	Sequence	579	9.4	47.0	18	6	AX115023	Sequence
C 507	9.6	48.0	20	6	AX293220	Sequence	580	9.4	47.0	18	6	AX172305	Sequence
C 508	9.6	48.0	20	6	AX293736	Sequence	581	9.4	47.0	18	8	ACE391720	Sequence
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C 510	9.6	48.0	20	6	AX294361	Sequence	583	9.4	47.0	19	6	AX129120	Sequence
C 511	9.6	48.0	20	6	AX295826	Sequence	584	9.4	47.0	19	6	AX130123	Sequence
C 512	9.6	48.0	20	6	AX298309	Sequence	585	9.4	47.0	19	6	AX132653	Sequence
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C 514	9.6	48.0	20	6	E11542	Sequence	587	9.4	47.0	20	6	A39864	Sequence
C 515	9.6	48.0	20	6	E15005	Sequence	588	9.4	47.0	20	6	A58761	Sequence
C 516	9.6	48.0	20	6	I30025	Sequence	589	9.4	47.0	20	6	A84076	Sequence
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C 520	9.6	48.0	21	6	AR049689	Sequence	593	9.4	47.0	20	6	AR058898	Sequence
C 521	9.6	48.0	21	6	AR129505	Sequence	594	9.4	47.0	20	6	AR071398	Sequence
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C 524	9.6	48.0	21	6	AX095982	Sequence	597	9.4	47.0	20	6	AR159424	Sequence
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C 526	9.6	48.0	21	6	AX096020	Sequence	599	9.4	47.0	20	6	AR159426	Sequence
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C 529	9.6	48.0	21	6	AX097116	Sequence	602	9.4	47.0	20	6	AR168604	Sequence
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C 532	9.6	48.0	21	6	BD002214	Remedy of	605	9.4	47.0	20	6	AR212411	Sequence
C 533	9.6	48.0	21	6	E10272	h2988 Alcohol deh	606	9.4	47.0	20	6	AX059413	Sequence
C 534	9.6	48.0	21	6	E42988	h10272 Primer for	607	9.4	47.0	20	6	AX073507	Sequence
C 535	9.6	48.0	21	6	S78400	S78400 CYP11B2-corr	608	9.4	47.0	20	6	AX106980	Sequence
C 536	9.6	48.0	22	6	AX055786	Sequence	609	9.4	47.0	20	6	AX110624	Sequence
C 537	9.6	48.0	22	6	AX081795	Sequence	610	9.4	47.0	20	6	AX111421	Sequence
C 538	9.6	48.0	22	6	AX083942	Sequence	611	9.4	47.0	20	6	AX293101	Sequence
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C 540	9.6	48.0	22	6	AX115167	Sequence	613	9.4	47.0	20	6	AX295646	Sequence
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C 542	9.6	48.0	23	6	A91553	Sequence 80	615	9.4	47.0	20	6	AX295723	Sequence
C 543	9.6	48.0	23	6	AX419073	Sequence	616	9.4	47.0	20	6	AX295823	Sequence
C 544	9.6	48.0	24	6	AX288587	Sequence	617	9.4	47.0	20	6	AX296762	Sequence
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C 546	9.6	48.0	24	6	AX289728	Sequence	619	9.4	47.0	20	6	AX298052	Sequence
C 547	9.6	48.0	24	6	AX290231	Sequence	620	9.4	47.0	20	6	AX298963	Sequence
C 548	9.6	48.0	24	6	AX291158	Sequence	621	9.4	47.0	20	6	AX316256	Sequence
C 549	9.6	48.0	24	6	AX291193	Sequence	622	9.4	47.0	20	6	AX397811	Sequence
C 550	9.6	48.0	24	6	AX292861	Sequence	623	9.4	47.0	20	6	AX399815	Sequence
C 551	9.6	48.0	24	6	AX417984	Sequence	624	9.4	47.0	20	6	AX488012	Sequence
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C 562	9.6	48.0	25	6	AX084193	Sequence	635	9.4	47.0	21	6	A06891	Oligonucleo
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C 574	9.4	47.0	17	6	I52637	Sequence 37	647	9.4	47.0	21	6	AR208941	Sequence
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C 666	9.4	47.0	21	6	E43280	E43280 Primer for	C 739	9.4	47.0	24	6	AX292152	AX292152 Sequence
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C 688	9.4	47.0	24	6	A30125	A30125 Probe F(1).	C 761	9.4	47.0	25	6	AX042840	AX042840 Sequence
C 689	9.4	47.0	24	6	A46030	A46030 Sequence 19	C 762	9.4	47.0	25	6	AX043076	AX043076 Sequence
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C 702	9.4	47.0	24	6	AR035371	AR035371 Sequence	C 775	9.4	47.0	25	6	E34109	E34109 Sequence
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C 709	9.4	47.0	24	6	AR091199	AR091199 Sequence	C 782	9.2	46.0	14	6	AX030173	AX030173 Sequence
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842	9.2	46.0	19	6	AX350616	Sequence	AX350616	Sequence	915	9.2	46.0	20	6	123911	Sequence	123911	Sequence
843	9.2	46.0	19	6	AX427598	Sequence	AX427598	Sequence	916	9.2	46.0	20	6	126786	Sequence	126786	Sequence
844	9.2	46.0	19	6	AX482171	Sequence	AX482171	Sequence	917	9.2	46.0	20	6	126894	Sequence	126894	Sequence
845	9.2	46.0	19	12	AB067868	Synthetic	AB067868	Synthetic	918	9.2	46.0	20	6	150734	Sequence	150734	Sequence
846	9.2	46.0	20	6	AR003686	Sequence	AR003686	Sequence	919	9.2	46.0	20	6	173239	Sequence	173239	Sequence
847	9.2	46.0	20	6	AR066773	Sequence	AR066773	Sequence	920	9.2	46.0	20	6	174761	Sequence	174761	Sequence
848	9.2	46.0	20	6	AR067069	Sequence	AR067069	Sequence	921	9.2	46.0	20	6	183796	Sequence	183796	Sequence
849	9.2	46.0	20	6	AR067608	Sequence	AR067608	Sequence	922	9.2	46.0	20	6	191527	Sequence	191527	Sequence
850	9.2	46.0	20	6	AR070686	Sequence	AR070686	Sequence	923	9.2	46.0	20	6	191635	Sequence	191635	Sequence
851	9.2	46.0	20	6	AR071595	Sequence	AR071595	Sequence	924	9.2	46.0	20	12	AB069375	Synthetic	AB069375	Synthetic
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853	9.2	46.0	20	6	AR091501	Sequence	AR091501	Sequence	926	9.2	46.0	21	6	AR050156	Sequence	AR050156	Sequence
854	9.2	46.0	20	6	AR100414	Sequence	AR100414	Sequence	927	9.2	46.0	21	6	AR067253	Sequence	AR067253	Sequence
855	9.2	46.0	20	6	AR100415	Sequence	AR100415	Sequence	928	9.2	46.0	21	6	AR074279	Sequence	AR074279	Sequence
856	9.2	46.0	20	6	AR101052	Sequence	AR101052	Sequence	929	9.2	46.0	21	6	AR076042	Sequence	AR076042	Sequence
857	9.2	46.0	20	6	AR101655	Sequence	AR101655	Sequence	930	9.2	46.0	21	6	AR103513	Sequence	AR103513	Sequence
858	9.2	46.0	20	6	AR130537	Sequence	AR130537	Sequence	931	9.2	46.0	21	6	AR103594	Sequence	AR103594	Sequence
859	9.2	46.0	20	6	AR150069	Sequence	AR150069	Sequence	932	9.2	46.0	21	6	AR106193	Sequence	AR106193	Sequence
860	9.2	46.0	20	6	AR150070	Sequence	AR150070	Sequence	933	9.2	46.0	21	6	AR120038	Sequence	AR120038	Sequence
861	9.2	46.0	20	6	AR152895	Sequence	AR152895	Sequence	934	9.2	46.0	21	6	AR130275	Sequence	AR130275	Sequence
862	9.2	46.0	20	6	AR152903	Sequence	AR152903	Sequence	935	9.2	46.0	21	6	AR131285	Sequence	AR131285	Sequence
863	9.2	46.0	20	6	AR154381	Sequence	AR154381	Sequence	936	9.2	46.0	21	6	AR138402	Sequence	AR138402	Sequence
864	9.2	46.0	20	6	AR154416	Sequence	AR154416	Sequence	937	9.2	46.0	21	6	AR139366	Sequence	AR139366	Sequence
865	9.2	46.0	20	6	AR159417	Sequence	AR159417	Sequence	938	9.2	46.0	21	6	AR141615	Sequence	AR141615	Sequence
866	9.2	46.0	20	6	AR162508	Sequence	AR162508	Sequence	939	9.2	46.0	21	6	AR141616	Sequence	AR141616	Sequence
867	9.2	46.0	20	6	AR173837	Sequence	AR173837	Sequence	940	9.2	46.0	21	6	AX032641	Sequence	AX032641	Sequence
868	9.2	46.0	20	6	AR174309	Sequence	AR174309	Sequence	941	9.2	46.0	21	6				

LOCUS	SEQUENCE	FROM	PATENT	GI	ALIGNMENTS
942	9.2	46.0	21	6	AX052546 Sequence
943	9.2	46.0	21	6	AX096415 Sequence
944	9.2	46.0	21	6	AX096728 Sequence
945	9.2	46.0	21	6	AX201207 Sequence
946	9.2	46.0	21	6	AX207166 Sequence
947	9.2	46.0	21	6	AX268956 Sequence
948	9.2	46.0	21	6	AX328535 Sequence
949	9.2	46.0	21	6	AX417171 Sequence
950	9.2	46.0	21	6	AX487899 Sequence
951	9.2	46.0	21	6	113834 Sequence 42
952	9.2	46.0	21	6	123731 Sequence 53
953	9.2	46.0	21	6	131423 Sequence 33
954	9.2	46.0	21	6	133645 Sequence 25
955	9.2	46.0	22	6	A2761 Synthetic c
956	9.2	46.0	22	6	A67543 Sequence 3
957	9.2	46.0	22	6	AR129576 Sequence
958	9.2	46.0	22	6	AR142907 Sequence
959	9.2	46.0	22	6	AX059300 Sequence
960	9.2	46.0	22	6	AX076897 Sequence
961	9.2	46.0	22	6	AX092984 Sequence
962	9.2	46.0	22	6	AX134108 Sequence
963	9.2	46.0	22	6	AX189717 Sequence
964	9.2	46.0	22	6	AX357835 Sequence
965	9.2	46.0	22	6	AX403734 Sequence
966	9.2	46.0	22	6	E31644 Method for
967	9.2	46.0	22	6	E31650 Method for
968	9.2	46.0	22	6	E31652 Method for
969	9.2	46.0	22	6	E31654 Method for
970	9.2	46.0	22	6	E37729 Genes of am
971	9.2	46.0	22	6	184326 Sequence 97
972	9.2	46.0	22	12	AB068490 Synthetic
973	9.2	46.0	22	12	AB251850 Artificial
974	9.2	46.0	22	6	AR195018 Sequence
975	9.2	46.0	23	6	AR12039 Sequence
976	9.2	46.0	23	6	AR118478 Sequence
977	9.2	46.0	23	6	AX135662 Sequence
978	9.2	46.0	23	6	AX375572 Sequence
979	9.2	46.0	23	6	AX430049 Sequence
980	9.2	46.0	23	6	AX486878 Sequence
981	9.2	46.0	23	6	AX487880 Sequence
982	9.2	46.0	23	6	E33212 Expression
983	9.2	46.0	23	6	E33212 Modified hu
984	9.2	46.0	24	6	AR022226 Sequence
985	9.2	46.0	24	6	AR037900 Sequence
986	9.2	46.0	24	6	AR059908 Sequence
987	9.2	46.0	24	6	AR071046 Sequence
988	9.2	46.0	24	6	AR077027 Sequence
989	9.2	46.0	24	6	AR077485 Sequence
990	9.2	46.0	24	6	AR090715 Sequence
991	9.2	46.0	24	6	AR099837 Sequence
992	9.2	46.0	24	6	AR117459 Sequence
993	9.2	46.0	24	6	AR142238 Sequence
994	9.2	46.0	24	6	AR153394 Sequence
995	9.2	46.0	24	6	AR158379 Sequence
996	9.2	46.0	24	6	AR181901 Sequence
997	9.2	46.0	24	6	AR187770 Sequence
998	9.2	46.0	24	6	AX036458 Sequence
999	9.2	46.0	24	6	AX085592 Sequence
1000	9.2	46.0	24	6	

ALIGNMENTS

11linear PAT 20-JUN-2002

RESULT 1
LOCUS AR210275
DEFINITION Sequence 187 from patent
ACCESSION AR210275
VERSION AR210275.1
KEYWORDS GI:21512464
SOURCE Unknown.
ORGANISM Unknown.

25 bp DNA
US 6387652

REFERENCE 1 (bases 1 to 25)
AUTHORS Haugland, R. and Vesper, S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: US 6387652-2017 14-MAY-2002;
FEATURES location/Qualifiers
source 1..25
/organism="unknown"

BASE COUNT 9 a 5 c 5 g 6 t

Query Match 75.0% Score 15; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GTTGGCCACTCAGAG 20
1 GTTGGCCACTCAGAG 15

RESULT 2
LOCUS AX402703
DEFINITION Sequence 187 from Patent WO0196612.
ACCESSION AX402703
VERSION AX402703.1
KEYWORDS GI:21387694

ORGANISM
Stachybotrys chartarum.
Stachybotrys chartarum.
Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Stachybotrys.

REFERENCE
AUTHORS Haugland, R. and Vesper, S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: WO 0196612-A 187 20-DEC-2001;
UNITED STATES ENVIRONMENTAL PROTECTION AGENCY (US)

FEATURES
source 1..25
/organism="Stachybotrys chartarum"
/db_xref="taxon:74722"

BASE COUNT 9 a 5 c 5 g 6 t

Query Match 75.0% Score 15; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GTTGGCCACTCAGAG 20
1 GTTGGCCACTCAGAG 15

RESULT 3
LOCUS AX164511
DEFINITION Sequence 341 from Patent WO0138564.
ACCESSION AX164511
VERSION AX164511.1
KEYWORDS GI:14545445

ORGANISM
synthetic construct.
synthetic construct.
artificial sequences.

REFERENCE
AUTHORS Rouleau, G. A., Lattemiere, R. G., Rochefort, D., Cossette, P. and
Ragdale, D.
TITLE Local for idiopathic generalized epilepsy, mutations thereof and
method using same to assess, diagnose, prognosis or treat epilepsy
JOURNAL Patent: WO 0138564-A 341 31-MAY-2001;
MCGill University (CA)

FEATURES
source 1..24
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

BASE COUNT 6 a 5 c 2 g 10 t 1 others
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 Best Local Similarity 83.3%; Pred. No. 5.4e+03;
 Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 TTGGCTTGGCAGCTCAG 18
 DB 6 TTGGCTTATTCAGCTCAG 23
 RESULT 4
 AR122463/c AR122463 20 bp DNA linear PAT 16-MAY-2001
 LOCUS
 DEFINITION Sequence 17 from patent US 6165728.
 ACCESSION AR122463
 VERSION AR122463.1 GI:14106780
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Ward, D.T. and Cowser, L.M.
 TITLE Antisense modulation of NCR-2 expression
 JOURNAL Patent: US 6165728-A 17 26-DEC-2000;
 FEATURES Location/Qualifiers
 source 1..20
 /organism="unknown"
 BASE COUNT 7 a 4 c 7 g 2 t
 ORIGIN
 Query Match 69.0%; Score 13.8; DB 6; Length 20;
 Best Local Similarity 88.2%; Pred. No. 1.1e+04;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 TTGGCTTGGCAGCTCA 17
 DB 19 TCTGCGTTTGGCAGCTCA 3
 RESULT 5
 BD000958/c BD000958 17 bp RNA linear PAT 31-JAN-2002
 LOCUS
 DEFINITION Method and reagent for inhibiting viral replication.
 ACCESSION BD000958
 VERSION BD000958.1 GI:18625517
 KEYWORDS UP 2000342285-A/118.
 SOURCE synthetic construct.
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Draper, K.G., Dadykzt, L.W., Macswigen, J.A., Maysejak, D.G.,
 Holeser, J.J., and Mamone, A.J.
 TITLE Method and reagent for inhibiting viral replication
 JOURNAL Patent: JP 2000342285-A 118 12-DEC-2000;
 COMMENT RIBOZYME PHARMACEUTICALS INC
 OS Artificial Sequence
 PN JP 2000342285-A/118
 PD 12-DEC-2000
 PF 01-MAY-2000 JP 2000132616
 PR 11-MAY-1992 US 07/882689, 14-MAY-1992 US 07/882712 PR
 14-MAY-1992 US 07/882713, 14-MAY-1992 US 07/882714 PR
 14-MAY-1992 US 07/882882, 14-MAY-1992 US 07/882884 PR
 14-MAY-1992 US 07/882886, 14-MAY-1992 US 07/882888 PR
 14-MAY-1992 US 07/882889, 14-MAY-1992 US 07/882922 PR
 14-MAY-1992 US 07/882922, 14-MAY-1992 US 07/882923 PR
 14-MAY-1992 US 07/883849, 14-MAY-1992 US 07/884073 PR
 14-MAY-1992 US 07/884074, 14-MAY-1992 US 07/884333 PR
 14-MAY-1992 US 07/884422, 14-MAY-1992 US 07/884431 PR
 14-MAY-1992 US 07/884436, 14-MAY-1992 US 07/884521 PR
 14-MAY-1992 US 07/923738, 26-AUG-1992 US 07/935855 PR
 26-AUG-1992 US 07/936086, 18-SEP-1992 US 07/948359 PR

15-OCT-1992 US 07/963322, 07-DEC-1992 US 07/987129 PR
 07-DEC-1992 US 07/987130, 07-DEC-1992 US 07/987133 PI
 KENNETH G DRAPER, LEC W DADYKZT, JAMES A MACSWIGEN, PI DENNIS G
 MAYSEJAK,
 PI JAMES J HOLESEK, ANTHONY J MAMONE
 PC C12N15/09, C12N5/10, C12N7/00, C12N9/22// (C12N5/10, C12R1.91), PC
 C12N15/00,
 PC C12N5/00, (C12N5/00, C12R1.91)
 CC
 FH Key Location/Qualifiers
 FT source 1..17
 /organism="Artificial Sequence".
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 source 1..17
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 BASE COUNT 4 a 6 c 4 g 3 t
 ORIGIN
 Query Match 67.0%; Score 13.4; DB 6; Length 17;
 Best Local Similarity 93.3%; Pred. No. 1.9e+04;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 GCGTTGGCAGCTCAG 18
 DB 15 GAGTTGGCAGCTCAG 1
 RESULT 6
 BD001387/c BD001387 17 bp RNA linear PAT 31-JAN-2002
 LOCUS
 DEFINITION Method and reagent for inhibiting viral replication.
 ACCESSION BD001387
 VERSION BD001387.1 GI:18625946
 KEYWORDS UP 2000342286-A/118.
 SOURCE synthetic construct.
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Draper, K.G., Dadykzt, L.W., Macswigen, J.A., Maysejak, D.G.,
 Holeser, J.J., and Mamone, A.J.
 TITLE Method and reagent for inhibiting viral replication
 JOURNAL Patent: JP 2000342286-A 118 12-DEC-2000;
 COMMENT RIBOZYME PHARMACEUTICALS INC
 OS Artificial Sequence
 PN JP 2000342286-A/118
 PD 12-DEC-2000
 PF 01-MAY-2000 JP 2000132651
 PR 11-MAY-1992 US 07/882689, 14-MAY-1992 US 07/882712 PR
 14-MAY-1992 US 07/882713, 14-MAY-1992 US 07/882714 PR
 14-MAY-1992 US 07/882882, 14-MAY-1992 US 07/882884 PR
 14-MAY-1992 US 07/882886, 14-MAY-1992 US 07/882888 PR
 14-MAY-1992 US 07/882889, 14-MAY-1992 US 07/882922 PR
 14-MAY-1992 US 07/882922, 14-MAY-1992 US 07/882923 PR
 14-MAY-1992 US 07/883849, 14-MAY-1992 US 07/884073 PR
 14-MAY-1992 US 07/884074, 14-MAY-1992 US 07/884333 PR
 14-MAY-1992 US 07/884422, 14-MAY-1992 US 07/884431 PR
 14-MAY-1992 US 07/884436, 14-MAY-1992 US 07/884521 PR
 14-MAY-1992 US 07/923738, 26-AUG-1992 US 07/935854 PR
 26-AUG-1992 US 07/936086, 18-SEP-1992 US 07/948359 PR
 15-OCT-1992 US 07/963322, 07-DEC-1992 US 07/987129 PR
 07-DEC-1992 US 07/987130, 07-DEC-1992 US 07/987133 PI
 KENNETH G DRAPER, LEC W DADYKZT, JAMES A MACSWIGEN, PI DENNIS G
 MAYSEJAK,
 PI JAMES J HOLESEK, ANTHONY J MAMONE
 PC C12N15/09, C12N5/10, C12N7/00//A61K38/43, A61K39/125, A61K39/13,
 PC A61K39/135,
 PC A61K39/145, A61K39/21, A61K39/23, A61K39/245, A61K39/29, A61K48/00,
 PC A61P1/16,
 PC A61P1/14, A61P31/16, A61P31/18, A61P31/22, A61P35/02, C12Q1/68, PC
 (C12N15/09, C12R1.93), C12N15/00, C12N5/00, A61K37/48, (C12N15/00, PC
 C12R1.93)

FEATURES
source
Location/Qualifiers
/organism='Artificial Sequence'

BASE COUNT
4 a 6 c 4 g 3 t

ORIGIN
Query Match 67.0%; Score 13.4; DB 6; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.9e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY
4 GCGTTGGCCACTCAG 18
15 GAGTTGCCACTCAG 1

RESULT 7
AX288902/c 24 bp DNA linear PAT 21-NOV-2001
LOCUS
DEFINITION
Sequence 664 from Patent WO0179548.
ACCESSION
AX288902
VERSION
AX288902.1 GI:17050585
KEYWORDS
synthetic construct.
synthetic construct
artificial sequences.

REFERENCE
1 Barany, F., Zivny, M., Gerry, N.P., Favis, R. and Kliman, R.
AUTHORS
TITLE
Method of designing addressable array for detection of nucleic acid
JOURNAL
Sequence differences using ligase detection reaction
Patent: WO 0179548-A 664 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)

FEATURES
source
Location/Qualifiers
1. 24
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"

BASE COUNT
3 a 9 c 6 g 6 t

ORIGIN
Query Match 64.0%; Score 12.8; DB 6; Length 24;
Best Local Similarity 87.5%; Pred. No. 4.1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY
4 GCGTTGGCCACTCAGA 19
16 GGGATTGCCACTCAGA 1

RESULT 8
AX150973/c 25 bp DNA linear PAT 22-JUN-2001
LOCUS
DEFINITION
Sequence 3 from Patent WO0140471.
ACCESSION
AX150973
VERSION
AX150973.1 GI:14533204
KEYWORDS
Mycoplasma mycoides.
Mycoplasma mycoides
Mycoplasma mycoides
Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;
Entomoplasmataceae.
1 (bases 1 to 25)
Prey, J.J., Nicolet, J.J. and Abdo, E.E.
Antigenic protein 1ppg of Mycoplasma mycoides subsp. (mycoides)
bc., its preparation and use
Patent: WO 0140471-A 3 07-JUN-2001;
Akzo Nobel N.V. (NL)

REFERENCE
AUTHORS
TITLE
JOURNAL
Akzo Nobel N.V. (NL)

FEATURES
source
Location/Qualifiers
1. 25
/organism="Mycoplasma mycoides"
/db_xref="taxon:2102"

primer_bind 1. 25
BASE COUNT 15 a 3 c 5 g 2 t

ORIGIN
Query Match 64.0%; Score 12.8; DB 6; Length 25;
Best Local Similarity 87.5%; Pred. No. 4.1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY
2 TTGGCTTGGCCACTCA 17
23 TTGTTTGGCCACTCA 8

RESULT 9
AX353540 20 bp DNA linear PAT 06-FEB-2002
LOCUS
DEFINITION
Sequence 72 from Patent WO0204636.
ACCESSION
AX353540
VERSION
AX353540.1 GI:18618615
KEYWORDS
synthetic construct.
synthetic construct
artificial sequences.

REFERENCE
1 van Roy, F., Goossens, S., Janssens, B. and Vampoucke, G.
AUTHORS
TITLE
Novel g(a) expressed in heart and testis
JOURNAL
Patent: WO 0204636-A 72 17-JAN-2002;
Vlaams Interuniversitair Instituut voor Biotechnologie vzw. (BE)

FEATURES
source
Location/Qualifiers
1. 20
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="lower primer FVR2536"

BASE COUNT
6 a 5 c 5 g 4 t

ORIGIN
Query Match 63.0%; Score 12.6; DB 6; Length 20;
Best Local Similarity 78.9%; Pred. No. 5.2e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY
2 TTGGCTTGGCCACTCAG 20
1 TGGCACTTGACACTCAG 19

RESULT 10
AX039884 21 bp DNA linear PAT 18-NOV-2000
LOCUS
DEFINITION
Sequence 273 from Patent WO0063441.
ACCESSION
AX039884
VERSION
AX039884.1 GI:11229913
KEYWORDS
synthetic construct.
synthetic construct
artificial sequences.

REFERENCE
1 (bases 1 to 21)
Herrnstadt, C. and Davis, R.E.
Single nucleotide polymorphisms in mitochondrial genes that segregate with Alzheimer's disease
Patent: WO 0063441-A 273 26-OCT-2000;
MITOXOR (US)

FEATURES
source
Location/Qualifiers
1. 21
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="PCR primer"

BASE COUNT
5 a 2 c 6 g 8 t

ORIGIN
Query Match 63.0%; Score 12.6; DB 6; Length 21;
Best Local Similarity 78.9%; Pred. No. 5.2e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTTGGCTTGCACCTCAGA 19
DB 1 TTTGAGTTTGCTAGGACAGA 19

RESULT 11
AX217169
LOCUS AX217169
DEFINITION Sequence 2611 from Patent WO0159103.
ACCESSION AX217169
VERSION AX217169.1 GI:15527230
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE artificial sequences.
AUTHORS 1 (bases 1 to 17)
TITLE Blatt, L., McSwiggen, J. and Chowrita, B.M.
JOURNAL Method and reagent for the modulation and diagnosis of cd20 and
PATENT: WO 0159103-A 2611 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrita, Bharat M. (US)
FEATURES
source Location/Qualifiers
1..17
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Nucleic Acid"

BASE COUNT 2 a 6 c 3 g 6 t

ORIGIN

Query Match 61.0%; Score 12.2; DB 6; Length 17;
Best Local Similarity 82.4%; Pred. No. 8.4e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTGGCTTGCACCTCA 17
DB 1 TCTGCTTGCACCTCA 17

RESULT 12
AX422057/c
LOCUS AX422057
DEFINITION Sequence 393 from Patent WO0188124.
ACCESSION AX422057
VERSION AX422057.1 GI:21525439
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Jarvis, T., von Carlowitz, I., McSwiggen, J.A., McLaughlin, F.G. and
Randi, A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 393 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 3 a 5 c 5 g 4 t

ORIGIN

Query Match 61.0%; Score 12.2; DB 6; Length 17;
Best Local Similarity 82.4%; Pred. No. 8.4e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GGGTTGCACCTCAGAG 20
DB 17 GCGTTCGACCTCAAG 1

RESULT 13

DOGPA1402
LOCUS DOGPA1402
DEFINITION Dog (clone: CXK.414) primer for STS 414, 3' end.
ACCESSION L24303
VERSION L24303.1 GI:401997
KEYWORDS PCR identification; PCR primer; STS.
SEGMENT 2 of 2
SOURCE Canis familiaris (library: E. Osterander, in pbluescript+) adult
splenic DNA.
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 20)
AUTHORS Osterander, E.A., Mapa, F.A., Yee, M. and Rine, J.
TITLE One hundred and one new simple sequence repeat-based markers for
the canine genome
JOURNAL Mamm. Genome 6 (3), 192-195 (1995)
MEDLINE 95268214
PUBMED 7749226
COMMENT Submitted by:
Fred Hutchinson Cancer Research Center
Transplantation Biology Dept
1124 Columbia; Mailstop M318
Seattle, WA 98104, USA
e-mail: EOsterander@bl.gov
PCR Buffer: PCR buffer (Perkin-Elmer/Cetus)
PCR Profile: Denaturation: 94 degrees C for 1.00 minute
Annealing: 55 or 59 degrees C for 0.45 minutes
Polymerization: 74 degrees C for 1.00 minutes
PCR Cycles: 33
Final Extension: 74 degrees C for 5.00 minutes.
FEATURES
source Location/Qualifiers
1..20
/organism="Canis familiaris"
/db_xref="taxon:9615"
/tissue.type="spleen"
/dev stage="adult"
/tissue_lbp="E. Osterander, in pbluescript+"
complement(1..20)

BASE COUNT 4 a 5 c 5 g 6 t

ORIGIN

primer_bind
complement(1..20)

Query Match 61.0%; Score 12.2; DB 4; Length 20;
Best Local Similarity 82.4%; Pred. No. 8.6e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTTGGCTTGCACCTCAG 18
DB 1 TTTGGCTTGCACCTCAG 17

RESULT 14
AR003705/c
LOCUS AR003705
DEFINITION Sequence 2 from patent US 5744368.
ACCESSION AR003705
VERSION AR003705.1 GI:3964964
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 22)
TITLE Goldgaber, D.Y., Schwartzman, A.L. and Eisenberg-Grunberg, M.
METHODS For the detection of soluble amyloid, beta-protein
(beta.AP) or soluble transthyretin (TTR)
JOURNAL Patent: US 5744368-A 2 28-APR-1998;
FEATURES
source Location/Qualifiers
1..22
/organism="unknown"

BASE COUNT 8 a 2 c 10 g 2 t

ORIGIN

Query Match 61.0%; Score 12.2; DB 6; Length 22;

Best Local Similarity 82.4%; Pred. No. 8.6e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTTCGCTTGGCACTCA 17
19 TTTCGCTTGGCCCTCA 3

RESULT 15
AR210196 24 bp DNA linear PAT 20-JUN-2002
LOCUS
DEFINITION Sequence 108 from patent US 6387652.
ACCESSION AR210196
VERSION AR210196.1 GI:21512365
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Haugland, R. and Vesper, S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: US 6387652-A 108 14-MAY-2002;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"

BASE COUNT 9 a 4 c 6 g 5 t
ORIGIN

Query Match 61.0%; Score 12.2; DB 6; Length 24;
Best Local Similarity 82.4%; Pred. No. 8.7e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCGTTGGCACTCAGAG 20
1 GCTGTGCACTCAGAG 17

RESULT 16
AX402624 24 bp DNA linear PAT 07-JUN-2002
LOCUS
DEFINITION Sequence 108 from Patent W00196612.
ACCESSION AX402624
VERSION AX402624.1 GI:21387615
KEYWORDS
SOURCE nematode egg-parasitic fungus.
ORGANISM Paecilomyces lilacinus
REFERENCE 1
AUTHORS Haugland, R. and Vesper, S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: WO 0196612-A 108 20-DEC-2001;
UNITED STATES ENVIRONMENTAL PROTECTION AGENCY (US)
FEATURES Location/Qualifiers
source 1..24
/organism="Paecilomyces lilacinus"
/db_xref="taxon:33203"

BASE COUNT 9 a 4 c 6 g 5 t
ORIGIN

Query Match 61.0%; Score 12.2; DB 6; Length 24;
Best Local Similarity 82.4%; Pred. No. 8.7e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCGTTGGCACTCAGAG 20
1 GCTGTGCACTCAGAG 17

RESULT 17
AR040151 17 bp DNA linear PAT 29-SEP-1999
LOCUS

DEFINITION Sequence 999 from patent US 5807743.
ACCESSION AR040151
VERSION AR040151.1 GI:5959514
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb, D.T. and McSwiggen, J.A.
TITLE Interleukin-2 receptor gamma-chain ribozymes
JOURNAL Patent: US 5807743-A 999 15-SEP-1998;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"

BASE COUNT 3 a 7 c 2 g 5 t
ORIGIN

Query Match 60.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TTCCCACTCAGA 19
1 TTCCCACTCAGA 12

RESULT 18
AR166679 21 bp DNA linear PAT 17-OCT-2001
LOCUS
DEFINITION Sequence 29 from patent US 6281346.
ACCESSION AR166679
VERSION AR166679.1 GI:16242091
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Hees, J.W., Caskey, C., Thomas, L., Liu, Q. and Phillips, M. Sean.
TITLE Rat ob-receptor and nucleotides encoding them
JOURNAL Patent: US 6281346-A 29 28-AUG-2001;
FEATURES Location/Qualifiers
source 1..21
/organism="unknown"

BASE COUNT 5 a 3 c 7 g 6 t
ORIGIN

Query Match 60.0%; Score 12; DB 6; Length 21;
Best Local Similarity 75.0%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TTTCGCTTGGCACTCAGAG 20
2 TTTCGCTTGGCACTCAGAG 21

RESULT 19
AX268543 23 bp DNA linear PAT 29-OCT-2001
LOCUS
DEFINITION Sequence 22 from Patent W00174903.
ACCESSION AX268543
VERSION AX268543.1 GI:16541697
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Welcher, A.A. and Calzone, F.J.
TITLE Cd20/lige-receptor like molecules and uses thereof
JOURNAL Patent: WO 0174903-A 22 11-OCT-2001;
Amgen, Inc. (US)
FEATURES Location/Qualifiers
source 1..23
/organism="synthetic construct"

BASE COUNT 7 a 7 c 4 g 5 t
 ORIGIN

Query Match 60.0%; Score 12; DB 6; Length 23;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TGGCCTGAG 20
 23 TGGCCTGAG 12

RESULT 20
 AX216558
 LOCUS AX216558 17 bp mRNA linear PAT 07-SEP-2001
 DEFINITION Sequence 2000 from Patent WO0159103.
 ACCESSION AX216558
 VERSION AX216558.1 GI:15526619
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE

1 (bases 1 to 17)
 1.17
 Location/Qualifiers
 1.17
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="Nucleic Acid"
 3 a 6 c 3 g 5 t

BASE COUNT 3 a 6 c 3 g 5 t
 ORIGIN

Query Match 59.0%; Score 11.8; DB 6; Length 17;
 Best Local Similarity 86.7%; Pred. No. 1.4e+05;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TGGCTTGGCCTCA 17
 2 TGGCTTGGCCTCA 16

RESULT 21
 AX059295/c
 LOCUS AX059295 20 bp DNA linear PAT 17-JAN-2001
 DEFINITION Sequence 28 from Patent WO0055325.
 ACCESSION AX059295
 VERSION AX059295.1 GI:12311400
 KEYWORDS
 SOURCE

thale cress.
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons, core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 20)
 1.20
 Location/Qualifiers
 1.20
 /organism="Arabidopsis thaliana"
 /db_xref="taxon:3702"

BASE COUNT 9 a 4 c 5 g 2 t
 ORIGIN

Query Match 59.0%; Score 11.8; DB 6; Length 20;

Best Local Similarity 86.7%; Pred. No. 1.4e+05;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTTCGTTGGCACT 15
 17 TTTCGTTGGCACT 3

RESULT 22
 AX467734
 LOCUS AX467734 22 bp DNA linear PAT 16-JUL-2002
 DEFINITION Sequence 14 from Patent WO0244332.
 ACCESSION AX467734
 VERSION AX467734.1 GI:21900906
 KEYWORDS
 SOURCE

human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 FEATURES
 source
 1.22
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 6 a 8 c 2 g 6 t
 ORIGIN

Query Match 59.0%; Score 11.8; DB 6; Length 22;
 Best Local Similarity 86.7%; Pred. No. 1.4e+05;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TGGCTTGGCCTCA 17
 5 TGGCTTGGCCTCA 19

RESULT 23
 AX291474/c
 LOCUS AX291474 24 bp DNA linear PAT 21-NOV-2001
 DEFINITION Sequence 3236 from Patent WO0179548.
 ACCESSION AX291474
 VERSION AX291474.1 GI:17053157
 KEYWORDS
 SOURCE

synthetic construct.
 artificial sequences.
 1
 1.24
 Location/Qualifiers
 1.24
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="Hypothetical Probe Sequence"

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 FEATURES
 source
 1.24
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="Hypothetical Probe Sequence"

BASE COUNT 4 a 7 c 7 g 6 t
 ORIGIN

Query Match 59.0%; Score 11.8; DB 6; Length 24;
 Best Local Similarity 86.7%; Pred. No. 1.4e+05;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CGTTGGCACTGAG 19
 23 CGTTGGCACTGAG 9

FEATURES	source	Location/Qualifiers
TITLE	Probes and decoder oligonucleotides	
JOURNAL	Patent: WO 0216649-A 2248 28-FEB-2002; Illumina, Inc. (US)	
BASE COUNT	8 a 5 c 7 g 4 t	
ORIGIN		
Query Match	58.0%; Score 11.6; DB 6; Length 24;	
Best Local Similarity	77.8%; Pred. No. 1.9e+05;	
Matches	14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	
QY	1 TTTCGTTTGCCTCAG 18 	
Db	18 TTTCGTTTTCACCG 1	
RESULT 29		
LOCUS	AX116728 25 bp DNA	linear PAT 11-MAY-2001
DEFINITION	Sequence 1851 from Patent W00129262.	
ACCESSION	AX116728	
VERSION	AX116728.1 GI:14033670	
KEYWORDS		
SOURCE	synthetic construct.	
ORGANISM	synthetic construct	
REFERENCE	artificial sequences.	
AUTHORS	1 (bases 1 to 25)	
TITLE	Picoult-Newburg, L. and Pohl, M.	
JOURNAL	Genotyping reagents, kits and methods of use thereof Patent: WO 0129262-A 1851 26-APR-2001; Orchid Biosciences, Inc. (US)	
FEATURES	location/Qualifiers	
source	1..25 /organism="synthetic construct" /db_xref="taxon:32630" /note="Primer"	
BASE COUNT	6 a 8 c 4 g 7 t	
ORIGIN		
Query Match	58.0%; Score 11.6; DB 6; Length 25;	
Best Local Similarity	77.8%; Pred. No. 1.9e+05;	
Matches	14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	
QY	2 TTGCGTTGCCTCAGA 19 	
Db	3 TTGCGTTGCTCTCTGA 20	
RESULT 30		
LOCUS	AX001122 21 bp DNA	linear PAT 10-MAR-2000
DEFINITION	Sequence 1 from Patent W09901563.	
ACCESSION	AX001122	
VERSION	AX001122.1 GI:7241321	
KEYWORDS		
SOURCE	unidentified.	
ORGANISM	unidentified	
REFERENCE	unclassified.	
AUTHORS	1 (bases 1 to 21)	
TITLE	Goddijn, O. J. and Ohl, S. A.	
JOURNAL	PLASMIDS FOR PLANT TRANSFORMATION AND METHOD FOR USING THE SAME Patent: WO 9901563-A 1 14-JAN-1999; GODDIJN OSCAR JOHANN MARIA (NL); OHL STEPHAN ANDREAS (NL)	
FEATURES	location/Qualifiers	
source	1..21 /organism="unidentified" /db_xref="taxon:32644"	
BASE COUNT	8 a 3 c 7 g 3 t	
ORIGIN		

	Query Match	57.0%;	Score 11.4;	DB 6;	Length 21;	
	Best Local Similarity	92.3%;	Pred. No. 2.4e+05;			
	Matches 12; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;	
QY	1 TTGCGTTTGCCA 13					
Dd	15 TTAGCGTTTGCCA 3					
RESULT 31						
LOCUS	AXI53966	21 bp	DNA		linear	PAT 22-JUN-2001
DEFINITION	Sequence 64 from Patent WO0138576.					
ACCESSION	AXI53966					
VERSION	AXI53966.1	GI:14535580				
KEYWORDS						
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 21)					
AUTHORS	Cargill,W.; Ireland,J.S. and Lander,E.S.					
TITLE	Human single nucleotide polymorphisms					
JOURNAL	Patent: WO 0138576-A 64 31-MAY-2001; WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) Location/Qualifiers					
FEATURES	1..21					
source	/organism="Homo sapiens" /db_xref="taxon:9606"					
BASE COUNT	3 a 2 c 5 g 10 t 1 others					
ORIGIN						
Query Match	57.0%;	Score 11.4;	DB 6;	length 21;		
Best Local Similarity	80.0%;	Pred. No. 2.4e+05;				
Matches 12; Conservative	1;	Mismatches 2;	Indels 0;	Gaps 0;		
QY	4 GCGTTTGCCTACTCAG 18					
Dd	3 GTGTTCGCAATTCAG 17					
RESULT 32						
LOCUS	AJ2924	24 bp	DNA		linear	PAT 11-DEC-1996
DEFINITION	synthetic PCR primer FDPcRFOR.					
ACCESSION	AJ2924					
VERSION	AJ2924.1	GI:1926573				
KEYWORDS						
SOURCE	synthetic construct.					
ORGANISM	synthetic construct					
FEATURES	artificial sequences.					
source	Location/Qualifiers 1..24 /organism="synthetic construct" /db_xref="taxon:32630"					
BASE COUNT	4 a 8 c 4 g 8 t					
ORIGIN						
Query Match	57.0%;	Score 11.4;	DB 6;	length 24;		
Best Local Similarity	92.3%;	Pred. No. 2.4e+05;				
Matches 12; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;		
QY	1 TTTGCGTTTGCCA 13					
Dd	12 TTAGCGTTTGCCA 24					
RESULT 33						
LOCUS	AXI75376	24 bp	DNA		linear	PAT 03-JUL-2001
DEFINITION	Sequence 53 from Patent WO0142308.					
ACCESSION	AXI75376					

VERSION AX175376.1 GI:14598736
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 FEATURES
 source
 1. .24
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="gback primer"
 BASE COUNT 3 a 9 c 4 g 8 t
 ORIGIN
 Query Match 57.0%; Score 11.4; DB 6; Length 24;
 Best Local Similarity 92.3%; Pred. No. 2.4e+05;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 TTGGCGTTGCCA 13
 Db 10 TTAGCGTTGCCA 22
 RESULT 34
 AR090389/c 25 bp DNA linear PAT 07-SEP-2000
 LOCUS
 DEFINITION Sequence 509 from patent US 5994076.
 ACCESSION AR090389
 VERSION AR090389.1 GI:10017144
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 FEATURES
 source
 1. .25
 /organism="unknown"
 BASE COUNT 7 a 7 c 8 g 3 t
 ORIGIN
 Query Match 57.0%; Score 11.4; DB 6; Length 25;
 Best Local Similarity 92.3%; Pred. No. 2.4e+05;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 8 TTGCCACTCAGAG 20
 Db 17 TTGCCACTCTGAG 5
 RESULT 35
 AR197424/c 25 bp DNA linear PAT 20-APR-2002
 LOCUS
 DEFINITION Sequence 509 from patent US 6352829.
 ACCESSION AR197424
 VERSION AR197424.1 GI:20247273
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 FEATURES
 source
 1. .25
 /organism="unknown"
 BASE COUNT 7 a 7 c 8 g 3 t
 ORIGIN
 Query Match 57.0%; Score 11.4; DB 6; Length 25;
 Best Local Similarity 92.3%; Pred. No. 2.4e+05;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 8 TTGCCACTCAGAG 20
 Db 17 TTGCCACTCTGAG 5

BASE COUNT 7 a 7 c 8 g 3 t
 ORIGIN
 Query Match 57.0%; Score 11.4; DB 6; Length 25;
 Best Local Similarity 92.3%; Pred. No. 2.4e+05;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 8 TTGCCACTCAGAG 20
 Db 17 TTGCCACTCTGAG 5
 RESULT 36
 BD006741/c 25 bp DNA linear PAT 31-JAN-2002
 LOCUS
 DEFINITION Novel polypeptide.
 ACCESSION BD006741
 VERSION BD006741.1 GI:18635112
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Ito, Y., Mogi, S., Tanaka, H., Okubo, S. and Ogi, K.
 Novel polypeptide
 Patent: JP 2001029090-A 44 06-FEB-2001,
 TAKEDA CHEMICAL INDUSTRIES LTD
 OS Artificial Sequence
 PN JP 2001029090-A/44
 PD 06-FEB-2001 JP 2000147530
 PF 19-MAY-2000 JP 2000147530
 PR
 PI YASUAKI ITO, SHINICHI MOGI, HIDEYUKI TANAKA, SHOICHI OKUBO, PI
 KAZUHIRO OGI
 PC C12N15/09, A61K38/00, A61K39/395, A61K39/395, A61K45/00, A61K48/00,
 PC A61P1/00,
 PC A61P5/00, A61P9/00, A61P11/00, A61P25/00, A61P25/18, A61P31/00, PC
 A61P35/00,
 PC A61P37/00, C07K14/47, C07K16/18, C12P21/02, G01N33/15, G01N33/50,
 PC G01N33/566//
 PC C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/08, C12P21/02, PC
 C12R1:91),
 PC (C12N5/10, C12R1:91), (C12P21/08, C12R1:91), C12N15/00, A61K37/02,
 PC C12N5/00,
 PC (C12N5/00, C12R1:91)
 CC
 FH Key Location/Qualifiers
 FT source 1. .25
 FT /organism="Artificial Sequence".
 Location/Qualifiers
 source
 1. .25
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 BASE COUNT 8 a 5 c 8 g 4 t
 ORIGIN
 Query Match 57.0%; Score 11.4; DB 6; Length 25;
 Best Local Similarity 92.3%; Pred. No. 2.4e+05;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 2 TTGGCTTGGCAC 14
 Db 20 TTGCATTGGCCAC 8
 RESULT 37
 AX215063 17 bp mRNA linear PAT 07-SEP-2001
 LOCUS
 DEFINITION Sequence 505 from Patent WO0159103.
 ACCESSION AX215063
 VERSION AX215063.1 GI:15525106
 KEYWORDS

SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt, L., McSwigen, J. and Chowira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL RHOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwigen, James (US) ; Chowira, Bharat M. (US)
FEATURES
source 1..17
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Nucleic Acid"
BASE COUNT 1 a 6 c 3 g 7 t
ORIGIN

Query Match 56.0%; Score 11.2; DB 6; Length 17;
Best Local Similarity 81.2%; Pred. No. 3e+05; 3; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTGGCTTGGCCACTC 16
| | | | | | | | | | | | | | | | | |
2 TCTGCTTGGCCACTC 17

RESULT 38
AX422987 17 bp mRNA linear PAT 18-JUN-2002
LOCUS AX422987/c
DEFINITION Sequence 1323 from Patent WO0188124.
ACCESSION AX422987
VERSION AX422987.1 GI:21526369
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Jarvis, T., von Carlwitz, I., McSwigen, J.A., McLaughlin, F.G. and
Randi, A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 1323 22-NOV-2001, GLAXO GROUP LIMITED (GB)
FEATURES
source 1..17
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 3 a 4 c 5 g 5 t
ORIGIN

Query Match 56.0%; Score 11.2; DB 6; Length 17;
Best Local Similarity 81.2%; Pred. No. 3e+05; 3; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCGTTGCCACTCAGA 19
| | | | | | | | | | | | | | | | | |
16 GCGTTGCCACTCAGA 1

RESULT 39
AX119996 19 bp DNA linear PAT 11-MAY-2001
LOCUS AX119996
DEFINITION Sequence 18 from Patent WO0129217.
ACCESSION AX119996
VERSION AX119996.1 GI:114036730
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 19)
AUTHORS Prayaga, S.K., Taupier, R.J. and Bandaru, R.
TITLE Polypeptides and polynucleotides encoding same

JOURNAL Patent: WO 0129217-A 18 26-APR-2001;
Curagen Corporation (US)
FEATURES
source 1..19
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Primer"
BASE COUNT 3 a 6 c 7 g 3 t
ORIGIN

Query Match 56.0%; Score 11.2; DB 6; Length 19;
Best Local Similarity 81.2%; Pred. No. 3e+05; 3; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 TGCCTTGGCCACTCAG 18
| | | | | | | | | | | | | | | | | |
4 TGCCTTGGCCACTCAG 19

RESULT 40
I25829/c 19 bp DNA linear PAT 07-OCT-1996
LOCUS I25829
DEFINITION Sequence 9 from patent US 5552390.
ACCESSION I25829
VERSION I25829.1 GI:1605699
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Scholar, E.M. and Iversen, P.L.
TITLE Phosphorothioate inhibitors of metastatic breast cancer
JOURNAL Patent: US 5552390-A 9 03-SEP-1996;
FEATURES
source 1..19
/organism="Unknown"
BASE COUNT 4 a 3 c 9 g 3 t
ORIGIN

Query Match 56.0%; Score 11.2; DB 6; Length 19;
Best Local Similarity 81.2%; Pred. No. 3e+05; 3; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TTGGCTTGGCCACTCA 17
| | | | | | | | | | | | | | | | | |
19 TTGGCTTGGCCACTCA 4

Search completed: June 7, 2003, 08:51:04
Job time : 453.909 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 7, 2003, 08:19:34 ; Search time 35.8545 Seconds

(without alignments)
145,407 Million cell updates/sec

Title: US-10-080-959A-1

Perfect score: 17
1 gtcgttcgsgcggaac 17

Scoring table: IDENTITY_NUC
Gapop 10.0 ; Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 364338

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	12.4	72.9	21	4	US-09-593-012-191
3	12.4	72.9	21	4	US-09-593-012-194
4	12.4	72.9	21	4	US-09-593-012-203
5	12.4	72.9	22	4	US-09-593-012-31
6	12.2	71.8	20	1	US-08-233-608-24
7	12.2	71.8	20	1	US-08-887-480-24
8	12.2	71.8	20	2	US-08-723-187-24
9	12.2	71.8	20	5	PCT-US95-04712-24
10	12	70.6	17	4	US-09-593-012-120
11	11.8	69.4	20	4	US-09-428-219-70
12	11.4	67.1	16	1	US-08-291-932A-812
13	11.4	67.1	16	1	US-08-887-480-57
14	11.4	67.1	16	1	US-08-887-480-64
15	11.4	67.1	16	2	US-08-722-187-57
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21	11.4	67.1	18	4	US-09-616-990-19
22	11.4	67.1	21	1	US-08-652-127C-1
23	11.2	65.9	18	2	US-08-358-556A-1
24	11.2	65.9	20	3	US-08-281-203-6
25	11.2	65.9	20	4	US-09-326-186B-146
26	11.2	65.9	25	1	US-08-005-283-4
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C 104	9.8	57.6	18	4	US-09-808-126-26	Sequence 26, Appl	C 177	9.4	55.3	21	2	US-08-472-659-15	Sequence 15, Appl
C 105	9.8	57.6	18	4	US-09-803-951-26	Sequence 26, Appl	C 178	9.4	55.3	21	2	US-08-611-977-15	Sequence 15, Appl
C 106	9.8	57.6	19	1	US-08-655-220-5	Sequence 5, Appl	C 179	9.4	55.3	21	5	PCT-US95-04477-63	Sequence 63, Appl
C 107	9.8	57.6	19	2	US-08-818-408B-5	Sequence 5, Appl	C 180	9.4	55.3	21	5	US-08-231-990-44	Sequence 44, Appl
C 108	9.8	57.6	19	3	US-08-818-256A-9	Sequence 9, Appl	C 181	9.4	55.3	22	1	US-08-367-122-44	Sequence 44, Appl
C 109	9.8	57.6	19	3	US-09-911-692-5	Sequence 5, Appl	C 182	9.4	55.3	22	1	US-07-951-715A-86	Sequence 86, Appl
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C 111	9.8	57.6	20	1	US-08-379-295-52	Sequence 52, Appl	C 184	9.4	55.3	22	1	US-08-459-448A-86	Sequence 86, Appl
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C 115	9.8	57.6	20	4	US-09-428-219-43	Sequence 43, Appl	C 188	9.4	55.3	22	3	US-08-459-444-86	Sequence 86, Appl
C 116	9.8	57.6	20	4	US-09-593-711A-192	Sequence 192, Appl	C 189	9.4	55.3	22	4	US-09-547-422-86	Sequence 86, Appl
C 117	9.8	57.6	20	4	US-09-326-186B-65	Sequence 65, Appl	C 190	9.4	55.3	22	4	US-09-547-422-86	Sequence 86, Appl
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C 125	9.8	57.6	22	1	US-08-462-577B-38	Sequence 38, Appl	C 198	9.4	55.3	25	4	US-08-062-023-10	Sequence 10, Appl
C 126	9.8	57.6	22	2	US-09-018-422-1	Sequence 1, Appl	C 199	9.4	55.3	25	4	US-09-493-352A-3	Sequence 3, Appl
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C 168	9.4	55.3	17	3	US-08-968-505-40	Sequence 40, Appl	C 241	9.4	55.3	25	1	US-08-991-932A-136	Sequence 136, Appl
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C 276	9.2	54.1	25	2	US-08-117-952-566	Sequence 566, App	C 349	9	52.9	25	2	US-08-260-546-12	Sequence 12, Appl
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C 278	9.2	54.1	25	3	US-08-839-765-32	Sequence 32, Appl	C 351	9	52.9	25	2	US-08-910-856-11	Sequence 11, Appl
C 279	9.2	54.1	25	3	US-09-136-389-32	Sequence 32, Appl	C 352	9	52.9	25	3	US-08-859-998-777	Sequence 777, App
C 280	9.2	54.1	25	4	US-08-943-731-379	Sequence 379, App	C 353	9	52.9	25	3	US-08-913-374-5	Sequence 5, Appl
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C 286	9.2	54.1	16	2	US-08-282-197C-4	Sequence 4, Appl	C 359	8.8	51.8	14	1	US-08-687-551-14	Sequence 14, Appl
C 287	9.2	54.1	17	1	US-08-373-124A-187	Sequence 1387, Ap	C 360	8.8	51.8	14	1	US-08-333-030-27	Sequence 27, Appl
C 288	9.2	54.1	17	1	US-08-435-628-1387	Sequence 1387, Ap	C 361	8.8	51.8	15	1	US-09-063-667-18	Sequence 18, Appl
C 289	9.2	54.1	18	3	US-09-071-710-21	Sequence 21, Appl	C 362	8.8	51.8	15	1	US-08-434-503-50	Sequence 50, Appl
C 290	9.2	54.1	18	4	US-09-825-397-21	Sequence 21, Appl	C 363	8.8	51.8	15	1	US-08-241-372-10	Sequence 10, Appl
C 291	9.2	54.1	18	4	US-08-651-155B-2	Sequence 2, Appl	C 364	8.8	51.8	15	1	US-08-291-932A-130	Sequence 130, Appl
C 292	9.2	54.1	18	4	US-09-545-686-32	Sequence 32, Appl	C 365	8.8	51.8	15	1	US-08-110-294A-4	Sequence 4, Appl
C 293	9.2	54.1	19	1	US-08-717-526-38	Sequence 38, Appl	C 366	8.8	51.8	15	2	US-08-389-926-4	Sequence 2, App
C 294	9.2	54.1	19	2	US-08-671-978A-22	Sequence 22, Appl	C 367	8.8	51.8	15	4	US-08-585-684B-2259	Sequence 2259, Ap
C 295	9.2	54.1	19	2	US-08-671-978A-24	Sequence 24, Appl	C 368	8.8	51.8	15	4	US-09-038-073-2259	Sequence 2259, Ap
C 296	9.2	54.1	20	1	US-08-535-697-12	Sequence 12, Appl	C 369	8.8	51.8	15	4	US-09-180-437-146	Sequence 146, App
C 297	9.2	54.1	20	2	US-08-743-637B-229	Sequence 229, App	C 370	8.8	51.8	15	4	US-09-081-646-415	Sequence 415, App
C 298	9.2	54.1	20	3	US-09-287-796-105	Sequence 105, App	C 371	8.8	51.8	15	5	PCT-US95-05420-10	Sequence 10, Appl
C 299	9.2	54.1	20	3	US-09-288-461-27	Sequence 27, Appl	C 372	8.8	51.8	17	1	US-08-286-856C-14	Sequence 14, Appl
C 300	9.2	54.1	20	4	US-09-130-616-105	Sequence 105, App	C 373	8.8	51.8	18	1	US-08-717-526-45	Sequence 45, Appl
C 301	9.2	54.1	20	4	US-09-489-869-34	Sequence 34, Appl	C 374	8.8	51.8	18	1	US-08-742-023-28	Sequence 28, Appl
C 302	9.2	54.1	20	4	US-09-488-295-17	Sequence 17, Appl	C 375	8.8	51.8	18	2	US-08-533-306A-13	Sequence 13, Appl
C 303	9.2	54.1	20	4	US-09-705-299-71	Sequence 71, Appl	C 376	8.8	51.8	18	2	US-08-742-923A-13	Sequence 13, Appl
C 304	9.2	54.1	21	1	US-07-718-274A-48	Sequence 48, Appl	C 377	8.8	51.8	18	2	US-08-222-617A-22	Sequence 22, Appl
C 305	9.2	54.1	21	1	US-08-149-106-48	Sequence 48, Appl	C 378	8.8	51.8	18	2	US-08-912-129A-42	Sequence 42, Appl
C 306	9.2	54.1	21	1	US-08-298-021-48	Sequence 48, Appl	C 379	8.8	51.8	18	2	US-09-256-496-79	Sequence 79, Appl
C 307	9.2	54.1	21	2	US-07-662-764D-5	Sequence 5, Appl	C 380	8.8	51.8	18	3	US-09-144-579-11	Sequence 11, Appl
C 308	9.2	54.1	21	2	US-08-101-624-9	Sequence 9, Appl	C 381	8.8	51.8	18	3	US-08-868-505-28	Sequence 28, Appl
C 309	9.2	54.1	21	3	US-08-479-744A-9	Sequence 9, Appl	C 382	8.8	51.8	18	4	US-09-387-341-209	Sequence 209, App
C 310	9.2	54.1	21	3	US-08-280-757B-9	Sequence 9, Appl	C 383	8.8	51.8	18	4	US-09-387-341-213	Sequence 213, App
C 311	9.2	54.1	21	3	US-08-611-587-28	Sequence 28, Appl	C 384	8.8	51.8	20	1	US-08-102-863-5	Sequence 5, Appl
C 312	9.2	54.1	21	4	US-09-168-406A-39	Sequence 39, Appl	C 385	8.8	51.8	20	1	US-08-033-081B-17	Sequence 17, Appl
C 313	9.2	54.1	21	4	US-09-471-016-11	Sequence 11, Appl	C 386	8.8	51.8	20	1	US-08-243-542-18	Sequence 18, Appl
C 314	9.2	54.1	21	4	US-09-249-697A-13	Sequence 13, Appl	C 387	8.8	51.8	20	1	US-08-250-856A-18	Sequence 18, Appl
C 315	9.2	54.1	21	4	US-09-363-316B-13	Sequence 13, Appl	C 388	8.8	51.8	20	1	US-08-477-407-18	Sequence 18, Appl
C 316	9.2	54.1	22	1	US-08-233-030-50	Sequence 50, Appl	C 389	8.8	51.8	20	1	US-08-435-529-2	Sequence 2, Appl
C 317	9.2	54.1	22	4	US-09-302-812-35	Sequence 35, Appl	C 390	8.8	51.8	20	1	US-08-110-429A-6	Sequence 6, Appl
C 318	9.2	54.1	22	4	US-09-511-477-35	Sequence 35, Appl	C 391	8.8	51.8	20	1	US-08-484-355-18	Sequence 18, Appl
C 319	9.2	54.1	22	4	US-09-511-507-35	Sequence 35, Appl	C 392	8.8	51.8	20	1	US-08-531-556-113	Sequence 113, App

C 393	8.8	51.8	20	2	US-08-448-386A-13	Sequence 13, Appl
C 394	8.8	51.8	20	2	US-08-117-952-417	Sequence 417, Appl
C 395	8.8	51.8	20	2	US-08-690-734A-5	Sequence 5, Appl
C 396	8.8	51.8	20	2	US-08-690-734A-76	Sequence 76, Appl
C 397	8.8	51.8	20	2	US-08-483-528B-77	Sequence 77, Appl
C 398	8.8	51.8	20	2	US-08-483-528B-78	Sequence 78, Appl
C 399	8.8	51.8	20	2	US-08-756-806A-18	Sequence 18, Appl
C 400	8.8	51.8	20	2	US-08-031-538-23	Sequence 23, Appl
C 401	8.8	51.8	20	3	US-08-589-939-45	Sequence 45, Appl
C 402	8.8	51.8	20	3	US-08-742-185-5	Sequence 5, Appl
C 403	8.8	51.8	20	3	US-08-742-185-76	Sequence 76, Appl
C 404	8.8	51.8	20	3	US-08-816-426-13	Sequence 13, Appl
C 405	8.8	51.8	20	3	US-08-673-799C-77	Sequence 77, Appl
C 406	8.8	51.8	20	3	US-08-673-799C-78	Sequence 78, Appl
C 407	8.8	51.8	20	3	US-09-143-214-18	Sequence 18, Appl
C 408	8.8	51.8	20	3	US-09-418-640-67	Sequence 67, Appl
C 409	8.8	51.8	20	4	US-09-433-699-24	Sequence 24, Appl
C 410	8.8	51.8	20	4	US-09-488-857B-16	Sequence 16, Appl
C 411	8.8	51.8	20	4	US-09-593-711A-158	Sequence 158, Appl
C 412	8.8	51.8	20	4	US-09-484-617-99	Sequence 99, Appl
C 413	8.8	51.8	20	4	US-09-593-529-17	Sequence 17, Appl
C 414	8.8	51.8	20	4	US-09-506-073-18	Sequence 18, Appl
C 415	8.8	51.8	20	4	US-09-393-385B-78	Sequence 78, Appl
C 416	8.8	51.8	20	4	US-09-658-679A-25	Sequence 25, Appl
C 417	8.8	51.8	20	4	US-09-853-768-50	Sequence 50, Appl
C 418	8.8	51.8	20	5	PCT-US92-10885-5	Sequence 5, Appl
C 419	8.8	51.8	20	5	PCT-US93-12161-13	Sequence 13, Appl
C 420	8.8	51.8	20	5	PCT-US95-07111A-18	Sequence 18, Appl
C 421	8.8	51.8	21	1	US-08-663-325-119	Sequence 119, Appl
C 422	8.8	51.8	21	1	US-08-653-740-22	Sequence 22, Appl
C 423	8.8	51.8	21	2	US-09-073-594-22	Sequence 22, Appl
C 424	8.8	51.8	21	3	US-09-715-925-22	Sequence 22, Appl
C 425	8.8	51.8	21	3	US-08-881-037-104	Sequence 104, Appl
C 426	8.8	51.8	21	3	US-09-338-685-3	Sequence 3, Appl
C 427	8.8	51.8	21	4	US-09-374-099C-350	Sequence 350, Appl
C 428	8.8	51.8	21	4	US-09-553-231-27	Sequence 27, Appl
C 429	8.8	51.8	21	4	US-08-442-680-5	Sequence 5, Appl
C 430	8.8	51.8	22	1	US-07-977-284A-152	Sequence 152, Appl
C 431	8.8	51.8	22	1	US-08-717-526-21	Sequence 21, Appl
C 432	8.8	51.8	22	1	US-08-482-577B-33	Sequence 33, Appl
C 433	8.8	51.8	22	1	US-08-482-577B-37	Sequence 37, Appl
C 434	8.8	51.8	22	2	US-08-288-508C-24	Sequence 24, Appl
C 435	8.8	51.8	22	2	US-08-288-508C-28	Sequence 28, Appl
C 436	8.8	51.8	22	2	US-08-751-305-29	Sequence 29, Appl
C 437	8.8	51.8	22	2	US-08-289-222E-41	Sequence 41, Appl
C 438	8.8	51.8	22	2	US-08-289-222E-37	Sequence 37, Appl
C 439	8.8	51.8	22	3	US-08-289-222E-37	Sequence 37, Appl
C 440	8.8	51.8	22	3	US-08-289-222E-37	Sequence 37, Appl
C 441	8.8	51.8	22	3	US-08-289-222E-37	Sequence 37, Appl
C 442	8.8	51.8	22	3	US-08-289-222E-37	Sequence 37, Appl
C 443	8.8	51.8	22	4	US-09-218-176-16	Sequence 16, Appl
C 444	8.8	51.8	22	4	US-09-054-526B-37	Sequence 37, Appl
C 445	8.8	51.8	22	4	US-09-054-526B-41	Sequence 41, Appl
C 446	8.8	51.8	22	4	US-09-269-136B-12	Sequence 12, Appl
C 447	8.8	51.8	22	4	US-08-903-446A-17	Sequence 17, Appl
C 448	8.8	51.8	22	4	US-08-881-784-33	Sequence 33, Appl
C 449	8.8	51.8	23	3	US-09-292-768-34	Sequence 34, Appl
C 450	8.8	51.8	23	3	US-08-464-148-7	Sequence 7, Appl
C 451	8.8	51.8	24	1	US-08-385-500-7	Sequence 7, Appl
C 452	8.8	51.8	24	1	US-08-846-784-7	Sequence 7, Appl
C 453	8.8	51.8	24	1	US-08-846-784-7	Sequence 7, Appl
C 454	8.8	51.8	24	3	US-08-569-221A-3	Sequence 3, Appl
C 455	8.8	51.8	24	3	US-09-245-041-47	Sequence 47, Appl
C 456	8.8	51.8	25	5	PCT-US93-07603-10	Sequence 10, Appl
C 457	8.8	51.8	25	1	US-08-321-071A-2	Sequence 2, Appl
C 458	8.8	51.8	25	1	US-08-465-590-46	Sequence 46, Appl
C 459	8.8	51.8	25	4	US-08-954-395A-21	Sequence 21, Appl
C 460	8.8	51.8	25	4	US-08-711-417C-46	Sequence 46, Appl
C 461	8.8	51.8	25	4	US-08-853-774-19	Sequence 19, Appl
C 462	8.8	51.8	25	4	US-08-934-386-40	Sequence 40, Appl
C 463	8.8	51.8	25	4	US-09-538-709-147	Sequence 147, Appl
C 464	8.8	51.8	25	4	US-09-538-709-147	Sequence 147, Appl
C 465	8.8	51.8	25	4	US-09-538-709-147	Sequence 147, Appl

466	8.8	51.8	25	5	PCT-US93-08743-46	Sequence 46, Appl
467	8.8	50.6	15	1	US-08-311-486C-267	Sequence 267, Appl
468	8.8	50.6	16	4	US-09-102-528-15	Sequence 15, Appl
C 469	8.8	50.6	17	2	US-08-308-818-10	Sequence 10, Appl
C 470	8.8	50.6	17	4	US-09-383-630-10	Sequence 10, Appl
C 471	8.8	50.6	17	4	US-08-584-040-2463	Sequence 2463, Appl
C 472	8.8	50.6	17	4	US-08-584-040-2464	Sequence 2464, Appl
C 473	8.8	50.6	17	4	US-08-679-645-727	Sequence 727, Appl
C 474	8.8	50.6	17	4	US-08-679-645-728	Sequence 728, Appl
C 475	8.8	50.6	17	4	US-09-457-066-7	Sequence 7, Appl
C 476	8.8	50.6	18	2	US-08-505-377-13	Sequence 13, Appl
C 477	8.8	50.6	18	2	US-09-197-378-29	Sequence 29, Appl
C 478	8.8	50.6	18	3	US-09-205-921-9	Sequence 9, Appl
C 479	8.8	50.6	18	3	US-08-798-269-13	Sequence 13, Appl
C 480	8.8	50.6	18	3	US-09-213-719-88	Sequence 88, Appl
C 481	8.8	50.6	18	4	US-09-102-558-17	Sequence 17, Appl
C 482	8.8	50.6	18	4	US-09-230-637-12	Sequence 12, Appl
C 483	8.8	50.6	18	4	US-09-496-694B-99	Sequence 99, Appl
C 484	8.8	50.6	18	4	US-09-055-210-13	Sequence 13, Appl
C 485	8.8	50.6	19	1	US-08-438-500-4	Sequence 4, Appl
C 486	8.8	50.6	19	1	US-08-438-500-4	Sequence 4, Appl
C 487	8.8	50.6	19	3	US-08-945-086-27	Sequence 27, Appl
C 488	8.8	50.6	19	4	US-09-258-967-11	Sequence 11, Appl
C 489	8.8	50.6	19	4	US-09-110-517-31	Sequence 31, Appl
C 490	8.8	50.6	19	5	PCT-US94-05910-4	Sequence 4, Appl
C 491	8.8	50.6	20	1	US-08-129-719-13	Sequence 13, Appl
C 492	8.8	50.6	20	1	US-08-306-871-13	Sequence 13, Appl
C 493	8.8	50.6	20	1	US-08-569-959-13	Sequence 13, Appl
C 494	8.8	50.6	20	1	US-08-484-192-73	Sequence 73, Appl
C 495	8.8	50.6	20	2	US-08-470-426B-9	Sequence 9, Appl
C 496	8.8	50.6	20	2	US-08-775-009-27	Sequence 27, Appl
C 497	8.8	50.6	20	2	US-09-058-489-63	Sequence 63, Appl
C 498	8.8	50.6	20	3	US-08-855-588A-8	Sequence 8, Appl
C 499	8.8	50.6	20	4	US-09-147-051-70	Sequence 70, Appl
C 500	8.8	50.6	20	4	US-09-258-967-10	Sequence 10, Appl
C 501	8.8	50.6	20	4	US-09-619-444-28	Sequence 28, Appl
C 502	8.8	50.6	20	4	US-09-657-042A-23	Sequence 23, Appl
C 503	8.8	50.6	20	4	US-09-462-606-23	Sequence 23, Appl
C 504	8.8	50.6	20	4	US-09-470-443-112	Sequence 112, Appl
C 505	8.8	50.6	20	4	US-08-433-126A-441	Sequence 441, Appl
C 506	8.8	50.6	21	1	US-08-477-877B-10	Sequence 10, Appl
C 507	8.8	50.6	21	1	US-08-433-124A-241	Sequence 241, Appl
C 508	8.8	50.6	21	1	US-08-410-779B-63	Sequence 63, Appl
C 509	8.8	50.6	21	1	US-08-410-779B-62	Sequence 62, Appl
C 510	8.8	50.6	21	1	US-08-410-779B-81	Sequence 81, Appl
C 511	8.8	50.6	21	1	US-08-410-779B-80	Sequence 80, Appl
C 512	8.8	50.6	21	1	US-08-410-779B-81	Sequence 81, Appl
C 513	8.8	50.6	21	1	US-08-410-779B-81	Sequence 81, Appl
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C 536	8.8	50.6	21	1	US-08-410-779B-81	Sequence 81, Appl
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C 538	8.8	50.6	21	1	US-08-410-779B-81	Sequence 81, Appl

C 539	8.6	50.6	21	5	PCT-US95-04477-81	Sequence 81, Appl	C 612	8.4	49.4	12	5	PCT-US95-04712-55	Sequence 55, Appl
C 540	8.6	50.6	21	5	PCT-US95-04477-88	Sequence 88, Appl	C 613	8.4	49.4	13	3	US-09-289-750-7	Sequence 7, Appl
C 541	8.6	50.6	21	5	PCT-US95-04477-89	Sequence 89, Appl	C 614	8.4	49.4	13	4	US-09-503-859-7	Sequence 7, Appl
C 542	8.6	50.6	21	5	PCT-US95-04477-104	Sequence 104, Appl	C 615	8.4	49.4	14	4	US-09-177-917-2	Sequence 2, Appl
C 543	8.6	50.6	21	5	PCT-US95-04477-105	Sequence 105, Appl	C 616	8.4	49.4	14	4	US-08-535-249-41	Sequence 41, Appl
C 544	8.6	50.6	21	5	PCT-US95-04477-126	Sequence 126, Appl	C 617	8.4	49.4	15	1	US-08-311-486C-265	Sequence 265, Appl
C 545	8.6	50.6	21	5	PCT-US95-04477-127	Sequence 127, Appl	C 618	8.4	49.4	15	1	US-08-311-486C-266	Sequence 266, Appl
C 546	8.6	50.6	21	5	PCT-US95-04477-134	Sequence 134, Appl	C 619	8.4	49.4	15	1	US-08-887-480-73	Sequence 73, Appl
C 547	8.6	50.6	21	5	PCT-US95-04477-135	Sequence 135, Appl	C 620	8.4	49.4	15	2	US-08-585-684B-1915	Sequence 1815, Ap
C 548	8.6	50.6	21	5	PCT-US96-06059-241	Sequence 241, Appl	C 621	8.4	49.4	15	2	US-08-585-684B-2135	Sequence 2135, Ap
C 549	8.6	50.6	21	5	PCT-US96-09472-71	Sequence 71, Appl	C 622	8.4	49.4	15	3	US-08-722-187-73	Sequence 73, Appl
C 550	8.6	50.6	22	1	US-08-105-761-6	Sequence 6, Appl	C 623	8.4	49.4	15	3	US-08-781-891-65	Sequence 65, Appl
C 551	8.6	50.6	22	1	US-07-722-798A-110	Sequence 110, Appl	C 624	8.4	49.4	15	4	US-09-038-073-1815	Sequence 1815, Ap
C 552	8.6	50.6	22	1	US-08-379-081B-313	Sequence 313, Appl	C 625	8.4	49.4	15	4	US-09-038-073-2135	Sequence 2135, Ap
C 553	8.6	50.6	22	1	US-08-379-081B-314	Sequence 314, Appl	C 626	8.4	49.4	15	5	PCT-US95-04712-73	Sequence 73, Appl
C 554	8.6	50.6	22	1	US-08-379-081B-313	Sequence 313, Appl	C 627	8.4	49.4	16	1	US-08-402-964-11	Sequence 11, Appl
C 555	8.6	50.6	22	1	US-08-379-078-314	Sequence 314, Appl	C 628	8.4	49.4	16	1	US-08-402-964-15	Sequence 15, Appl
C 556	8.6	50.6	22	1	US-08-486-408-15	Sequence 15, Appl	C 629	8.4	49.4	17	4	US-09-356-118A-10	Sequence 10, Appl
C 557	8.6	50.6	22	1	US-08-486-408-15	Sequence 15, Appl	C 630	8.4	49.4	17	4	US-09-324-667-54	Sequence 54, Appl
C 558	8.6	50.6	22	2	US-08-371-001-3	Sequence 3, Appl	C 631	8.4	49.4	17	4	US-08-679-645-80	Sequence 80, Appl
C 559	8.6	50.6	22	2	US-08-173-489C-365	Sequence 365, Appl	C 632	8.4	49.4	17	4	US-08-679-645-80	Sequence 80, Appl
C 560	8.6	50.6	22	2	US-08-837-302-1	Sequence 15, Appl	C 633	8.4	49.4	17	4	US-08-679-645-82	Sequence 82, Appl
C 561	8.6	50.6	22	3	US-08-798-668-1	Sequence 1, Appl	C 634	8.4	49.4	17	4	US-08-679-645-84	Sequence 84, Appl
C 562	8.6	50.6	22	3	US-08-765-332-60	Sequence 60, Appl	C 635	8.4	49.4	18	1	US-09-549-804C-3	Sequence 3, Appl
C 563	8.6	50.6	22	4	US-08-855-825-1	Sequence 1, Appl	C 636	8.4	49.4	18	1	US-07-780-973-14	Sequence 14, Appl
C 564	8.6	50.6	22	4	US-09-448-894-60	Sequence 60, Appl	C 637	8.4	49.4	18	2	US-08-585-684B-2683	Sequence 2683, Ap
C 565	8.6	50.6	22	4	US-09-608-285A-18	Sequence 18, Appl	C 638	8.4	49.4	18	3	US-09-133-212-42	Sequence 42, Appl
C 566	8.6	50.6	22	4	US-09-395-345-28	Sequence 28, Appl	C 639	8.4	49.4	18	3	US-09-143-212-63	Sequence 63, Appl
C 567	8.6	50.6	22	4	US-09-350-836B-18	Sequence 18, Appl	C 640	8.4	49.4	18	3	US-09-280-409-53	Sequence 53, Appl
C 568	8.6	50.6	22	4	US-09-462-569B-3	Sequence 3, Appl	C 641	8.4	49.4	18	4	US-09-038-073-2683	Sequence 2683, Ap
C 569	8.6	50.6	22	4	US-09-370-265-18	Sequence 18, Appl	C 642	8.4	49.4	18	4	US-09-071-433-72	Sequence 72, Appl
C 570	8.6	50.6	22	5	PCT-US92-11076-6	Sequence 6, Appl	C 643	8.4	49.4	18	4	US-09-632-580A-12	Sequence 12, Appl
C 571	8.6	50.6	22	5	PCT-US96-00331-3	Sequence 3, Appl	C 644	8.4	49.4	18	4	US-09-187-946-11	Sequence 11, Appl
C 572	8.6	50.6	23	1	US-08-105-761-12	Sequence 12, Appl	C 645	8.4	49.4	18	4	US-09-215-221-47	Sequence 47, Appl
C 573	8.6	50.6	23	1	US-08-466-033-120	Sequence 120, Appl	C 646	8.4	49.4	18	4	US-09-393-529-19	Sequence 19, Appl
C 574	8.6	50.6	23	1	US-08-444-733-120	Sequence 120, Appl	C 647	8.4	49.4	18	4	US-08-679-645-565	Sequence 565, Appl
C 575	8.6	50.6	23	2	US-08-464-134-120	Sequence 120, Appl	C 648	8.4	49.4	18	4	US-08-679-645-565	Sequence 565, Appl
C 576	8.6	50.6	23	2	US-08-461-361-120	Sequence 120, Appl	C 649	8.4	49.4	18	4	US-08-679-645-565	Sequence 565, Appl
C 577	8.6	50.6	23	2	US-08-485-910-120	Sequence 120, Appl	C 650	8.4	49.4	18	4	US-08-535-249-40	Sequence 40, Appl
C 578	8.6	50.6	23	2	US-08-825-426-8	Sequence 8, Appl	C 651	8.4	49.4	19	4	PCT-US93-05240-11	Sequence 11, Appl
C 579	8.6	50.6	23	4	US-08-943-731-600	Sequence 600, Appl	C 652	8.4	49.4	20	1	US-09-150-999-9	Sequence 9, Appl
C 580	8.6	50.6	23	4	US-09-538-709-23	Sequence 23, Appl	C 653	8.4	49.4	20	1	US-07-841-652-4	Sequence 4, Appl
C 581	8.6	50.6	23	5	PCT-US92-11076-12	Sequence 12, Appl	C 654	8.4	49.4	20	1	US-07-922-828C-28	Sequence 28, Appl
C 582	8.6	50.6	24	1	US-07-722-798A-109	Sequence 109, Appl	C 655	8.4	49.4	20	1	US-07-799-828C-28	Sequence 28, Appl
C 583	8.6	50.6	24	1	US-08-703-809-7	Sequence 7, Appl	C 656	8.4	49.4	20	1	US-07-722-798A-98	Sequence 98, Appl
C 584	8.6	50.6	24	1	US-08-703-809-7	Sequence 7, Appl	C 657	8.4	49.4	20	1	US-07-681-703B-28	Sequence 28, Appl
C 585	8.6	50.6	24	1	US-08-545-562A-27	Sequence 27, Appl	C 658	8.4	49.4	20	1	US-08-355-892-55	Sequence 55, Appl
C 586	8.6	50.6	24	2	US-08-703-807-7	Sequence 7, Appl	C 659	8.4	49.4	20	1	US-08-293-237-1	Sequence 7, Appl
C 587	8.6	50.6	24	2	US-08-747-108A-7	Sequence 7, Appl	C 660	8.4	49.4	20	1	US-08-525-697-8	Sequence 8, Appl
C 588	8.6	50.6	24	3	US-09-211-631-7	Sequence 7, Appl	C 661	8.4	49.4	20	1	US-08-715-142-11	Sequence 11, Appl
C 589	8.6	50.6	24	3	US-09-265-628-7	Sequence 7, Appl	C 662	8.4	49.4	20	2	US-08-651-692-1	Sequence 1, Appl
C 590	8.6	50.6	24	4	US-09-518-386B-16	Sequence 16, Appl	C 663	8.4	49.4	20	2	US-07-952-277A-28	Sequence 28, Appl
C 591	8.6	50.6	25	2	US-08-902-623-21	Sequence 21, Appl	C 664	8.4	49.4	20	2	US-08-468-819-29	Sequence 29, Appl
C 592	8.6	50.6	25	2	US-08-983-108-14	Sequence 14, Appl	C 665	8.4	49.4	20	2	US-08-468-819-29	Sequence 29, Appl
C 593	8.6	50.6	25	2	US-08-983-108-14	Sequence 14, Appl	C 666	8.4	49.4	20	2	US-08-468-819-29	Sequence 29, Appl
C 594	8.6	50.6	25	4	US-09-230-288-15	Sequence 15, Appl	C 667	8.4	49.4	20	2	US-08-651-692-2	Sequence 2, Appl
C 595	8.6	50.6	25	4	US-09-147-751-11	Sequence 11, Appl	C 668	8.4	49.4	20	2	US-08-468-819-29	Sequence 29, Appl
C 596	8.6	50.6	25	4	US-09-177-650-50	Sequence 50, Appl	C 669	8.4	49.4	20	2	US-08-468-819-29	Sequence 29, Appl
C 597	8.6	50.6	25	4	US-09-350-969-65	Sequence 65, Appl	C 670	8.4	49.4	20	2	US-08-468-819-29	Sequence 29, Appl
C 598	8.6	50.6	25	4	US-09-538-709-391	Sequence 391, Appl	C 671	8.4	49.4	20	2	US-07-965-285-17	Sequence 17, Appl
C 599	8.6	50.6	25	4	US-09-538-709-391	Sequence 391, Appl	C 672	8.4	49.4	20	2	US-08-474-450A-40	Sequence 40, Appl
C 600	8.6	50.6	25	4	US-09-538-709-391	Sequence 391, Appl	C 673	8.4	49.4	20	2	US-08-363-124A-7	Sequence 7, Appl
C 601	8.4	49.4	12	1	US-08-441-887A-41	Sequence 41, Appl	C 674	8.4	49.4	20	2	US-08-487-231-17	Sequence 17, Appl
C 602	8.4	49.4	12	1	US-08-887-480-55	Sequence 55, Appl	C 675	8.4	49.4	20	2	US-08-487-231-17	Sequence 17, Appl
C 603	8.4	49.4	12	2	US-08-547-214-47	Sequence 47, Appl	C 676	8.4	49.4	20	2	US-08-911-434A-11	Sequence 11, Appl
C 604	8.4	49.4	12	2	US-08-722-187-55	Sequence 55, Appl	C 677	8.4	49.4	20	2	US-08-911-434A-11	Sequence 11, Appl
C 605	8.4	49.4	12	3	US-08-663-823B-47	Sequence 47, Appl	C 678	8.4	49.4	20	3	US-08-663-823B-47	Sequence 47, Appl
C 606	8.4	49.4	12	4	US-08-942-406-47	Sequence 47, Appl	C 679	8.4	49.4	20	3	US-08-663-823B-47	Sequence 47, Appl
C 607	8.4	49.4	12	4	US-09-322-617-47	Sequence 47, Appl	C 680	8.4	49.4	20	3	US-08-663-823B-47	Sequence 47, Appl
C 608	8.4	49.4	12	4	US-09-281-418-119	Sequence 119, Appl	C 681	8.4	49.4	20	3	US-08-663-823B-47	Sequence 47, Appl
C 609	8.4	49.4	12	4	US-09-203-318-51	Sequence 51, Appl	C 682	8.4	49.4	20	3	US-09-249-730-148	Sequence 148, Appl
C 610	8.4	49.4	12	4	US-09-751-561-47	Sequence 47, Appl	C 683	8.4	49.4	20	3	US-09-249-730-148	Sequence 148, Appl
C 611	8.4	49.4	12	4	US-09-724-385-47	Sequence 47, Appl	C 684	8.4	49.4	20	3	US-09-249-730-148	Sequence 148, Appl
					US-09-757-528-47	Sequence 47, Appl						US-09-206-537-10	Sequence 10, Appl
												US-09-287-796-13	Sequence 13, Appl

C 685	8.4	49.4	20	3	US-09-429-323-32	Sequence 32, Appl	C 758	8.4	49.4	24	4	US-09-043-303-13	Sequence 16, Appl
C 686	8.4	49.4	20	3	US-08-481-341-12	Sequence 12, Appl	C 759	8.4	49.4	24	4	US-09-349-677-16	Sequence 16, Appl
C 687	8.4	49.4	20	3	US-09-490-693-17	Sequence 17, Appl	C 760	8.4	49.4	24	4	US-09-430-503-11	Sequence 11, Appl
C 688	8.4	49.4	20	4	US-08-983-466-71	Sequence 71, Appl	C 761	8.4	49.4	24	4	US-09-455-960-17	Sequence 17, Appl
C 689	8.4	49.4	20	4	US-09-201-912-17	Sequence 17, Appl	C 762	8.4	49.4	24	5	PCT-US95-12624-3	Sequence 3, Appl
C 690	8.4	49.4	20	4	US-09-103-912-17	Sequence 117, App	C 763	8.4	49.4	25	1	US-08-261-206A-11	Sequence 11, Appl
C 691	8.4	49.4	20	4	US-09-130-616-13	Sequence 13, Appl	C 764	8.4	49.4	25	2	US-08-338-530A-9	Sequence 9, Appl
C 692	8.4	49.4	20	4	US-09-487-445-42	Sequence 42, Appl	C 765	8.4	49.4	25	3	US-08-733-607-14	Sequence 14, Appl
C 693	8.4	49.4	20	4	US-08-797-358B-4	Sequence 10, Appl	C 766	8.4	49.4	25	3	US-08-737-607-28	Sequence 28, Appl
C 694	8.4	49.4	20	4	US-09-430-854-10	Sequence 10, Appl	C 767	8.4	49.4	25	3	US-08-589-028-33	Sequence 33, Appl
C 695	8.4	49.4	20	4	US-09-031-006-12	Sequence 12, Appl	C 768	8.4	49.4	25	3	US-08-784-582-33	Sequence 33, Appl
C 696	8.4	49.4	20	4	US-09-309-317-8	Sequence 19, Appl	C 769	8.4	49.4	25	4	US-09-077-205-6	Sequence 6, Appl
C 697	8.4	49.4	20	4	US-09-593-589-19	Sequence 20, Appl	C 770	8.4	49.4	25	4	US-09-267-384-9	Sequence 9, Appl
C 698	8.4	49.4	20	4	US-09-593-589-20	Sequence 20, Appl	C 771	8.4	49.4	25	4	US-08-785-271-33	Sequence 33, Appl
C 700	8.4	49.4	20	4	US-09-082-6498-74	Sequence 74, Appl	C 772	8.4	49.4	25	4	US-08-943-731-410	Sequence 410, App
C 701	8.4	49.4	20	4	US-09-082-6498-78	Sequence 78, Appl	C 773	8.4	49.4	25	4	US-08-182-968A-33	Sequence 459, Appl
C 702	8.4	49.4	20	4	US-09-68-992-84	Sequence 84, Appl	C 774	8.4	49.4	25	4	US-09-538-709-459	Sequence 19, Appl
C 703	8.4	49.4	20	4	US-09-657-474-84	Sequence 84, Appl	C 775	8.4	49.4	25	5	PCT-US93-10106-19	Sequence 47, Appl
C 704	8.4	49.4	20	4	US-09-792-594-43	Sequence 43, Appl	C 776	8.2	48.2	14	1	US-08-259-148A-47	Sequence 63, Appl
C 705	8.4	49.4	20	4	US-09-817-4678-39	Sequence 39, Appl	C 777	8.2	48.2	15	1	US-08-182-968A-33	Sequence 33, Appl
C 706	8.4	49.4	20	4	US-09-100-0088-39	Sequence 39, Appl	C 778	8.2	48.2	15	1	US-08-182-968A-382	Sequence 382, App
C 707	8.4	49.4	20	5	PCT-US94-00265-12	Sequence 12, Appl	C 779	8.2	48.2	15	1	US-08-795-788-20	Sequence 20, Appl
C 708	8.4	49.4	20	5	PCT-US94-02471-4	Sequence 4, Appl	C 780	8.2	48.2	15	1	US-08-795-788-20	Sequence 414, Appl
C 709	8.4	49.4	21	1	US-07-697-421-4	Sequence 4, Appl	C 781	8.2	48.2	15	2	US-08-774-306A-333	Sequence 333, App
C 710	8.4	49.4	21	1	US-07-714-687-45	Sequence 45, Appl	C 782	8.2	48.2	15	2	US-08-774-306A-333	Sequence 382, App
C 711	8.4	49.4	21	1	US-08-283-203-4	Sequence 45, Appl	C 783	8.2	48.2	15	2	US-08-774-306A-382	Sequence 1746, App
C 712	8.4	49.4	21	1	US-08-224-391-45	Sequence 45, Appl	C 785	8.2	48.2	15	2	US-08-053-451B-132	Sequence 132, App
C 713	8.4	49.4	21	1	US-08-884-304-45	Sequence 45, Appl	C 786	8.2	48.2	15	3	US-08-271-882B-30	Sequence 30, App
C 714	8.4	49.4	21	1	US-08-351-4								

C 831	8.2	48.2	18	3	US-09-344-520-44	Sequence 44, Appl	C 904	8.2	48.2	19	4	US-09-178-098A-6	Sequence 6, Appl
C 832	8.2	48.2	18	3	US-09-444-579-20	Sequence 20, Appl	C 905	8.2	48.2	19	5	PCT-US94-09318-1	Sequence 1, Appl
C 833	8.2	48.2	18	3	US-08-867-381A-7	Sequence 7, Appl	C 906	8.2	48.2	19	6	5168062-3	Patent No. 5168062
C 834	8.2	48.2	18	3	US-09-443-212-25	Sequence 25, Appl	C 907	8.2	48.2	20	1	US-07-613-083B-5	Sequence 5, Appl
C 835	8.2	48.2	18	3	US-09-143-212-45	Sequence 45, Appl	C 908	8.2	48.2	20	1	US-08-036-217-5	Sequence 5, Appl
C 836	8.2	48.2	18	3	US-08-472-040A-55	Sequence 55, Appl	C 909	8.2	48.2	20	1	US-08-105-483-5	Sequence 5, Appl
C 837	8.2	48.2	18	3	US-09-280-409-31	Sequence 31, Appl	C 910	8.2	48.2	20	1	US-08-073-962-21	Sequence 21, Appl
C 838	8.2	48.2	18	3	US-08-606-505B-20	Sequence 20, Appl	C 911	8.2	48.2	20	1	US-07-714-687-5	Sequence 28, Appl
C 839	8.2	48.2	18	3	US-08-606-505B-22	Sequence 22, Appl	C 912	8.2	48.2	20	1	US-08-220-161-28	Sequence 28, Appl
C 840	8.2	48.2	18	3	US-08-606-505B-24	Sequence 24, Appl	C 913	8.2	48.2	20	1	US-07-977-284A-163	Sequence 163, Appl
C 841	8.2	48.2	18	3	US-08-606-505B-29	Sequence 29, Appl	C 914	8.2	48.2	20	1	US-08-435-529-18	Sequence 18, Appl
C 842	8.2	48.2	18	3	US-09-082-614A-5	Sequence 5, Appl	C 915	8.2	48.2	20	1	US-08-188-434A-9	Sequence 9, Appl
C 843	8.2	48.2	18	3	US-08-894-736-21	Sequence 21, Appl	C 916	8.2	48.2	20	1	US-08-233-030-24	Sequence 24, Appl
C 844	8.2	48.2	18	3	US-08-894-736-21	Sequence 21, Appl	C 917	8.2	48.2	20	1	US-08-043-390-9	Sequence 9, Appl
C 845	8.2	48.2	18	4	US-08-276-776-55	Sequence 55, Appl	C 918	8.2	48.2	20	1	US-08-413-118-28	Sequence 28, Appl
C 846	8.2	48.2	18	4	US-08-471-209-55	Sequence 55, Appl	C 919	8.2	48.2	20	1	US-08-530-492-86	Sequence 86, Appl
C 847	8.2	48.2	18	4	US-09-616-990-20	Sequence 20, Appl	C 920	8.2	48.2	20	1	US-08-131-625B-3	Sequence 3, Appl
C 848	8.2	48.2	18	4	US-09-616-990-22	Sequence 22, Appl	C 921	8.2	48.2	20	1	US-08-535-230A-9	Sequence 9, Appl
C 849	8.2	48.2	18	4	US-09-616-990-24	Sequence 24, Appl	C 922	8.2	48.2	20	1	US-08-411-020-16	Sequence 16, Appl
C 850	8.2	48.2	18	4	US-09-616-990-29	Sequence 29, Appl	C 923	8.2	48.2	20	1	US-08-411-020-17	Sequence 17, Appl
C 851	8.2	48.2	18	4	US-08-878-750-4	Sequence 4, Appl	C 924	8.2	48.2	20	1	US-08-224-391-5	Sequence 5, Appl
C 852	8.2	48.2	18	4	US-08-428-596A-15	Sequence 15, Appl	C 925	8.2	48.2	20	1	US-08-484-304-5	Sequence 5, Appl
C 853	8.2	48.2	18	4	US-08-537-732A-22	Sequence 22, Appl	C 926	8.2	48.2	20	1	US-08-224-657-5	Sequence 5, Appl
C 854	8.2	48.2	18	4	US-09-521-144-7	Sequence 7, Appl	C 927	8.2	48.2	20	1	US-08-475-063-5	Sequence 5, Appl
C 855	8.2	48.2	18	4	US-08-584-040-8307	Sequence 8307, Ap	C 928	8.2	48.2	20	1	US-08-207-792-5	Sequence 5, Appl
C 856	8.2	48.2	18	4	US-09-387-341-171	Sequence 171, Ap	C 929	8.2	48.2	20	1	US-08-487-412-21	Sequence 21, Appl
C 857	8.2	48.2	18	4	US-09-375-318-23	Sequence 23, Appl	C 930	8.2	48.2	20	1	US-08-709-209-5	Sequence 5, Appl
C 858	8.2	48.2	18	5	PCT-US96-00845-14	Sequence 14, Appl	C 931	8.2	48.2	20	1	US-08-257-073-1	Sequence 1, Appl
C 859	8.2	48.2	19	1	US-08-116-388-1	Sequence 1, Appl	C 932	8.2	48.2	20	1	US-08-303-275-5	Sequence 5, Appl
C 860	8.2	48.2	19	1	US-08-474-542A-78	Sequence 78, Appl	C 933	8.2	48.2	20	1	US-08-458-101-5	Sequence 5, Appl
C 861	8.2	48.2	19	1	US-08-502-185-48	Sequence 48, Appl	C 934	8.2	48.2	20	1	US-08-343-281A-2	Sequence 2, Appl
C 862	8.2	48.2	19	1	US-08-457-648-78	Sequence 78, Appl	C 935	8.2	48.2	20	1	US-08-715-142-23	Sequence 23, Appl
C 863	8.2	48.2	19	1	US-08-398-945-48	Sequence 48, Appl	C 936	8.2	48.2	20	1	US-08-410-779B-70	Sequence 70, Appl
C 864	8.2	48.2	19	1	US-08-569-926-18	Sequence 18, Appl	C 937	8.2	48.2	20	1	US-08-410-779B-71	Sequence 71, Appl
C 865	8.2	48.2	19	1	US-08-501-779-48	Sequence 48, Appl	C 938	8.2	48.2	20	2	US-08-913-050A-4	Sequence 4, Appl
C 866	8.2	48.2	19	1	US-08-440-103-13	Sequence 13, Appl	C 939	8.2	48.2	20	2	US-08-184-009-5	Sequence 5, Appl
C 867	8.2	48.2	19	1	US-08-440-542-13	Sequence 13, Appl	C 940	8.2	48.2	20	2	US-08-486-969-5	Sequence 5, Appl
C 868	8.2	48.2	19	1	US-08-501-713-48	Sequence 48, Appl	C 941	8.2	48.2	20	2	US-08-412-376-11	Sequence 11, Appl
C 869	8.2	48.2	19	1	US-08-510-032A-7	Sequence 7, Appl	C 942	8.2	48.2	20	2	US-08-457-273B-16	Sequence 16, Appl
C 870	8.2	48.2	19	1	US-08-378-860-48	Sequence 48, Appl	C 943	8.2	48.2	20	2	US-07-963-538B-13	Sequence 13, Appl
C 871	8.2	48.2	19	1	US-08-211-368-13	Sequence 13, Appl	C 944	8.2	48.2	20	2	US-08-417-210A-5	Sequence 5, Appl
C 872	8.2	48.2	19	1	US-08-440-210-13	Sequence 13, Appl	C 945	8.2	48.2	20	2	US-08-876-766-9	Sequence 9, Appl
C 873	8.2	48.2	19	1	US-08-742-023-34	Sequence 34, Appl	C 946	8.2	48.2	20	2	US-08-478-178A-71	Sequence 71, Appl
C 874	8.2	48.2	19	1	US-08-501-626-48	Sequence 48, Appl	C 947	8.2	48.2	20	2	US-08-488-177-71	Sequence 71, Appl
C 875	8.2	48.2	19	1	US-08-501-356-48	Sequence 48, Appl	C 948	8.2	48.2	20	2	US-08-481-177-71	Sequence 71, Appl
C 876	8.2	48.2	19	1	US-08-110-294A-44	Sequence 44, Appl	C 949	8.2	48.2	20	2	US-08-664-336-71	Sequence 71, Appl
C 877	8.2	48.2	19	2	US-08-359-705B-21	Sequence 21, Appl	C 950	8.2	48.2	20	2	US-08-458-336-5	Sequence 5, Appl
C 878	8.2	48.2	19	2	US-08-117-952-151	Sequence 151, Ap	C 951	8.2	48.2	20	2	US-08-256-426B-163	Sequence 163, Appl
C 879	8.2	48.2	19	2	US-08-389-926-44	Sequence 44, Appl	C 952	8.2	48.2	20	2	US-08-481-066A-71	Sequence 71, Appl
C 880	8.2	48.2	19	2	US-08-386-846A-21	Sequence 21, Appl	C 953	8.2	48.2	20	2	US-08-837-201C-4	Sequence 4, Appl
C 881	8.2	48.2	19	2	US-08-457-880A-21	Sequence 21, Appl	C 954	8.2	48.2	20	2	US-08-471-025-5	Sequence 5, Appl
C 882	8.2	48.2	19	3	US-08-688-514-7	Sequence 7, Appl	C 955	8.2	48.2	20	2	US-08-658-665-5	Sequence 5, Appl
C 883	8.2	48.2	19	3	US-08-444-622A-21	Sequence 21, Appl	C 956	8.2	48.2	20	2	US-08-904-901-59	Sequence 59, Appl
C 884	8.2	48.2	19	3	US-08-942-562-21	Sequence 21, Appl	C 957	8.2	48.2	20	3	US-08-947-965-15	Sequence 15, Appl
C 885	8.2	48.2	19	3	US-09-344-579-2	Sequence 2, Appl	C 958	8.2	48.2	20	3	US-08-975-698A-13	Sequence 13, Appl
C 886	8.2	48.2	19	3	US-09-199-859-3	Sequence 3, Appl	C 959	8.2	48.2	20	3	US-08-473-446-28	Sequence 28, Appl
C 887	8.2	48.2	19	3	US-08-968-505-34	Sequence 34, Appl	C 960	8.2	48.2	20	3	US-09-366-257-37	Sequence 37, Appl
C 888	8.2	48.2	19	3	US-08-912-772-65	Sequence 65, Appl	C 961	8.2	48.2	20	3	US-09-357-073-34	Sequence 34, Appl
C 889	8.2	48.2	19	3	US-09-156-923-21	Sequence 21, Appl	C 962	8.2	48.2	20	3	US-09-289-267-58	Sequence 58, Appl
C 890	8.2	48.2	19	4	US-08-938-669A-6	Sequence 6, Appl	C 963	8.2	48.2	20	3	US-08-882-501-8	Sequence 8, Appl
C 891	8.2	48.2	19	4	US-09-050-159-18	Sequence 18, Appl	C 964	8.2	48.2	20	3	US-09-166-186-128	Sequence 128, Appl
C 892	8.2	48.2	19	4	US-09-050-159-19	Sequence 19, Appl	C 965	8.2	48.2	20	3	US-07-933-035A-3	Sequence 3, Appl
C 893	8.2	48.2	19	4	US-09-338-907-442	Sequence 442, Appl	C 966	8.2	48.2	20	3	US-08-353-901-4	Sequence 4, Appl
C 894	8.2	48.2	19	4	US-09-177-349-11	Sequence 11, Appl	C 967	8.2	48.2	20	3	US-08-855-531D-3	Sequence 3, Appl
C 895	8.2	48.2	19	4	US-09-046-604-13	Sequence 13, Appl	C 968	8.2	48.2	20	3	US-09-449-730-59	Sequence 59, Appl
C 896	8.2	48.2	19	4	US-08-761-708-18	Sequence 18, Appl	C 969	8.2	48.2	20	3	US-09-286-904-10	Sequence 10, Appl
C 897	8.2	48.2	19	4	US-09-026-039-65	Sequence 65, Appl	C 970	8.2	48.2	20	3	US-09-277-016-32	Sequence 32, Appl
C 898	8.2	48.2	19	4	US-09-218-207-442	Sequence 442, Appl	C 971	8.2	48.2	20	3	US-09-277-016-33	Sequence 33, Appl
C 899	8.2	48.2	19	4	US-09-342-681C-48	Sequence 48, Appl	C 972	8.2	48.2	20	3	US-09-288-461-4	Sequence 4, Appl
C 900	8.2	48.2	19	4	US-08-970-166-6	Sequence 6, Appl	C 973	8.2	48.2	20	3	US-09-288-461-5	Sequence 5, Appl
C 901	8.2	48.2	19	4	US-09-320-911-18	Sequence 18, Appl	C 974	8.2	48.2	20	4	US-09-428-696-13	Sequence 13, Appl
C 902	8.2	48.2	19	4	US-08-098-942C-3	Sequence 3, Appl	C 975	8.2	48.2	20	4	US-09-428-696-59	Sequence 59, Appl
C 903	8.2	48.2	19	4	US-09-091-952A-131	Sequence 131, Appl	C 976	8.2	48.2	20	4	US-09-433-694-35	Sequence 35, Appl

C 977 8.2 48.2 20 4 US-09-435-296-48 Sequence 48, Appl
C 978 8.2 48.2 20 4 US-09-428-219-11 Sequence 11, Appl
C 979 8.2 48.2 20 4 US-09-490-692-59 Sequence 59, Appl
C 980 8.2 48.2 20 4 US-08-906-517-86 Sequence 86, Appl
C 981 8.2 48.2 20 4 US-09-280-805-34 Sequence 34, Appl
C 982 8.2 48.2 20 4 US-09-280-805-51 Sequence 51, Appl
C 983 8.2 48.2 20 4 US-09-050-159-30 Sequence 30, Appl
C 984 8.2 48.2 20 4 US-09-101-8868-15 Sequence 15, Appl
C 985 8.2 48.2 20 4 US-09-290-640-27 Sequence 27, Appl
C 986 8.2 48.2 20 4 US-08-983-466-20 Sequence 20, Appl
C 987 8.2 48.2 20 4 US-09-417-090-13 Sequence 13, Appl
C 988 8.2 48.2 20 4 US-09-067-400-15 Sequence 15, Appl
C 989 8.2 48.2 20 4 US-09-313-932-128 Sequence 128, Appl
C 990 8.2 48.2 20 4 US-09-313-930-19 Sequence 19, Appl
C 991 8.2 48.2 20 4 US-09-313-930-19 Sequence 11, Appl
C 992 8.2 48.2 20 4 US-09-467-082-10 Sequence 10, Appl
C 993 8.2 48.2 20 4 US-08-478-316-88 Sequence 88, Appl
C 994 8.2 48.2 20 4 US-08-855-5268-3 Sequence 3, Appl
C 995 8.2 48.2 20 4 US-09-487-445-83 Sequence 83, Appl
C 996 8.2 48.2 20 4 US-09-117-927-1 Sequence 1, Appl
C 997 8.2 48.2 20 4 US-09-117-927-1 Sequence 11, Appl
C 998 8.2 48.2 20 4 US-08-460-736-5 Sequence 5, Appl
C 999 8.2 48.2 20 4 US-09-085-273-5 Sequence 5, Appl
1000 8.2 48.2 20 4 US-09-593-711A-162 Sequence 162, Appl

ALIGNMENTS

RESULT 1
US-09-593-012-195
Sequence 195, Application US/09593012

Patent No. 6387652
GENERAL INFORMATION:
APPLICANT: HAUGLAND, Richard
TITLE OF INVENTION: METHOD OF IDENTIFYING AND QUANTIFYING SPECIFIC FUNGI AND BACTERIA
FILE REFERENCE: HAUGLAND=1A
CURRENT APPLICATION NUMBER: US/09/593, 012
CURRENT FILING DATE: 2000-06-13
PRIOR APPLICATION NUMBER: US 09/290, 990
PRIOR FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: US 60/081, 773
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 225
SOFTWARE: Patentin version 3.0
SEQ ID NO 195
LENGTH: 15
TYPE: DNA
ORGANISM: Trichoderma harzianum
US-09-593-012-195

Query Match 72.9%; Score 12.4; DB 4; Length 15;
Best Local Similarity 92.9%; Pred. No. 4.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTGCTTGGCGGG 15
Db 1 TTGCTTGGCGGG 14

RESULT 2
US-09-593-012-191

Sequence 191, Application US/09593012
Patent No. 6387652
GENERAL INFORMATION:
APPLICANT: HAUGLAND, Richard
TITLE OF INVENTION: METHOD OF IDENTIFYING AND QUANTIFYING SPECIFIC FUNGI AND BACTERIA
FILE REFERENCE: HAUGLAND=1A
CURRENT APPLICATION NUMBER: US/09/593, 012
CURRENT FILING DATE: 2000-06-13
PRIOR APPLICATION NUMBER: US 09/290, 990

PRIOR FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: US 60/081, 773
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 225
SOFTWARE: Patentin version 3.0
SEQ ID NO 191
LENGTH: 21
TYPE: DNA
ORGANISM: Trichoderma asperellum/namatum
US-09-593-012-191

Query Match 72.9%; Score 12.4; DB 4; Length 21;
Best Local Similarity 92.9%; Pred. No. 4.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTGCTTGGCGGG 14
Db 8 GTTGCTTGGCGGG 21

RESULT 3
US-09-593-012-194
Sequence 194, Application US/09593012

Patent No. 6387652
GENERAL INFORMATION:
APPLICANT: HAUGLAND, Richard
TITLE OF INVENTION: METHOD OF IDENTIFYING AND QUANTIFYING SPECIFIC FUNGI AND BACTERIA
FILE REFERENCE: HAUGLAND=1A
CURRENT APPLICATION NUMBER: US/09/593, 012
CURRENT FILING DATE: 2000-06-13
PRIOR APPLICATION NUMBER: US 09/290, 990
PRIOR FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: US 60/081, 773
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 225
SOFTWARE: Patentin version 3.0
SEQ ID NO 194
LENGTH: 21
TYPE: DNA
ORGANISM: Trichoderma asperellum/namatum/viride
US-09-593-012-194

Query Match 72.9%; Score 12.4; DB 4; Length 21;
Best Local Similarity 92.9%; Pred. No. 4.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTGCTTGGCGGG 14
Db 8 GTTGCTTGGCGGG 21

RESULT 4
US-09-593-012-203

Sequence 203, Application US/09593012
Patent No. 6387652
GENERAL INFORMATION:
APPLICANT: HAUGLAND, Richard
TITLE OF INVENTION: METHOD OF IDENTIFYING AND QUANTIFYING SPECIFIC FUNGI AND BACTERIA
FILE REFERENCE: HAUGLAND=1A
CURRENT APPLICATION NUMBER: US/09/593, 012
CURRENT FILING DATE: 2000-06-13
PRIOR APPLICATION NUMBER: US 09/290, 990
PRIOR FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: US 60/081, 773
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 225
SOFTWARE: Patentin version 3.0
SEQ ID NO 203
LENGTH: 21
TYPE: DNA
ORGANISM: Trichoderma viride/atroviride/koningii

US-09-593-012-203

Query Match 72.9%; Score 12.4; DB 4; Length 21;
Best Local Similarity 92.9%; Pred. No. 4.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGGG 14
|||||
DB 8 GTTGCTTCGGCGGG 21

RESULT 5

US-09-593-012-31
Sequence 31, Application US/09593012
Patent No. 6387652

GENERAL INFORMATION:
APPLICANT: HAUGLAND, Richard
APPLICANT: VESPER, Stephen
TITLE OF INVENTION: METHOD OF IDENTIFYING AND QUANTIFYING SPECIFIC FUNGI AND BACTERIA
FILE REFERENCE: HAUGLAND=1A
CURRENT APPLICATION NUMBER: US/09/593,012
CURRENT FILING DATE: 2000-06-13
PRIOR APPLICATION NUMBER: US 09/290,990
PRIOR FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: US 60/081,773
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 225
SOFTWARE: Patentin version 3.0
SEQ ID NO 31
LENGTH: 22
TYPE: DNA
ORGANISM: Aspergillus ochraceus/Oestianus/auricomus
US-09-593-012-31

Query Match: 72.9%; Score 12.4; DB 4; Length 22;
Best Local Similarity 92.9%; Pred. No. 4.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGGG 14
|||||
DB 6 GTTGCTTCGGCGGG 19

RESULT 6

US-08-233-608-24
Sequence 24, Application US/08233608
Patent No. 5585238

GENERAL INFORMATION:
APPLICANT: Ligon, James M
APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
TITLE OF INVENTION: Polymerase Chain Reaction
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,608
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Spurrill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: CGC 1739

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-541-8615

TELEFAX: 919-541-8689

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Other nucleic acid

DESCRIPTION: Oligonucleotide primer JB548

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-233-608-24

Query Match 71.8%; Score 12.2; DB 1; Length 20;
Best Local Similarity 82.4%; Pred. No. 5.4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGGAGC 17
|||||
DB 1 GTTGCTTCGGCGGAGC 17

RESULT 7

US-08-887-480-24
Sequence 24, Application US/08887480
Patent No. 5814453

GENERAL INFORMATION:

APPLICANT: Beck, James J

TITLE OF INVENTION: Detection of Fungal Pathogens Using the

TITLE OF INVENTION: Polymerase Chain Reaction

NUMBER OF SEQUENCES: 96

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 5814453artis Corporation

STREET: 520 White Plains Road

CITY: Tarrytown

STATE: NY

COUNTRY: USA

ZIP: 10591

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/887,480

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/722,187

FILING DATE: 15-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP

TELEPHONE: 919-541-8587

TELEFAX: 919-541-8689

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Other nucleic acid

DESCRIPTION: Oligonucleotide primer JB548

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-887-480-24

Query Match 71.8%; Score 12.2; DB 1; Length 20;
Best Local Similarity 82.4%; Pred. No. 5.4e+02;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGGGAAC 17
|||||
Db 1 GTTGCTTCGGCGGCGAC 17

RESULT 8

US-08-722-187-24
; Sequence 24, Application US/08722187
; Patent No. 5955274
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M
; APPLICANT: Beck, James J
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,187
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/233,608
; FILING DATE: 04-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Walsh, Andrea C.
; REGISTRATION NUMBER: 34,988
; REFERENCE/DOCKET NUMBER: CGC 1739
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8666
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; DESCRIPTION: Oligonucleotide primer JB548
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-722-187-24

Query Match 71.8%; Score 12.2; DB 2; Length 20;
Best Local Similarity 82.4%; Pred. No. 5.4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGGGAAC 17
|||||
Db 1 GTTGCTTCGGCGGCGAC 17

RESULT 9

PCT-US95-04712-24
; Sequence 24, Application PC/TUS9504712
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M
; APPLICANT: Beck, James J
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 86

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04712
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,608
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: CGC 1739
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8666
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: Oligonucleotide primer JB548
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US95-04712-24

Query Match 71.8%; Score 12.2; DB 5; Length 20;
Best Local Similarity 82.4%; Pred. No. 5.4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGGGAAC 17
|||||
Db 1 GTTGCTTCGGCGGCGAC 17

RESULT 10

US-09-593-012-120
; Sequence 120, Application US/09593012
; Patent No. 6387652
; GENERAL INFORMATION:
; APPLICANT: HAUGLAND, Richard
; APPLICANT: VESPER, Stephen
; TITLE OF INVENTION: METHOD OF IDENTIFYING AND QUANTIFYING SPECIFIC FUNGI AND BACTER.
; FILE REFERENCE: HAUGLAND-1A
; CURRENT APPLICATION NUMBER: US/09/593,012
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US 09/290,990
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 60/081,773
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 225
; SOFTWARE: Patent version 3.0
; SEQ ID NO 120
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Penicillium brevicompactum/alberechti
US-09-593-012-120

Query Match 70.6%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTGTGGCG 12
|||||
Db 5 GTTGTGGCG 16

RESULT 11

US-09-428-219-70/c
Sequence 70, Application US/09428219
Patent No. 6177273
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Lex M. Cowser
TITLE OF INVENTION: ANTISENSE MODULATION OF INTEGRIN-LINKED KINASE EXPRESSION
FILE REFERENCE: RTS-0101
CURRENT APPLICATION NUMBER: US/09/428,219
CURRENT FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 70
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-428-219-70

Query Match 69.4%; Score 11.8; DB 4; Length 20;
Best Local Similarity 86.7%; Pred. No. 8.9e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGCTTGGGGGAC 17
|||||
Db 18 TGCTTGTGGGAC 4

RESULT 12

US-08-291-932A-812/c
Sequence 812, Application US/08291932A
Patent No. 5658780
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth G.
APPLICANT: McSwigen, James
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: NF-KB
NUMBER OF SEQUENCES: 830
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/291,932A
FILING DATE: August 15, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992

Two

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/157
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 812:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-291-932A-812

Query Match 67.1%; Score 11.4; DB 1; Length 16;
Best Local Similarity 92.3%; Pred. No. 1.4e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTGTGGCG 13
|||||
Db 16 GTTGTGGCG 4

RESULT 13

US-08-887-480-57
Sequence 57, Application US/08887480
Patent No. 5814453
GENERAL INFORMATION:
APPLICANT: Beck, James J.
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
TITLE OF INVENTION: Polymerase Chain Reaction
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 5814453artis Corporation
STREET: 520 White Plains Road
CITY: Tarrytown
STATE: NY
COUNTRY: USA
ZIP: 10591

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,480
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/722,187
FILING DATE: 15-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide primer
DESCRIPTION: JBS70"
HYPOTHETICAL: NO
US-08-887-480-57

Query Match 67.1%; Score 11.4; DB 1; Length 16;

Best Local Similarity 92.3%; Pred. No. 1.4e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGG 13
|||||
Db 4 GTTGCTTCGGCGG 16

RESULT 14

US-08-887-480-64
; Sequence 64, Application US/08887480
; Patent No. 5814453
; GENERAL INFORMATION:
; APPLICANT: Beck, James J
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5814453artis Corporation
; STREET: 520 White Plains Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,480
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/722,187
; FILING DATE: 15-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotide primer
; DESCRIPTION: JB577"
; HYPOTHETICAL: NO
; US-08-887-480-64

Query Match 67.1%; Score 11.4; DB 1; Length 16;
Best Local Similarity 92.3%; Pred. No. 1.4e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGG 13
|||||
Db 1 GTTGCTTCGGCGG 13

RESULT 15
US-08-722-187-57
; Sequence 57, Application US/08722187
; Patent No. 5955274
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M
; APPLICANT: Beck, James J
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
; TITLE OF INVENTION: Polymerase Chain Reaction

NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,187
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,608
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea G.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: CGC 1739
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8666
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide primer
DESCRIPTION: JB570"
HYPOTHETICAL: NO
US-08-722-187-57

Query Match 67.1%; Score 11.4; DB 2; Length 16;
Best Local Similarity 92.3%; Pred. No. 1.4e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGG 13
|||||
Db 4 GTTGCTTCGGCGG 16

RESULT 16
US-08-722-187-64
; Sequence 64, Application US/08722187
; Patent No. 5955274
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M
; APPLICANT: Beck, James J
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,187
; FILING DATE:

```

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/233,608
; FILING DATE: 04-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Walsh, Andrea C.
; REGISTRATION NUMBER: 34,988
; REFERENCE/DOCKET NUMBER: CGC 1739
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8666
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotide primer
; DESCRIPTION: JB577"
; HYPOTHETICAL: NO
; US-08-722-187-64

Query Match      67.1%; Score 11.4; DB 2; Length 16;
Best Local Similarity 92.3%; Pred. No. 1.4e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GTTGCTTCGGCGG 13
DB      1 GTTGCTTCGGCGG 13

RESULT 17
US-09-593-012-198
; Sequence 198; Application US/09593012
; Patent No. 6387652.
; GENERAL INFORMATION:
; APPLICANT: HAUGLAND, Richard
; APPLICANT: VESPER, Stephen
; TITLE OF INVENTION: METHOD OF IDENTIFYING AND QUANTIFYING SPECIFIC FUNGI AND BACTERIA
; FILE REFERENCE: HAUGLAND-1A
; CURRENT APPLICATION NUMBER: US/09/593,012
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US 09/290,990
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 60/081,773
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 198
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Trichoderma longibrachiatum/citreoviride
; US-09-593-012-198

Query Match      67.1%; Score 11.4; DB 4; Length 16;
Best Local Similarity 92.3%; Pred. No. 1.4e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 TGCTTCGGCGGGA 15
DB      1 TGCTTCGGCGGGA 13

RESULT 18
PCT-US95-04712-57
; Sequence 57; Application PC/TUS9504712
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M
; APPLICANT: Beck, James J
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 86
```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04712
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION:
; APPLICATION NUMBER: US 08/233,608
; FILING DATE: 04-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Walsh, Andrea C.
; REGISTRATION NUMBER: 34,988
; REFERENCE/DOCKET NUMBER: CGC 1739
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8666
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotide primer
; DESCRIPTION: JB570"
; HYPOTHETICAL: NO
; PCT-US95-04712-57

Query Match      67.1%; Score 11.4; DB 5; Length 16;
Best Local Similarity 92.3%; Pred. No. 1.4e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GTTGCTTCGGCGG 13
DB      4 GTTGCTTCGGCGG 16

RESULT 19
PCT-US95-04712-64
; Sequence 64; Application PC/TUS9504712
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M
; APPLICANT: Beck, James J
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04712
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: US 08/233,606
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: WALSH, ANDREA C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: CGC 1739
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8666
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide primer"
DESCRIPTION: JB577"
HYPOTHETICAL: NO
PCT-US95-04712-64

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Query Match 67.1%; Score 11.4; DB 5; Length 16;
Best Local Similarity 92.3%; Pred. No. 1.4e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCTTGGCGG 13
DB 1 GTTCTTGGCGG 13

RESULT 20
US-08-606-505B-19/C
Sequence 19, Application US/08606505B
Patent No. 6114601
GENERAL INFORMATION:
APPLICANT: KIKUCHI, Yasuhiro
APPLICANT: KIYOKAWA, Shigeto
APPLICANT: SHIMADA, Yukihisa
APPLICANT: OHBAYASHI, Masaya
APPLICANT: SHIMADA, Ritsuko
APPLICANT: OKINAKA, Yasushi
TITLE OF INVENTION: NOVEL PLANT GENES
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: FITZPATRICK, CELLA, HARPER & SCINTO
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112-3801
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.50 inch, 720 Kb storage.
COMPUTER: IBM PS/V
OPERATING SYSTEM: MS-DOS Ver3.30
SOFTWARE: PATENT AID Ver1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,505B
FILING DATE: 23-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP44963/92
FILING DATE: 02-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: PERRY, Lawrence S.
REGISTRATION NUMBER: 31865
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-218-2100
TELEFAX: 212-218-2200
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: Other nucleic acid
DESCRIPTION: Synthetic RNA
US-09-606-505B-19

Query Match 67.1%; Score 11.4; DB 3; Length 17;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TGCTTGGCGGGAAC 17
DB 18 TGCTTGGCGGGAAC 4

RESULT 21
US-09-616-990-19/C
Sequence 19, Application US/09616990
Patent No. 6232109
GENERAL INFORMATION:
APPLICANT: KIKUCHI, Yasuhiro
APPLICANT: KIYOKAWA, Shigeto
APPLICANT: SHIMADA, Yukihisa
APPLICANT: OHBAYASHI, Masaya
APPLICANT: SHIMADA, Ritsuko
APPLICANT: OKINAKA, Yasushi
TITLE OF INVENTION: NOVEL PLANT GENES
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: FITZPATRICK, CELLA, HARPER & SCINTO
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112-3801
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.50 inch, 720 Kb storage.
COMPUTER: IBM PS/V
OPERATING SYSTEM: MS-DOS Ver3.30
SOFTWARE: PATENT AID Ver1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/616,990
FILING DATE: 14-JUL-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP44963/92
FILING DATE: 02-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: PERRY, Lawrence S.
REGISTRATION NUMBER: 31865
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-218-2100
TELEFAX: 212-218-2200
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: Synthetic DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 19
US-09-616-990-19

Query Match 67.1%; Score 11.4; DB 4; Length 18;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TGCTTGGCGGGAAC 17
DB 18 TGCTTGGCGGGAAC 4

RESULT 22
US-08-652-127C-1
Sequence 1, Application US/08652127C

Patent No. 5792611
GENERAL INFORMATION:
APPLICANT: Richard C. Hamelin
TITLE OF INVENTION: DETECTION OF PLANT
TITLE OF INVENTION: PATHOGEN FUNGI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: George A. Seaby
ADDRESS: Seaby & Maclean
STREET: 880 Wellington Street, Suite 708
CITY: Ottawa
COUNTRY: Canada
ZIP: K1R 6K7
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652.127C
FILING DATE: May 23, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: George A. Seaby
REGISTRATION NUMBER: 24,034
REFERENCE/DOCKET NUMBER: 1898
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 232-5815
TELEFAX: (613) 232-5831
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-652-127C-1

Query Match 67.1%; Score 11.4; DB 1; Length 21;
Best Local Similarity 92.3%; Pred. No. 1.5e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTGCTTGGCGG 13
||| ||| ||| |||
Db 3 GTTGCTTGGCGG 15

RESULT 23
US-08-358-556A-1
Sequence 1, Application US/08358556A
Patent No. 5869643
GENERAL INFORMATION:
APPLICANT: Chatelet, Francois
APPLICANT: Kumarev, Viktor
TITLE OF INVENTION: Process for Preparing Polynucleotides on
TITLE OF INVENTION: a Solid Support and Apparatus Permitting its
TITLE OF INVENTION: Implementation
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CITY: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358.556A
FILING DATE: 14-DEC-1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 9315164
FILING DATE: 16-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577/P58418
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-5350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
FEATURE:
NAME/KEY: CDS
LOCATION: 1..18
US-08-358-556A-1

Query Match 65.9%; Score 11.2; DB 2; Length 18;
Best Local Similarity 81.2%; Pred. No. 1.8e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTGCTTGGCGGAA 16
||| ||| ||| ||| |||
Db 3 GTTGCTTGGCGGAA 18

RESULT 24
US-08-281-203-6
Sequence 6, Application US/08281203
Patent No. 6033909
GENERAL INFORMATION:
APPLICANT: Uhlmann, Eugen
APPLICANT: Peyman, Anuschirvan
APPLICANT: O'Malley, Gerard
APPLICANT: Heisberg, Matthias
APPLICANT: Winkler, Irvin
TITLE OF INVENTION: Oligonucleotide Analogs, Their
TITLE OF INVENTION: Preparation and Use
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/281.203
FILING DATE: 27-JULY-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/003,972
FILING DATE: 19-JAN-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 02481.1269-01000
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-281-203-6

Query Match 65.9%; Score 11.2; DB 3; Length 20;
Best Local Similarity 81.2%; Pred. No. 1.9e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTCCTTCGGCGGAA 16
DB 4 GTTCCTTCGGCGGAA 19

RESULT 25
US-09-326-1868-146
Sequence 146, Application US/093261868
Patent No. 6319806
GENERAL INFORMATION:
APPLICANT: Bennett, Clarence Frank
APPLICANT: Vickers, Timothy A.
TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
FILE REFERENCE: ISPH-0376
CURRENT APPLICATION NUMBER: US/09/326,1868
PRIOR FILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: 08/777,266
NUMBER OF SEQ ID NOS: 226
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 146
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-326-1868-146

Query Match 65.9%; Score 11.2; DB 4; Length 20;
Best Local Similarity 81.2%; Pred. No. 1.9e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTGCTTCGGCGGAA 17
DB 3 TTGCTTCGGCGGAA 18

RESULT 26
US-08-005-283-4/C
Sequence 4, Application US/08005283
Patent No. 5646261
GENERAL INFORMATION:
APPLICANT: Uhlmann, Eugen
APPLICANT: Peyman, Anuschirwan
APPLICANT: O'Malley, Gerard
APPLICANT: Helberg, Matthias
APPLICANT: Winkler, Irvin
TITLE OF INVENTION: 3'-Derivatized Oligonucleotide Analogs
TITLE OF INVENTION: 3'-Derivatized Oligonucleotide Analogs
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS: with No. 5646261-Nucleotide Groupings, Their Preparation and

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSER: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA

ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/005,283
FILING DATE: 19-JAN-1993
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4201663.0
FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Hammond, Alan W.
REGISTRATION NUMBER: 35,178
REFERENCE/DOCKET NUMBER: 02481.1270-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-005-283-4

Query Match 65.9%; Score 11.2; DB 1; Length 25;
Best Local Similarity 81.2%; Pred. No. 1.9e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTCCTTCGGCGGAA 16
DB 19 GTTCCTTCGGCGGAA 4

RESULT 27
US-08-005-283-6/C
Sequence 6, Application US/08005283
Patent No. 5646261
GENERAL INFORMATION:
APPLICANT: Uhlmann, Eugen
APPLICANT: Peyman, Anuschirwan
APPLICANT: O'Malley, Gerard
APPLICANT: Helberg, Matthias
APPLICANT: Winkler, Irvin
TITLE OF INVENTION: 3'-Derivatized Oligonucleotide Analogs
TITLE OF INVENTION: 3'-Derivatized Oligonucleotide Analogs
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS: with No. 5646261-Nucleotide Groupings, Their Preparation and
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSER: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/005,283
FILING DATE: 19-JAN-1993
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4201663.0
FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Hammond, Alan W.

REGISTRATION NUMBER: 35,178
REFERENCE/DOCKET NUMBER: 02481.1270-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-005-283-6

Query Match 65.9%; Score 11.2; DB 1; Length 25;
Best Local Similarity 81.2%; Pred. No. 1.9e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTGCTTGGCGGGA 16
DB 19 GTTCTCTGCGGGA 4

RESULT 28
US-09-593-012-48/c
Sequence 48, Application US/09593012
Patent No. 6387652
GENERAL INFORMATION:
APPLICANT: HAUGLAND, Richard
APPLICANT: VESPER, Stephen
TITLE OF INVENTION: METHOD OF IDENTIFYING AND QUANTIFYING SPECIFIC FUNGI AND BACTERIA
FILE REFERENCE: HAUGLAND-1A
CURRENT APPLICATION NUMBER: US/09/593,012
CURRENT FILING DATE: 2000-06-13
PRIOR APPLICATION NUMBER: US 09/290,990
PRIOR FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: US 60/081,773
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 48
LENGTH: 18
TYPE: DNA
ORGANISM: Aspergillus natus
US-09-593-012-48

Query Match 64.7%; Score 11; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTGCTTGGC 11
DB 11 GTTGCTTGGC 1

RESULT 29
US-08-472-255A-56
Sequence 56, Application US/08472255A
Patent No. 5766853
GENERAL INFORMATION:
APPLICANT: PARMA, DAVID
APPLICANT: GOLD, LARRY
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
TITLE OF INVENTION: TO SELECTS (AS AMENDED)
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,255A
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX40-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All C's are 2'-NH2 cytosine
OTHER INFORMATION: All U's are 2'-NH2 uracil
US-08-472-255A-56

Query Match 64.7%; Score 11; DB 1; Length 20;
Best Local Similarity 90.9%; Pred. No. 2.4e+03;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 TCGCGCGGAC 17
DB 6 UCGCGCGGAC 16

RESULT 30
US-08-479-724A-56
Sequence 56, Application US/08479724A
Patent No. 5780228
GENERAL INFORMATION:
APPLICANT: PARMA, DAVID
APPLICANT: GOLD, LARRY
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
TITLE OF INVENTION: TO SELECTS
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,724A
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/714,111
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1991
PRIOR APPLICATION DATA: 07/964,624
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX40-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All C's are 2'-NH2 cytosine
FEATURE:
OTHER INFORMATION: All U's are 2'-NH2 uracil
US-08-479-724A-56

Query Match 64.7%; Score 11; DB 1; Length 20;
Best Local Similarity 90.9%; Pred. No. 2.4e+03;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 TCGGCGGGAAC 17
Db 6 UCGCGGGAAC 16

RESULT 31
US-08-472-256B-56
Sequence 56, Application US/08472256B
Patent No. 6001988
GENERAL INFORMATION:
APPLICANT: PARMA, DAVID
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
TITLE OF INVENTION: TO LECTINS
NUMBER OF SEQUENCES: 177
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,256B
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:

NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All C's are 2'-NH2 cytosine
FEATURE:
OTHER INFORMATION: All U's are 2'-NH2 uracil
US-08-472-256B-56

Query Match 64.7%; Score 11; DB 3; Length 20;
Best Local Similarity 90.9%; Pred. No. 2.4e+03;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 TCGGCGGGAAC 17
Db 6 UCGCGGGAAC 16

RESULT 32
US-08-952-793-56
Sequence 56, Application US/08952793
Patent No. 6280932
GENERAL INFORMATION:
APPLICANT: PARMA, et al.
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
TITLE OF INVENTION: TO LECTINS
NUMBER OF SEQUENCES: 390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,793
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09455
FILING DATE: 05-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,724
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/472,256
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/472,255
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/477,829
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/477,829
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX40C/PCT
TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All C's are 2'-NH2 cytosine
FEATURE:
OTHER INFORMATION: All U's are 2'-NH2 uracil
US-08-952-793-56

Query Match 64.7% Score 11; DB 4; Length 20;
Best Local Similarity 90.9%; Pred. No. 2.4e+03;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 TCGGCGGGGAC 17
Db 6 UCGGCGGGGAC 16

RESULT 33

PCT-US96-09455A-56

Sequence 56, Application PC/TUS9609455A

GENERAL INFORMATION:

APPLICANT: PARMA, et al.

TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID

LIGANDS TO LECTINS

NUMBER OF SEQUENCES: 390

CORRESPONDENCE ADDRESS:

ADDRESSEE: Swanson & Bratschun, L.L.C.

STREET: 8400 E. Prentice Avenue, Suite 200

CITY: Englewood

STATE: Colorado

COUNTRY: USA

ZIP: 80111

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB

COMPUTER: IBM PC compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/09455A

FILING DATE: 05 JUNE 1996

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/479,724

FILING DATE: 07-JUNE-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/472,256

FILING DATE: 07-JUNE-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/472,255

FILING DATE: 07-JUNE-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/477,829

FILING DATE: 07-JUNE-1995

ATTORNEY/AGENT INFORMATION:

NAME: Barry J. Swanson

REGISTRATION NUMBER: 33,215

REFERENCE/DOCKET NUMBER: NEX40C/PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 793-3333

TELEFAX: (303) 793-3433

INFORMATION FOR SEQ ID NO: 56:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All C's are 2'-NH2 cytosine
FEATURE:
OTHER INFORMATION: All U's are 2'-NH2 uracil
PCT-US96-09455A-56

Query Match 64.7% Score 11; DB 5; Length 20;
Best Local Similarity 90.9%; Pred. No. 2.4e+03;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 TCGGCGGGGAC 17
Db 6 UCGGCGGGGAC 16

RESULT 34

US-08-679-645-539/C

Sequence 539, Application US/08679645

Patent No. 6350934

GENERAL INFORMATION:

APPLICANT: Zwick, Michael G.

APPLICANT: Edington, Brent E.

APPLICANT: McSwiggen, James A.

APPLICANT: Merlo, Patricia Ann Owens

APPLICANT: Guo, Lining

APPLICANT: Skokut, Thomas A.

APPLICANT: Young, Scott A.

APPLICANT: Folkerts, Otto

APPLICANT: Merlo, Donald J.

TITLE OF INVENTION: COMPOSITION AND METHODS FOR

MODULATION OF GENE EXPRESSION

TITLE OF INVENTION: IN PLANTS

NUMBER OF SEQUENCES: 1263

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/679,645

FILING DATE: July 12, 1996

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/001,135

FILING DATE: July 13, 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/300,726

FILING DATE: September 2, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 219/247

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

INFORMATION FOR SEQ ID NO: 539:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-679-645-539

LOCATION: 822..803
OTHER INFORMATION: Antisense primer hts-6b for PCR amplification of part
OTHER INFORMATION: of 890 base pair fragment of human TS gene
OTHER INFORMATION: from nucleotide 50 to the C-terminus
US-09-367-007C-14

Query Match 63.5% Score 10.8; DB 4; Length 20;
Best Local Similarity 85.7% Pred. No. 3.1e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCTTGGCGGCGAAC 17
DB 19 GCTTCAGCGAGAAC 6

RESULT 39
PCT-US95-09069-2/C
Sequence 2, Application PC/TUS9509069

GENERAL INFORMATION:
APPLICANT: Wilson, David B.
APPLICANT: Walker, Larry P.

APPLICANT: Zhang, Sheng
TITLE OF INVENTION: Thermostable Cellulase from A Thermomonospora Gene
NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
STREET: 1800 One M&T Plaza
CITY: Buffalo

STATE: New York
COUNTRY: United States
ZIP: 14203-2391

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1
SOFTWARE: Wordperfect for Windows 5.1
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/09069
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial No. 08/265,429
FILING DATE: 24/06/94

ATTORNEY/AGENT INFORMATION:
NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300

REFERENCE/DOCKET NUMBER: 18617.0008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 856-4000

TELEFAX: 716-849-0349
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 20 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single-stranded

MOLECULE TYPE: DNA
IMMEDIATE SOURCE: synthesized
ORIGINAL SOURCE:

ORGANISM: Thermomonospora fusca
STRAIN: YX36
CELL TYPE: bacterium

PCT-US95-09069-2

Query Match 63.5% Score 10.8; DB 5; Length 20;
Best Local Similarity 85.7% Pred. No. 3.1e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGCTTCGGCGGCGAA 16
DB 20 TGCAATGGCGGCGAA 7

RESULT 40
US-08-974-549A-510
Sequence 510, Application US/08974549A
Patent No. 6166178

GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.

APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.

APPLICANT: Morin, Gregg B.
APPLICANT: Hatley, Calvin B.
APPLICANT: Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco

STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 510:
SEQUENCE CHARACTERISTICS:

LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear

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OM nucleic - nucleic search, using sw model

Run on: June 7, 2003, 08:05:49 ; Search time 973.327 Seconds
(without alignments)
282.868 Million cell updates/sec

Title: US-10-080-959a-1

Perfect score: 17

Sequence: 1 gctcgtcggcgsgaac 17

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 18144

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :
EST:
1: em_estba:*
2: em_estbun:*
3: em_estlin:*
4: em_estlml:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_hnc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hnc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estcom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vit:*
22: em_gss_fun:*
23: em_gss_man:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11.2	65.9	25	13	BI094828
2	10.4	61.2	25	17	TA352B06Q
3	10	58.8	21	17	AZ307451
4	9.8	57.6	25	9	AI421881
5	9.6	56.5	22	17	TA114G12Q
6	9.4	55.3	24	17	AZ786547

C	7	9.2	54.1	18	13	BM398017
C	8	9.2	54.1	19	17	AZ781461
C	9	9.2	54.1	20	17	AZ432681
C	10	9.2	54.1	24	17	TA75A030
C	11	9.2	54.1	25	9	AI594892
C	12	9.2	54.1	25	17	BM854200
C	13	9.2	54.1	20	17	AZ659612
C	14	9.2	54.1	21	17	AZ663981
C	15	9.2	54.1	25	13	BM399936
C	16	9.2	54.1	25	17	AZ478429
C	17	9.2	54.1	25	17	AZ339811
C	18	9.2	54.1	23	17	TA106C010
C	19	9.2	54.1	23	17	TA266D03P
C	20	9.2	54.1	20	17	AZ345583
C	21	9.2	54.1	22	17	AZ247820
C	22	9.2	54.1	23	17	AZ780543
C	23	9.2	54.1	25	9	AA343350
C	24	9.2	54.1	25	9	AI091780
C	25	9.2	54.1	25	13	BM397307
C	26	9.2	54.1	25	17	TA307A07Q
C	27	9.2	54.1	22	9	AA91484
C	28	9.2	54.1	22	9	AI352536
C	29	9.2	54.1	22	9	AU006620
C	30	9.2	54.1	22	9	AU006633
C	31	9.2	54.1	22	17	AZ476310
C	32	9.2	54.1	22	17	TA219C09P
C	33	9.2	54.1	20	17	AZ475852
C	34	9.2	54.1	20	17	AZ511616
C	35	9.2	54.1	20	17	AZ789409
C	36	9.2	54.1	21	17	AZ354490
C	37	9.2	54.1	22	9	AA908627
C	38	9.2	54.1	22	9	AI721471
C	39	9.2	54.1	22	17	TA174D06Q
C	40	9.2	54.1	23	17	AZ785027
C	41	9.2	54.1	25	9	AI264778
C	42	9.2	54.1	25	13	BM401196
C	43	9.2	54.1	25	17	TA237D08Q
C	44	9.2	54.1	19	17	AZ449942
C	45	9.2	54.1	20	9	AU060353
C	46	9.2	54.1	22	17	AZ821049
C	47	9.2	54.1	22	17	TA28D01Q
C	48	9.2	54.1	22	17	TA368E02Q
C	49	9.2	54.1	23	17	AZ387178
C	50	9.2	54.1	23	17	AZ785889
C	51	9.2	54.1	23	17	AZ840388
C	52	9.2	54.1	23	17	BM848405
C	53	9.2	54.1	24	17	AZ405843
C	54	9.2	54.1	24	17	AZ584313
C	55	9.2	54.1	24	17	AZ595059
C	56	9.2	54.1	24	17	AZ809979
C	57	9.2	54.1	25	9	AA903841
C	58	9.2	54.1	25	17	TA72B02P
C	59	9.2	54.1	19	9	AI017937
C	60	9.2	54.1	19	17	AZ345964
C	61	9.2	54.1	19	17	AZ969805
C	62	9.2	54.1	20	9	AU257181
C	63	9.2	54.1	20	17	AZ592635
C	64	9.2	54.1	21	17	AZ318273
C	65	9.2	54.1	21	17	AZ581103
C	66	9.2	54.1	22	17	AM059920
C	67	9.2	54.1	22	14	DI8746
C	68	9.2	54.1	22	17	AZ644887
C	69	9.2	54.1	23	17	AZ308507
C	70	9.2	54.1	24	17	AZ316848
C	71	9.2	54.1	24	17	AZ492823
C	72	9.2	54.1	24	17	AZ792764
C	73	9.2	54.1	25	9	AA980269
C	74	9.2	54.1	25	9	AA933070
C	75	9.2	54.1	25	14	Z20702
C	76	9.2	54.1	25	17	AQ025268
C	77	9.2	54.1	25	17	AZ308557
C	78	9.2	54.1	25	17	AZ339351
C	79	9.2	54.1	25	17	AZ807246

83	11	55.0	20	20	AA93074	PCR primer used to	156	10.6	53.0	20	19	AAV06901	Modified oligonucleotide
84	11	55.0	20	21	AA63630	PCR primer used to	157	10.6	53.0	20	22	AAH81077	Oligonucleotide by
85	11	55.0	20	22	AA75019	PCR primer for hum	158	10.6	53.0	20	22	AAH81078	Oligonucleotide by
86	11	55.0	20	22	AAH75023	PCR primer for hum	159	10.6	53.0	20	22	AAH81079	Oligonucleotide by
87	11	55.0	20	24	ABN80813	Human IRF-1 PCR p	160	10.6	53.0	20	22	AAH81080	Oligonucleotide by
88	11	55.0	20	24	ABN50586	Human OST11 PCR p	161	10.6	53.0	20	22	AAH81081	Oligonucleotide by
89	11	55.0	20	24	ABN49377	Capture oligonucle	162	10.6	53.0	20	22	AAH81082	Oligonucleotide by
90	11	55.0	20	24	ABN49377	Human chromosome 1	163	10.6	53.0	20	24	AAH81083	Oligonucleotide by
91	11	55.0	21	19	AAV52632	Hepatocyte nuclear	164	10.6	53.0	20	24	AAH81084	Oligonucleotide by
92	11	55.0	21	22	AAV52632	Human gene single	165	10.6	53.0	20	24	AAH81085	Oligonucleotide by
93	11	55.0	21	22	AAV52632	Tyrosinase gene sp	166	10.6	53.0	20	24	AAH81086	Oligonucleotide by
94	11	55.0	22	20	AAZ28059	Human tumor suppl	167	10.6	53.0	21	19	AAV40597	Human TSC gene exo
95	11	55.0	22	17	AAZ28059	E. coli PBP 1B sol	168	10.6	53.0	21	20	AAV63758	PCR primer-1 for a
96	11	55.0	23	14	AAZ28059	PCR primer used to	169	10.6	53.0	22	20	AAV63759	Human JAGGED1 PCR
97	11	55.0	23	20	AAZ28059	Human vimentin PCR	170	10.6	53.0	22	20	AAV63760	Human GDNFR-beta c
98	11	55.0	24	19	AAV18979	Endothelin convert	171	10.6	53.0	24	18	AAH84805	Rat endothelial di
99	11	55.0	24	24	ABN55324	Capture oligonucle	172	10.6	53.0	24	24	AAZ32492	Human EDG family H
100	11	55.0	24	24	ABN55324	HLA DRB345 gene PC	173	10.6	53.0	24	24	ABN00912	Oligonucleotide ad
101	11	55.0	25	21	AAZ28059	Human ERG G-cleave	174	10.6	53.0	24	24	ABN01595	Oligonucleotide ad
102	11	55.0	25	21	AAZ28059	Human DRB345 gene PC	175	10.6	53.0	24	24	ABN05790	Oligonucleotide ad
103	11	55.0	25	21	AAZ28059	Human ICAM hammet	176	10.6	53.0	24	24	ABN05831	Oligonucleotide ad
104	11	55.0	15	16	AAZ28059	Hammerhead ribozym	177	10.6	53.0	24	24	ABN07120	Oligonucleotide ad
105	11	55.0	17	21	AAZ28059	Hammerhead ribozym	178	10.6	53.0	24	24	ABN07161	Capture oligonucle
106	11	55.0	17	21	AAZ28059	Human NOGO inozyme	179	10.6	53.0	24	24	ABN07161	Human MAT1 RING do
107	11	55.0	17	23	ABN01366	Chromosome 11 (loc	180	10.6	53.0	25	18	AAH89165	Human kinase MCX
108	11	55.0	17	23	ABN01366	Chromosome 11 (loc	181	10.6	53.0	25	18	AAH89165	SNP specific SNPE
109	11	55.0	17	23	ABN01366	Chromosome 11 (loc	182	10.6	53.0	25	22	AAH39759	Xenopus laevis ree
110	11	55.0	20	19	AAV85951	Human LRP-3 CDNA P	183	10.6	53.0	25	22	AAH39759	Human ICAM hammet
111	11	55.0	20	19	AAV85951	Primer extension p	184	10.6	53.0	25	22	AAH39759	Human phospholipid
112	11	55.0	20	20	AAZ74939	Human SHP-1 antis	185	10.6	53.0	25	22	AAH39759	Human PLTP gene a1
113	11	55.0	20	21	AAZ74939	Human CDNA clone-s	186	10.6	53.0	25	22	AAH39759	Integrin subunit b
114	11	55.0	20	21	AAZ74939	Human hmrp Al pho	187	10.6	53.0	25	22	AAH39759	Monomer DRB1013 fo
115	11	55.0	20	22	AAZ74939	3'-end primer RS 4	188	10.6	53.0	15	22	AAH39759	Single nucleotide
116	11	55.0	20	22	AAZ74939	Bglb536r primer c	189	10.6	53.0	17	20	AAZ24493	MMP25 (leukolysin)
117	11	55.0	20	24	AAZ74939	Capture oligonucle	190	10.6	53.0	18	14	AAZ24493	rtx gene PCR prime
118	11	55.0	20	24	AAZ74939	Neuropeptide Y Yx	191	10.6	53.0	18	21	AAZ24493	Human ballelic ma
119	11	55.0	20	24	AAZ74939	Human ballelic ma	192	10.6	53.0	19	21	AAZ24493	Single nucleotide
120	11	55.0	21	17	AAZ74939	Zs66 sequencing	193	10.6	53.0	19	21	AAZ24493	cdk-we-hu ribozyme
121	11	55.0	21	17	AAZ74939	Human gene single	194	10.6	53.0	19	21	AAZ24493	cdk-we-hu ribozyme
122	11	55.0	21	21	AAZ74939	Human gene single	195	10.6	53.0	19	21	AAZ24493	Dog genomic marker
123	11	55.0	21	21	AAZ74939	Human beta-globin	196	10.6	53.0	19	21	AAZ24493	Bacterial 16S RNA
124	11	55.0	21	21	AAZ74939	Human short inters	197	10.6	53.0	19	21	AAZ24493	Cdk-we-hu ribozyme
125	11	55.0	21	21	AAZ74939	Human short inters	198	10.6	53.0	19	21	AAZ24493	Cdk-we-hu ribozyme
126	11	55.0	21	21	AAZ74939	Human short inters	199	10.6	53.0	19	21	AAZ24493	Oligonucleotide (c
127	11	55.0	21	21	AAZ74939	Human short inters	200	10.6	53.0	19	21	AAZ24493	Human kappa oploid
128	11	55.0	21	21	AAZ74939	Human short inters	201	10.6	53.0	19	21	AAZ24493	Primer 201B for my
129	11	55.0	21	21	AAZ74939	Human short inters	202	10.6	53.0	20	17	AAZ24493	ATM region 9 (nt 2
130	11	55.0	21	21	AAZ74939	Human short inters	203	10.6	53.0	20	17	AAZ24493	Neospora caninum G
131	11	55.0	21	21	AAZ74939	Human short inters	204	10.6	53.0	20	17	AAZ24493	Forward primer #10
132	11	55.0	21	21	AAZ74939	Human short inters	205	10.6	53.0	20	17	AAZ24493	Human IL-5 antis
133	11	55.0	21	21	AAZ74939	Human short inters	206	10.6	53.0	20	17	AAZ24493	Human IL-5 antis
134	11	55.0	21	21	AAZ74939	Human short inters	207	10.6	53.0	20	17	AAZ24493	Newcastle disease
135	11	55.0	21	21	AAZ74939	Human short inters	208	10.6	53.0	20	17	AAZ24493	Newcastle disease
136	11	55.0	21	21	AAZ74939	Human short inters	209	10.6	53.0	20	17	AAZ24493	Newcastle disease
137	11	55.0	21	21	AAZ74939	Human short inters	210	10.6	53.0	20	17	AAZ24493	Newcastle disease
138	11	55.0	21	21	AAZ74939	Human short inters	211	10.6	53.0	20	17	AAZ24493	Newcastle disease
139	11	55.0	21	21	AAZ74939	Human short inters	212	10.6	53.0	20	17	AAZ24493	Newcastle disease
140	11	55.0	21	21	AAZ74939	Human short inters	213	10.6	53.0	20	17	AAZ24493	Newcastle disease
141	11	55.0	21	21	AAZ74939	Human short inters	214	10.6	53.0	20	17	AAZ24493	Newcastle disease
142	11	55.0	21	21	AAZ74939	Human short inters	215	10.6	53.0	20	17	AAZ24493	Newcastle disease
143	11	55.0	21	21	AAZ74939	Human short inters	216	10.6	53.0	20	17	AAZ24493	Newcastle disease
144	11	55.0	21	21	AAZ74939	Human short inters	217	10.6	53.0	20	17	AAZ24493	Newcastle disease
145	11	55.0	21	21	AAZ74939	Human short inters	218	10.6	53.0	20	17	AAZ24493	Newcastle disease
146	11	55.0	21	21	AAZ74939	Human short inters	219	10.6	53.0	20	17	AAZ24493	Newcastle disease
147	11	55.0	21	21	AAZ74939	Human short inters	220	10.6	53.0	20	17	AAZ24493	Newcastle disease
148	11	55.0	21	21	AAZ74939	Human short inters	221	10.6	53.0	20	17	AAZ24493	Newcastle disease
149	11	55.0	21	21	AAZ74939	Human short inters	222	10.6	53.0	20	17	AAZ24493	Newcastle disease
150	11	55.0	21	21	AAZ74939	Human short inters	223	10.6	53.0	20	17	AAZ24493	Newcastle disease
151	11	55.0	21	21	AAZ74939	Human short inters	224	10.6	53.0	20	17	AAZ24493	Newcastle disease
152	11	55.0	21	21	AAZ74939	Human short inters	225	10.6	53.0	20	17	AAZ24493	Newcastle disease
153	11	55.0	21	21	AAZ74939	Human short inters	226	10.6	53.0	20	17	AAZ24493	Newcastle disease
154	11	55.0	21	21	AAZ74939	Human short inters	227	10.6	53.0	20	17	AAZ24493	Newcastle disease
155	11	55.0	21	21	AAZ74939	Human short inters	228	10.6	53.0	20	17	AAZ24493	Newcastle disease

C 226	7	41.2	22	9	AU009067	AU009067	AU009067	299	6.8	40.0	20	17	AZ591658	AZ591658	IM0401F19
C 227	7	41.2	22	17	AZ366437	AZ366437	IM015K11	300	6.8	40.0	20	17	AZ766411	AZ766411	IM0564B02
C 228	7	41.2	22	17	AZ459715	AZ459715	IM0264E13	301	6.8	40.0	20	17	AZ776071	AZ776071	2M0009L24
C 229	7	41.2	22	17	AZ484391	AZ484391	IM0310M15	302	6.8	40.0	21	13	BM400884	BM400884	5009-0-8
C 230	7	41.2	22	17	AZ598225	AZ598225	IM041K222	303	6.8	40.0	21	17	AZ307817	AZ307817	IM0010I09
C 231	7	41.2	22	17	AZ785163	AZ785163	2M0028B20	304	6.8	40.0	21	17	AZ447969	AZ447969	IM0245U19
C 232	7	41.2	22	17	AZ785474	AZ785474	2M0029E19	305	6.8	40.0	21	17	AZ583481	AZ583481	IM0378X06
C 233	7	41.2	22	17	AZ840252	AZ840252	2M0136P10	306	6.8	40.0	21	17	TA72A04P	TA72A04P	
C 234	7	41.2	22	17	TA133E06P	TA133E06P		307	6.8	40.0	22	9	AA936651	AA936651	0167b12.8
C 235	7	41.2	22	17	TA13D05Q	TA13D05Q		308	6.8	40.0	22	9	AA978171	AA978171	ny36f08.B
C 236	7	41.2	23	9	AU256828	AU256828		309	6.8	40.0	22	9	A1442754	A1442754	8a26a02.x
C 237	7	41.2	23	9	AU259528	AU259528		310	6.8	40.0	22	9	A1567845	A1567845	cg87e02.x
C 238	7	41.2	23	10	AW249405	AW249405	2819235.5	311	6.8	40.0	22	9	A1568336	A1568336	cn68b01.x
C 239	7	41.2	23	17	BG927413	BG927413	HNC1-1-G1	312	6.8	40.0	22	9	A1735392	A1735392	at10e10.x
C 240	7	41.2	23	17	AZ309657	AZ309657	IM016U24	313	6.8	40.0	22	13	BM398330	BM398330	5009-0-44
C 241	7	41.2	23	17	AZ320709	AZ320709	IM0040I20	314	6.8	40.0	22	13	BM398330	BM398330	5009-0-44
C 242	7	41.2	23	17	AZ335717	AZ335717	IM0065J20	315	6.8	40.0	22	13	BM399045	BM399045	5009-0-52
C 243	7	41.2	23	17	AZ392457	AZ392457	IM0155O03	316	6.8	40.0	22	13	BM399475	BM399475	5009-0-58
C 244	7	41.2	23	17	AZ398730	AZ398730	IM0164F15	317	6.8	40.0	22	13	BM399475	BM399475	5009-0-58
C 245	7	41.2	23	17	AZ617124	AZ617124	IM0448E15	318	6.8	40.0	22	13	BM400176	BM400176	5009-0-68
C 246	7	41.2	23	17	AZ828013	AZ828013	2M0104H13	319	6.8	40.0	22	13	AZ321399	AZ321399	IM0041G24
C 247	7	41.2	23	17	BM848110	BM848110	SAUK_0675	320	6.8	40.0	22	17	AZ321399	AZ321399	IM0202J03
C 248	7	41.2	23	17	TA133D03P	TA133D03P		321	6.8	40.0	22	17	AZ423444	AZ423444	IM0202D20
C 249	7	41.2	23	17	TA175H02P	TA175H02P		322	6.8	40.0	22	17	AZ784043	AZ784043	2M0106B06
C 250	7	41.2	23	17	TA242D06P	TA242D06P		323	6.8	40.0	22	17	AZ828775	AZ828775	2M0106B06
C 251	7	41.2	23	17	TA265A03P	TA265A03P		324	6.8	40.0	22	17	BM747671	BM747671	SAUK_0324
C 252	7	41.2	24	13	BM399103	BM399103	5009-0-53	325	6.8	40.0	22	17	TA129801P	TA129801P	
C 253	7	41.2	24	17	AZ395193	AZ395193	IM0159D17	326	6.8	40.0	23	13	BM399821	BM399821	5009-0-62
C 254	7	41.2	24	17	AZ586050	AZ586050	IM0391N08	327	6.8	40.0	23	13	BM400852	BM400852	5009-0-8
C 255	7	41.2	24	17	AZ588844	AZ588844	IM0397M20	328	6.8	40.0	23	13	BM400852	BM400852	5009-0-8
C 256	7	41.2	24	17	AZ597727	AZ597727	IM0411P02	329	6.8	40.0	23	17	AZ308507	AZ308507	IM0011L02
C 257	7	41.2	24	17	AZ782545	AZ782545	2M0023E04	330	6.8	40.0	23	17	AZ340084	AZ340084	
C 258	7	41.2	24	17	TA207E11Q	TA207E11Q		331	6.8	40.0	23	17	AZ42625	AZ42625	IM0263C14
C 259	7	41.2	25	9	A1091780	A1091780	qa91e02.8	332	6.8	40.0	23	17	AZ472899	AZ472899	IM0288L22
C 260	7	41.2	25	9	A1444500	A1444500	fw25d04.x	333	6.8	40.0	23	17	AZ495857	AZ495857	IM0381P21
C 261	7	41.2	25	9	A1586975	A1586975	cb15g05.x	334	6.8	40.0	23	17	AZ593454	AZ593454	IM0405C03
C 262	7	41.2	25	9	A1589311	A1589311	cr58h04.x	335	6.8	40.0	23	17	AZ596987	AZ596987	IM0410O05
C 263	7	41.2	25	9	A1682835	A1682835	wc66h10.x	336	6.8	40.0	23	17	AZ619403	AZ619403	IM0451B09
C 264	7	41.2	25	9	A1745654	A1745654	tc24d07.x	337	6.8	40.0	23	17	AZ619403	AZ619403	IM0530E20
C 265	7	41.2	25	9	AU270690	AU270690		338	6.8	40.0	23	17	AZ655495	AZ655495	
C 266	7	41.2	25	14	L32056	L32056	HUMXP664B H	339	6.8	40.0	23	17	AZ813325	AZ813325	2M0080L02
C 267	7	41.2	25	17	AZ417175	AZ417175	IM0192D13	340	6.8	40.0	24	9	AU588263	AU588263	
C 268	7	41.2	25	17	AZ482946	AZ482946	IM0308K16	341	6.8	40.0	24	9	AU254162	AU254162	
C 269	7	41.2	25	17	AZ845871	AZ845871	2M0145B19	342	6.8	40.0	24	13	BM398765	BM398765	
C 270	7	41.2	25	17	BM850584	BM850584	SAUK_0715	343	6.8	40.0	24	13	BM398765	BM398765	
C 271	7	41.2	25	17	BM857193	BM857193	SAUK_0766	344	6.8	40.0	24	14	D19581	D19581	
C 272	7	41.2	25	17	BM866379	BM866379	SAUK_1012	345	6.8	40.0	24	17	AZ934113	AZ934113	
C 273	7	41.2	25	17	TA152H13Q	TA152H13Q		346	6.8	40.0	24	17	AZ991546	AZ991546	2M0275O13
C 274	6.8	40.0	14	9	AL584023	AL584023		347	6.8	40.0	24	17	TA113F01O	TA113F01O	
C 275	6.8	40.0	15	12	BF219911	BF219911	601296879	348	6.8	40.0	24	17	TA178F08P	TA178F08P	
C 276	6.8	40.0	17	14	BQ605828	BQ605828	BRX_1399	349	6.8	40.0	25	9	AA881443	AA881443	vx19a01.x
C 277	6.8	40.0	18	13	BM397051	BM397051	5009-0-28	350	6.8	40.0	25	9	AA894827	AA894827	cf61e08.8
C 278	6.8	40.0	18	13	BM397051	BM397051	5009-0-28	351	6.8	40.0	25	9	AI081705	AI081705	ow81d01.8
C 279	6.8	40.0	18	13	BM397954	BM397954	5009-0-39	352	6.8	40.0	25	9	AI1339004	AI1339004	
C 280	6.8	40.0	18	13	BM397954	BM397954	5009-0-39	353	6.8	40.0	25	9	AI559609	AI559609	cg58c02.x
C 281	6.8	40.0	18	13	BM399858	BM399858	5009-0-62	354	6.8	40.0	25	9	AI738003	AI738003	w134b01.x
C 282	6.8	40.0	18	13	BM399858	BM399858	5009-0-62	355	6.8	40.0	25	13	BM397307	BM397307	5009-0-30
C 283	6.8	40.0	19	9	A1719958	A1719958	as41d06.x	356	6.8	40.0	25	13	BM400776	BM400776	
C 284	6.8	40.0	19	17	AZ442378	AZ442378	IM0236K18	357	6.8	40.0	25	17	AZ328535	AZ328535	IM0052B21
C 285	6.8	40.0	19	17	AZ634666	AZ634666	IM0490O03	358	6.8	40.0	25	17	AZ588253	AZ588253	IM0396O23
C 286	6.8	40.0	19	17	AZ782308	AZ782308	2M0022B05	359	6.8	40.0	25	17	AZ775040	AZ775040	
C 287	6.8	40.0	19	17	AZ788326	AZ788326	2M0035F16	360	6.8	40.0	25	17	AZ991453	AZ991453	2M0275I11
C 288	6.8	40.0	19	17	AZ798425	AZ798425	2M0055D13	361	6.8	40.0	25	17	BH755405	BH755405	SAUK_0490
C 289	6.8	40.0	19	17	AZ806506	AZ806506	2M0068P03	362	6.8	40.0	25	17	BM851983	BM851983	0738
C 290	6.8	40.0	19	17	AZ824929	AZ824929	2M0099P16	363	6.8	40.0	25	17	TA216C10Q	TA216C10Q	
C 291	6.8	40.0	20	9	AL695159	AL695159		364	6.8	38.8	14	17	BH129645	BH129645	G-5K14.f
C 292	6.8	40.0	20	9	AU256704	AU256704		365	6.8	38.8	17	13	BM396941	BM396941	
C 293	6.8	40.0	20	9	AU257335	AU257335		366	6.8	38.8	18	13	EG929045	EG929045	
C 294	6.8	40.0	20	13	BM397553	BM397553	5009-0-34	367	6.8	38.8	19	9	A1597783	A1597783	cr92g04.x
C 295	6.8	40.0	20	13	BM398892	BM398892	5009-0-50	368	6.8	38.8	19	9	A1624451	A1624451	tz92h01.x
C 296	6.8	40.0	20	13	BM399755	BM399755	5009-0-60	369	6.8	38.8	19	9	A1635491	A1635491	cb65g09.x
C 297	6.8	40.0	20	17	AZ480598	AZ480598	IM0302B17	370	6.8	38.8	19	13	BM397047	BM397047	
C 298	6.8	40.0	20	17	AZ485309	AZ485309	IM0312H11	371	6.8	38.8	19	13	BM401213	BM401213	5009-0-84

C 375	10.2	51.0	21	18	AA780605	Antisense oligonuc	448	10	50.0	13	23	ABC30246	Oligonucleotide SE
C 376	10.2	51.0	21	18	AA780606	Antisense oligonuc	449	10	50.0	13	23	ABC30247	Oligonucleotide SE
C 377	10.2	51.0	21	19	AA226112	Human polymorphic	450	10	50.0	13	23	ABC47702	Oligonucleotide SE
C 378	10.2	51.0	21	19	AAV67343	Nucleotide firegmen	451	10	50.0	13	23	ABC47703	Oligonucleotide SE
C 379	10.2	51.0	21	19	AAV67343	Human endotheial	452	10	50.0	13	23	ABC80672	Oligonucleotide SE
C 380	10.2	51.0	21	20	AAV99727	Human AUR2 inhibit	453	10	50.0	13	23	ABC80673	Oligonucleotide SE
C 381	10.2	51.0	21	20	AAV99727	Human endogenous r	454	10	50.0	13	23	ABC82078	Oligonucleotide SE
C 382	10.2	51.0	21	21	AAV69338	Human ABC1 gene ex	455	10	50.0	13	23	ABC83914	Oligonucleotide SE
C 383	10.2	51.0	21	21	AAZ288915	Human wolfram ex	456	10	50.0	13	23	ABC83915	Oligonucleotide SE
C 384	10.2	51.0	21	21	AAZ288915	PCR primer for cap	457	10	50.0	13	23	ABF04484	Oligonucleotide SE
C 385	10.2	51.0	21	22	AAH2163	Kalixrein B plasm	458	10	50.0	13	23	ABF04485	Oligonucleotide SE
C 386	10.2	51.0	21	22	AAH2163	Polymorphic sequen	459	10	50.0	13	23	ABF17826	Oligonucleotide SE
C 387	10.2	51.0	21	22	AAH2163	T-DNA right border	460	10	50.0	13	23	ABF17827	Oligonucleotide SE
C 388	10.2	51.0	21	22	AAH2163	Human ADF-ribosyl	461	10	50.0	13	23	ABF29756	Oligonucleotide SE
C 389	10.2	51.0	21	22	AAH2163	AAV antisense prim	462	10	50.0	13	23	ABF29757	Oligonucleotide SE
C 390	10.2	51.0	21	24	AAH2163	Human single nucle	463	10	50.0	13	23	ABF30616	Oligonucleotide SE
C 391	10.2	51.0	22	15	AAH2163	Antisense oligonuc	464	10	50.0	13	23	ABF30617	Oligonucleotide SE
C 392	10.2	51.0	22	15	AAH2163	Antisense oligonuc	465	10	50.0	13	23	ABF30617	Oligonucleotide SE
C 393	10.2	51.0	22	16	AAH2163	ICAM antisense oli	466	10	50.0	13	23	ABF40670	Oligonucleotide SE
C 394	10.2	51.0	22	16	AAH2163	Peptide nucleic ac	467	10	50.0	13	23	ABF40671	Oligonucleotide SE
C 395	10.2	51.0	22	16	AAH2163	Peptide nucleic ac	468	10	50.0	13	23	ABF49644	Oligonucleotide SE
C 396	10.2	51.0	22	16	AAH2163	Antisense oligonuc	469	10	50.0	13	23	ABF49645	Oligonucleotide SE
C 397	10.2	51.0	22	18	AAH2163	ICAM inhibiting an	470	10	50.0	13	23	ABF50342	Oligonucleotide SE
C 398	10.2	51.0	22	18	AAH2163	PCR primer hmgp-74	471	10	50.0	13	23	ABF50343	Oligonucleotide SE
C 399	10.2	51.0	22	19	AAH2163	Human ICAM-1, E-se	472	10	50.0	13	23	ABF55570	Oligonucleotide SE
C 400	10.2	51.0	22	20	AAH2163	Human XIS gene fr	473	10	50.0	13	23	ABF55571	Oligonucleotide SE
C 401	10.2	51.0	22	20	AAH2163	Antisense chiol-de	474	10	50.0	13	23	ABF71648	Oligonucleotide SE
C 402	10.2	51.0	22	21	AAH2163	Protein production	475	10	50.0	13	23	ABF71649	Oligonucleotide SE
C 403	10.2	51.0	22	21	AAH2163	Human ICAM-1 antis	476	10	50.0	13	23	ABF81342	Oligonucleotide SE
C 404	10.2	51.0	22	22	AAH2163	Antisense oligo fo	477	10	50.0	13	23	ABH18788	Oligonucleotide SE
C 405	10.2	51.0	22	22	AAH2163	Human GPCR forwar	478	10	50.0	13	23	ABH18789	Oligonucleotide SE
C 406	10.2	51.0	22	24	AAH2163	Chromosomal locus	479	10	50.0	13	23	ABH18789	Oligonucleotide SE
C 407	10.2	51.0	23	18	AAH2163	Primer D8S349 for	480	10	50.0	15	22	AAH81570	Oligonucleotide SE
C 408	10.2	51.0	23	18	AAH2163	Mouse HYPLIP1 locu	481	10	50.0	15	22	AAH98004	Oligonucleotide SE
C 409	10.2	51.0	23	24	AAH2163	Mouse capniz spec	482	10	50.0	17	21	AAH98004	Oligonucleotide SE
C 410	10.2	51.0	23	24	AAH2163	Mouse capniz spec	483	10	50.0	17	21	AAH98004	Oligonucleotide SE
C 411	10.2	51.0	23	24	AAH2163	Helix-turn-helix d	484	10	50.0	17	21	AAH98004	Oligonucleotide SE
C 412	10.2	51.0	24	22	AAH2163	Human shear stress	485	10	50.0	18	20	AAH2163	Oligonucleotide SE
C 413	10.2	51.0	24	22	AAH2163	Oligonucleotide ad	486	10	50.0	18	20	AAH2163	Oligonucleotide SE
C 414	10.2	51.0	24	24	AAH2163	Oligonucleotide ad	487	10	50.0	18	22	AAH39265	Oligonucleotide SE
C 415	10.2	51.0	24	24	AAH2163	Oligonucleotide ad	488	10	50.0	18	22	AAH39265	Oligonucleotide SE
C 416	10.2	51.0	24	24	AAH2163	Oligonucleotide ad	489	10	50.0	18	24	AAH47145	Oligonucleotide SE
C 417	10.2	51.0	24	24	AAH2163	Oligonucleotide ad	490	10	50.0	19	15	AAH47145	Oligonucleotide SE
C 418	10.2	51.0	24	24	AAH2163	Oligonucleotide ad	491	10	50.0	19	15	AAH47145	Oligonucleotide SE
C 419	10.2	51.0	24	24	AAH2163	Oligonucleotide ad	492	10	50.0	19	20	AAH47145	Oligonucleotide SE
C 420	10.2	51.0	24	24	AAH2163	Oligonucleotide ad	493	10	50.0	19	20	AAH47145	Oligonucleotide SE
C 421	10.2	51.0	24	24	AAH2163	Capture oligonucle	494	10	50.0	19	21	AAH47145	Oligonucleotide SE
C 422	10.2	51.0	24	24	AAH2163	Capture oligonucle	495	10	50.0	19	21	AAH47145	Oligonucleotide SE
C 423	10.2	51.0	24	24	AAH2163	Capture oligonucle	496	10	50.0	19	21	AAH47145	Oligonucleotide SE
C 424	10.2	51.0	24	24	AAH2163	Capture oligonucle	497	10	50.0	19	21	AAH47145	Oligonucleotide SE
C 425	10.2	51.0	24	24	AAH2163	Capture oligonucle	498	10	50.0	19	22	AAH47145	Oligonucleotide SE
C 426	10.2	51.0	24	24	AAH2163	Capture oligonucle	499	10	50.0	19	22	AAH47145	Oligonucleotide SE
C 427	10.2	51.0	24	24	AAH2163	Capture oligonucle	500	10	50.0	19	24	AAH47145	Oligonucleotide SE
C 428	10.2	51.0	25	12	AAH2163	Probe RP based on	501	10	50.0	19	24	AAH47145	Oligonucleotide SE
C 429	10.2	51.0	25	12	AAH2163	PCR primer VR109 u	502	10	50.0	20	16	AAH47145	Oligonucleotide SE
C 430	10.2	51.0	25	21	AAH2163	Human growth hormo	503	10	50.0	20	17	AAH47145	Oligonucleotide SE
C 431	10.2	51.0	25	24	AAH2163	Human aquaporin 5	504	10	50.0	20	18	AAH47145	Oligonucleotide SE
C 432	10.2	51.0	25	24	AAH2163	P. patens Na+/H+ a	505	10	50.0	20	19	AAH47145	Oligonucleotide SE
C 433	10.2	51.0	25	24	AAH2163	Oligonucleotide ad	506	10	50.0	20	19	AAH47145	Oligonucleotide SE
C 434	10.2	51.0	25	24	AAH2163	Oligonucleotide ad	507	10	50.0	20	19	AAH47145	Oligonucleotide SE
C 435	10.2	51.0	25	24	AAH2163	Oligonucleotide ad	508	10	50.0	20	20	AAH47145	Oligonucleotide SE
C 436	10.2	51.0	25	24	AAH2163	Oligonucleotide ad	509	10	50.0	20	20	AAH47145	Oligonucleotide SE
C 437	10.2	51.0	25	24	AAH2163	Oligonucleotide ad	510	10	50.0	20	20	AAH47145	Oligonucleotide SE
C 438	10.2	51.0	25	24	AAH2163	Human interleukin	511	10	50.0	20	21	AAH47145	Oligonucleotide SE
C 439	10.2	51.0	25	24	AAH2163	Oligonucleotide pr	512	10	50.0	20	21	AAH47145	Oligonucleotide SE
C 440	10.2	51.0	25	24	AAH2163	Oligonucleotide pr	513	10	50.0	20	21	AAH47145	Oligonucleotide SE
C 441	10.2	51.0	25	24	AAH2163	Oligonucleotide pr	514	10	50.0	20	22	AAH47145	Oligonucleotide SE
C 442	10.2	51.0	25	24	AAH2163	Oligonucleotide pr	515	10	50.0	20	22	AAH47145	Oligonucleotide SE
C 443	10.2	51.0	25	24	AAH2163	Oligonucleotide pr	516	10	50.0	20	22	AAH47145	Oligonucleotide SE
C 444	10.2	51.0	25	24	AAH2163	Oligonucleotide pr	517	10	50.0	20	22	AAH47145	Oligonucleotide SE
C 445	10.2	51.0	25	24	AAH2163	Oligonucleotide SE	518	10	50.0	20	22	AAH47145	Oligonucleotide SE
C 446	10.2	51.0	25	24	AAH2163	Oligonucleotide SE	519	10	50.0	20	22	AAH47145	Oligonucleotide SE
C 447	10.2	51.0	25	24	AAH2163	Oligonucleotide SE	520	10	50.0	20	24	AAH47145	Oligonucleotide SE

C 518	6.4	37.6	20	17	AZ465809	AZ465809	1M0276112	C 591	6.4	37.6	22	17	TA140A04P	AL466405 T. brucei
C 519	6.4	37.6	20	17	AZ466238	AZ466238	1M0276116	C 592	6.4	37.6	22	17	TA272E02Q	AL487827 T. brucei
C 520	6.4	37.6	20	17	AZ466238	AZ466238	1M0407B18	C 593	6.4	37.6	22	17	TA272H06Q	AL491850 T. brucei
C 521	6.4	37.6	20	17	AZ603553	AZ603553	1M0422P21	C 594	6.4	37.6	22	17	TA338G08Q	AL494107 T. brucei
C 522	6.4	37.6	20	17	AZ615402	AZ615402	1M0444A16	C 595	6.4	37.6	22	17	TA346E12P	AL496439 T. brucei
C 523	6.4	37.6	20	17	AZ654725	AZ654725	1M0529003	C 596	6.4	37.6	22	17	TA372G12P	AL496638 T. brucei
C 524	6.4	37.6	20	17	AZ785547	AZ785547	2M0029A05	C 597	6.4	37.6	22	17	TA7H01P	AL452882 T. brucei
C 525	6.4	37.6	20	17	AZ799305	AZ799305	2M0056N05	C 598	6.4	37.6	23	13	AL584237	AL584237
C 526	6.4	37.6	20	17	AZ823352	AZ823352	2M0097A22	C 599	6.4	37.6	23	13	BG926069	BG926069 HNC23-1-E
C 527	6.4	37.6	20	17	AZ853126	AZ853126	2M0156G10	C 600	6.4	37.6	23	17	AZ387861	AZ387861
C 528	6.4	37.6	20	17	AZ860554	AZ860554	2M0166C07	C 601	6.4	37.6	23	17	AZ390689	AZ390689
C 529	6.4	37.6	20	17	AZ959504	AZ959504	2M0227N12	C 602	6.4	37.6	23	17	AZ439449	AZ439449
C 530	6.4	37.6	20	17	AZ972315	AZ972315	2M0246E09	C 603	6.4	37.6	23	17	AZ451117	AZ451117
C 531	6.4	37.6	21	9	AL585450	AL585450	AL585450	C 604	6.4	37.6	23	17	AZ470337	AZ470337
C 532	6.4	37.6	21	13	BM398406	BM398406	5009-0-45	C 605	6.4	37.6	23	17	AZ488138	AZ488138
C 533	6.4	37.6	21	14	BM121116	BM121116	EST606692	C 606	6.4	37.6	23	17	AZ514463	AZ514463
C 534	6.4	37.6	21	14	D20000	D20000	HUMGS00970	C 607	6.4	37.6	23	17	AZ514463	AZ514463
C 535	6.4	37.6	21	14	D20000	D20000	HUMGS00970	C 608	6.4	37.6	23	17	AZ561440	AZ561440
C 536	6.4	37.6	21	17	AZ307929	AZ307929	1M0010F24	C 609	6.4	37.6	23	17	AZ753387	AZ753387
C 537	6.4	37.6	21	17	AZ309732	AZ309732	1M0016K01	C 610	6.4	37.6	23	17	AZ780690	AZ780690
C 538	6.4	37.6	21	17	AZ320773	AZ320773	1M0041C24	C 611	6.4	37.6	23	17	AZ785466	AZ785466
C 539	6.4	37.6	21	17	AZ345955	AZ345955	1M0080P19	C 612	6.4	37.6	23	17	AZ818239	AZ818239
C 540	6.4	37.6	21	17	AZ467734	AZ467734	1M0279N18	C 613	6.4	37.6	23	17	AZ823567	AZ823567
C 541	6.4	37.6	21	17	AZ479997	AZ479997	1M0301G11	C 614	6.4	37.6	23	17	AZ849056	AZ849056
C 542	6.4	37.6	21	17	AZ482019	AZ482019	1M0306I17	C 615	6.4	37.6	23	17	BH790005	BH790005
C 543	6.4	37.6	21	17	AZ492310	AZ492310	1M0326D21	C 616	6.4	37.6	23	17	TA123G12Q	TA123G12Q
C 544	6.4	37.6	21	17	AZ503574	AZ503574	1M0343H19	C 617	6.4	37.6	23	17	TA158A06Q	TA158A06Q
C 545	6.4	37.6	21	17	AZ584607	AZ584607	1M0389E15	C 618	6.4	37.6	23	17	TA15C04Q	TA15C04Q
C 546	6.4	37.6	21	17	AZ598137	AZ598137	1M0412P16	C 619	6.4	37.6	23	17	TA162A12P	TA162A12P
C 547	6.4	37.6	21	17	AZ625565	AZ625565	1M0456H10	C 620	6.4	37.6	23	17	TA242D06P	TA242D06P
C 548	6.4	37.6	21	17	AZ654965	AZ654965	1M0529E11	C 621	6.4	37.6	23	17	TA296F01P	TA296F01P
C 549	6.4	37.6	21	17	AZ665199	AZ665199	1M0546E01	C 622	6.4	37.6	23	17	TA327G08Q	TA327G08Q
C 550	6.4	37.6	21	17	AZ765362	AZ765362	1M0562I14	C 623	6.4	37.6	23	17	TA363D03Q	TA363D03Q
C 551	6.4	37.6	21	17	AZ774524	AZ774524	2M004M011	C 624	6.4	37.6	24	9	AL588263	AL588263
C 552	6.4	37.6	21	17	AZ785791	AZ785791	1M0030019	C 625	6.4	37.6	24	13	BM397860	BM397860
C 553	6.4	37.6	21	17	AZ796205	AZ796205	2M0051013	C 626	6.4	37.6	24	13	BM401141	BM401141
C 554	6.4	37.6	21	17	AZ819369	AZ819369	2M0089021	C 627	6.4	37.6	24	13	BM401311	BM401311
C 555	6.4	37.6	21	17	AZ819992	AZ819992	2M0091M21	C 628	6.4	37.6	24	13	BM401729	BM401729
C 556	6.4	37.6	21	17	AZ834089	AZ834089	2M011C112	C 629	6.4	37.6	24	17	AZ307620	AZ307620
C 557	6.4	37.6	21	17	AZ862607	AZ862607	2M0170C23	C 630	6.4	37.6	24	17	AZ310221	AZ310221
C 558	6.4	37.6	21	17	AZ990424	AZ990424	2M0274F09	C 631	6.4	37.6	24	17	AZ339707	AZ339707
C 559	6.4	37.6	21	17	TA62F03Q	TA62F03Q	TA62F03Q	C 632	6.4	37.6	24	17	AZ341704	AZ341704
C 560	6.4	37.6	21	17	TA62F01P	TA62F01P	TA62F01P	C 633	6.4	37.6	24	17	AZ409513	AZ409513
C 561	6.4	37.6	22	9	AA868842	AA868842	AA868842	C 634	6.4	37.6	24	17	AZ464550	AZ464550
C 562	6.4	37.6	22	9	AA885905	AA885905	AA885905	C 635	6.4	37.6	24	17	AZ492651	AZ492651
C 563	6.4	37.6	22	9	AA911600	AA911600	AA911600	C 636	6.4	37.6	24	17	AZ587584	AZ587584
C 564	6.4	37.6	22	9	AA912871	AA912871	AA912871	C 637	6.4	37.6	24	17	AZ595616	AZ595616
C 565	6.4	37.6	22	9	AA923820	AA923820	AA923820	C 638	6.4	37.6	24	17	AZ601725	AZ601725
C 566	6.4	37.6	22	9	AA108045	AA108045	AA108045	C 639	6.4	37.6	24	17	AZ608837	AZ608837
C 567	6.4	37.6	22	9	AA112064	AA112064	AA112064	C 640	6.4	37.6	24	17	AZ663178	AZ663178
C 568	6.4	37.6	22	9	AA1158879	AA1158879	AA1158879	C 641	6.4	37.6	24	17	AZ682814	AZ682814
C 569	6.4	37.6	22	9	AA1256837	AA1256837	AA1256837	C 642	6.4	37.6	24	17	AZ682814	AZ682814
C 570	6.4	37.6	22	9	AA1267916	AA1267916	AA1267916	C 643	6.4	37.6	24	17	AZ682814	AZ682814
C 571	6.4	37.6	22	9	AA1723177	AA1723177	AA1723177	C 644	6.4	37.6	24	17	AZ682814	AZ682814
C 572	6.4	37.6	22	9	AU256604	AU256604	AU256604	C 645	6.4	37.6	24	17	AZ682814	AZ682814
C 573	6.4	37.6	22	13	BG926061	BG926061	BG926061	C 646	6.4	37.6	24	17	AZ682814	AZ682814
C 574	6.4	37.6	22	13	BM395019	BM395019	50072-2-7	C 647	6.4	37.6	24	17	AZ682814	AZ682814
C 575	6.4	37.6	22	13	BM400797	BM400797	5009-0-79	C 648	6.4	37.6	24	17	AZ682814	AZ682814
C 576	6.4	37.6	22	13	AZ309879	AZ309879	1M0017D13	C 649	6.4	37.6	24	17	AZ682814	AZ682814
C 577	6.4	37.6	22	17	AZ311479	AZ311479	1M0026M24	C 650	6.4	37.6	24	17	AZ682814	AZ682814
C 578	6.4	37.6	22	17	AZ326642	AZ326642	1M0049D09	C 651	6.4	37.6	24	17	AZ682814	AZ682814
C 579	6.4	37.6	22	17	AZ341858	AZ341858	1M0074D03	C 652	6.4	37.6	24	17	AZ682814	AZ682814
C 580	6.4	37.6	22	17	AZ380277	AZ380277	1M0316D07	C 653	6.4	37.6	24	17	AZ682814	AZ682814
C 581	6.4	37.6	22	17	AZ480841	AZ480841	1M0302A19	C 654	6.4	37.6	24	17	AZ682814	AZ682814
C 582	6.4	37.6	22	17	AZ486653	AZ486653	1M0314I14	C 655	6.4	37.6	24	17	AZ682814	AZ682814
C 583	6.4	37.6	22	17	AZ493044	AZ493044	1M0460F21	C 656	6.4	37.6	24	17	AZ682814	AZ682814
C 584	6.4	37.6	22	17	AZ623308	AZ623308	1M0461F07	C 657	6.4	37.6	24	17	AZ682814	AZ682814
C 585	6.4	37.6	22	17	AZ623422	AZ623422	1M0461F07	C 658	6.4	37.6	24	17	AZ682814	AZ682814
C 586	6.4	37.6	22	17	AZ806109	AZ806109	2M0067O20	C 659	6.4	37.6	24	17	AZ682814	AZ682814
C 587	6.4	37.6	22	17	AZ829430	AZ829430	2M0107A09	C 660	6.4	37.6	24	17	AZ682814	AZ682814
C 588	6.4	37.6	22	17	AZ836104	AZ836104	2M0130C17	C 661	6.4	37.6	24	17	AZ682814	AZ682814
C 589	6.4	37.6	22	17	AZ958287	AZ958287	2M0255G02	C 662	6.4	37.6	24	17	AZ682814	AZ682814
C 590	6.4	37.6	22	17	TA110B07P	TA110B07P	TA110B07P	C 663	6.4	37.6	25	9	AL464946 T. brucei	AL464946 T. brucei

C 667	9.8	49.0	20	24	ABN95191	C. glutamicum air	C 740	9.8	49.0	24	21	AAA99024	H. influenzae adhe
C 668	9.8	49.0	20	24	ABK41160	Human obesity-asso	C 741	9.8	49.0	24	21	AAAD01305	Primer EC280W-R to
C 669	9.8	49.0	20	24	AB192994	Capture oligonucle	C 742	9.8	49.0	24	21	AAZ29056	PCR primer 3 for R
C 670	9.8	49.0	20	24	AB193983	Capture oligonucle	C 743	9.8	49.0	24	21	AAH22236	Anti-A33 antigen a
C 671	9.8	49.0	20	24	AB194202	Capture oligonucle	C 744	9.8	49.0	24	22	AAH20101	Chimeric antibody
C 672	9.8	49.0	20	24	AB194281	Capture oligonucle	C 745	9.8	49.0	24	22	AAH39806	SNP specific lower
C 673	9.8	49.0	20	24	AB194393	Capture oligonucle	C 746	9.8	49.0	24	22	AAH76329	Human C2-4-4 micro
C 674	9.8	49.0	20	24	AB194404	Capture oligonucle	C 747	9.8	49.0	24	22	AAH44578	Mouse DSS-induced
C 675	9.8	49.0	20	24	AB196297	Capture oligonucle	C 748	9.8	49.0	24	22	ABT03725	Human Olf-1-homol g
C 676	9.8	49.0	21	13	AAQ95063	3' - 5' DNA sequen	C 749	9.8	49.0	24	24	ABL54194	Streptococcus pneu
C 677	9.8	49.0	21	13	AAQ28665	ORL ANTISENSE I p	C 750	9.8	49.0	24	24	ABK66864	Escherichia canis p2
C 678	9.8	49.0	21	14	AAQ38853	Sequence of primer	C 751	9.8	49.0	24	24	ABK00059	Oligonucleotide ad
C 679	9.8	49.0	21	14	AAQ50104	PCR primer used in	C 752	9.8	49.0	24	24	ABQ000310	Oligonucleotide ad
C 680	9.8	49.0	21	16	AAQ11981	CMV antisense oligo	C 753	9.8	49.0	24	24	ABQ000324	Oligonucleotide ad
C 681	9.8	49.0	21	16	AAQ09528	Simple tandem repe	C 754	9.8	49.0	24	24	ABQ01080	Oligonucleotide ad
C 682	9.8	49.0	21	16	AAQ090024	PCR primer SK 69 d	C 755	9.8	49.0	24	24	ABQ004094	Oligonucleotide ad
C 683	9.8	49.0	21	17	AAQ19822	Antisense oligo RA	C 756	9.8	49.0	24	24	ABQ004135	Oligonucleotide ad
C 684	9.8	49.0	21	17	AAQ19822	Primer SK69 for HI	C 757	9.8	49.0	24	24	ABQ004587	Oligonucleotide ad
C 685	9.8	49.0	21	19	AAZ26484	Human polymorphic	C 758	9.8	49.0	24	24	ABQ004600	Oligonucleotide ad
C 686	9.8	49.0	21	19	AAZ26484	Human polymorphic	C 759	9.8	49.0	24	24	ABQ004628	Oligonucleotide ad
C 687	9.8	49.0	21	19	AAZ26484	Anti-CMV oligonucle	C 760	9.8	49.0	24	24	ABQ004641	Oligonucleotide ad
C 688	9.8	49.0	21	19	AAZ26484	Human biallelic po	C 761	9.8	49.0	24	24	ABQ006122	Oligonucleotide ad
C 689	9.8	49.0	21	19	AAZ26484	PCR primer 11LF-1	C 762	9.8	49.0	24	24	ABQ006163	Oligonucleotide ad
C 690	9.8	49.0	21	19	AAZ26484	Human BRCA1 exon 1	C 763	9.8	49.0	24	24	ABQ10422	Oligonucleotide ad
C 691	9.8	49.0	21	19	AAZ26484	Human BRCA1 PCR pr	C 764	9.8	49.0	24	24	ABQ10422	Oligonucleotide ad
C 692	9.8	49.0	21	19	AAZ26484	SK69 primer for am	C 765	9.8	49.0	24	24	ABQ10915	Oligonucleotide ad
C 693	9.8	49.0	21	20	AAZ23105	HIV-1 gp41 env gen	C 766	9.8	49.0	24	24	ABQ10928	Oligonucleotide ad
C 694	9.8	49.0	21	20	AAZ23105	Human cancer antiq	C 767	9.8	49.0	24	24	ABQ10966	Oligonucleotide ad
C 695	9.8	49.0	21	20	AAZ23105	BRCA1 gene specif	C 768	9.8	49.0	24	24	ABL55137	Oligonucleotide ad
C 696	9.8	49.0	21	20	AAZ23105	Fehos exon 2 ampl	C 769	9.8	49.0	24	24	ABL55137	Oligonucleotide ad
C 697	9.8	49.0	21	21	AAZ272451	Human biallelic ma	C 770	9.8	49.0	24	24	ABL55137	Random DNA arrange
C 698	9.8	49.0	21	21	AAZ272451	Human biallelic ma	C 771	9.8	49.0	24	24	ABL55137	Human ubiquitin C-
C 699	9.8	49.0	21	21	AAZ272451	Sequence surroundi	C 772	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 700	9.8	49.0	21	21	AAZ272451	Primer Ubi3-3 used	C 773	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 701	9.8	49.0	21	21	AAZ272451	A. gossypii ribofl	C 774	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 702	9.8	49.0	21	21	AAZ272451	SSP1 cDNA amplif	C 775	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 703	9.8	49.0	21	21	AAZ272451	Human BTD gene ass	C 776	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 704	9.8	49.0	21	22	AAH48927	Human BTD gene ass	C 777	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 705	9.8	49.0	21	22	AAH48927	Human BTD gene ass	C 778	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 706	9.8	49.0	21	22	AAH23154	Nitric oxide synth	C 779	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 707	9.8	49.0	21	22	AAH23154	Arginine kinase an	C 780	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 708	9.8	49.0	21	22	AAH23154	Maize mRNAs DNA amp	C 781	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 709	9.8	49.0	21	22	AAH23154	Primer derived f	C 782	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 710	9.8	49.0	21	22	AAH23154	Human ecdys gene p	C 783	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 711	9.8	49.0	21	24	ABLA94921	Maturation/activat	C 784	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 712	9.8	49.0	21	24	ABLA94921	Human chromosome 2	C 785	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 713	9.8	49.0	21	24	ABLA94921	Human PGE-2/NF-3 p	C 786	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 714	9.8	49.0	21	24	ABLA94921	Human short inters	C 787	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 715	9.8	49.0	21	24	ABLA94921	Helicobacter 16S r	C 788	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 716	9.8	49.0	21	24	ABLA94921	Reverse PCR primer	C 789	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 717	9.8	49.0	21	24	ABLA94921	PCR primer for pro	C 790	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 718	9.8	49.0	21	24	ABLA94921	Probe for human po	C 791	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 719	9.8	49.0	21	24	ABLA94921	Tail primer #247 f	C 792	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 720	9.8	49.0	21	24	ABLA94921	Human ABCD1 gene r	C 793	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 721	9.8	49.0	21	24	ABLA94921	Human androgen rec	C 794	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 722	9.8	49.0	21	24	ABLA94921	Ras gene PCR prime	C 795	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 723	9.8	49.0	21	24	ABLA94921	Human ATP-binding	C 796	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 724	9.8	49.0	21	24	ABLA94921	Lactococcus lactis	C 797	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 725	9.8	49.0	21	24	ABLA94921	Degenerate probe f	C 798	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 726	9.8	49.0	21	24	ABLA94921	Mimp18 reverse p	C 799	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 727	9.8	49.0	21	24	ABLA94921	Elongation factor	C 800	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 728	9.8	49.0	21	24	ABLA94921	Sequence of primer	C 801	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 729	9.8	49.0	21	24	ABLA94921	PTEN/MAK1 exon 6	C 802	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 730	9.8	49.0	21	24	ABLA94921	PTEN/MAK1 exon 6	C 803	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 731	9.8	49.0	21	24	ABLA94921	Primer #16 used in	C 804	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 732	9.8	49.0	21	24	ABLA94921	Lactococcus lactis	C 805	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 733	9.8	49.0	21	24	ABLA94921	Non-coding strand	C 806	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 734	9.8	49.0	21	24	ABLA94921	SK69 primer. Synt	C 807	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 735	9.8	49.0	21	24	ABLA94921	sk69-galactosid ch	C 808	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 736	9.8	49.0	21	24	ABLA94921	Oligonucleotide ch	C 809	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 737	9.8	49.0	21	24	ABLA94921	HIV-1 PCR primer b	C 810	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 738	9.8	49.0	21	24	ABLA94921	Oligonucleotide pr	C 811	9.8	49.0	24	24	ABL55137	Capture oligonucle
C 739	9.8	49.0	21	24	ABLA94921	Oligonucleotide pr	C 812	9.8	49.0	24	24	ABL55137	Capture oligonucle

C 810	6.2	36.5	23	9	AU014520	AU014520	883	6.2	36.5	25	17	AZ377071
C 811	6.2	36.5	23	9	AU256868	AU256868	C 884	6.2	36.5	25	17	AZ462642
C 812	6.2	36.5	23	9	AU258717	AU258717	C 885	6.2	36.5	25	17	AZ765933
C 813	6.2	36.5	23	10	AM063953	AM063953	C 886	6.2	36.5	25	17	AZ765933
C 814	6.2	36.5	23	13	BM395635	BM395635	C 887	6.2	36.5	25	17	AZ861588
C 815	6.2	36.5	23	13	BM396297	BM396297	C 888	6.2	36.5	25	17	AZ937578
C 816	6.2	36.5	23	13	BM397693	BM397693	C 889	6.2	36.5	25	17	BH840643
C 817	6.2	36.5	23	13	BM398156	BM398156	C 890	6.2	36.5	25	17	TA114E04P
C 818	6.2	36.5	23	13	BM398329	BM398329	C 891	6.2	36.5	25	17	TA131D07P
C 819	6.2	36.5	23	13	BM399677	BM399677	C 892	6.2	36.5	25	17	TA330H09Q
C 820	6.2	36.5	23	13	BM400878	BM400878	C 893	6.2	36.5	25	17	BH170808
C 821	6.2	36.5	23	13	L32041	L32041	C 894	6.2	36.5	25	17	BM396889
C 822	6.2	36.5	23	14	AZ309461	AZ309461	C 895	6.2	36.5	25	17	BM401092
C 823	6.2	36.5	23	17	AZ351113	AZ351113	C 896	6.2	36.5	25	17	BM397906
C 824	6.2	36.5	23	17	AZ345458	AZ345458	C 897	6.2	36.5	25	17	BM401274
C 825	6.2	36.5	23	17	AZ595375	AZ595375	C 898	6.2	36.5	25	17	BM397800
C 826	6.2	36.5	23	17	AZ763749	AZ763749	C 899	6.2	36.5	25	17	BM398488
C 827	6.2	36.5	23	17	AZ769365	AZ769365	C 900	6.2	36.5	25	17	BM399416
C 828	6.2	36.5	23	17	AZ819914	AZ819914	C 901	6.2	36.5	25	17	BM399640
C 829	6.2	36.5	23	17	AZ833328	AZ833328	C 902	6.2	36.5	25	17	BM400473
C 830	6.2	36.5	23	17	AZ833407	AZ833407	C 903	6.2	36.5	25	17	BM400473
C 831	6.2	36.5	23	17	AZ833407	AZ833407	C 904	6.2	36.5	25	17	BM400473
C 832	6.2	36.5	23	17	AZ833407	AZ833407	C 905	6.2	36.5	25	17	BM400473
C 833	6.2	36.5	23	17	AZ833407	AZ833407	C 906	6.2	36.5	25	17	BM400473
C 834	6.2	36.5	23	17	AZ833407	AZ833407	C 907	6.2	36.5	25	17	BM400473
C 835	6.2	36.5	23	17	AZ833407	AZ833407	C 908	6.2	36.5	25	17	BM400473
C 836	6.2	36.5	23	17	AZ833407	AZ833407	C 909	6.2	36.5	25	17	BM400473
C 837	6.2	36.5	23	17	AZ833407	AZ833407	C 910	6.2	36.5	25	17	BM400473
C 838	6.2	36.5	23	17	AZ833407	AZ833407	C 911	6.2	36.5	25	17	BM400473
C 839	6.2	36.5	23	17	AZ833407	AZ833407	C 912	6.2	36.5	25	17	BM400473
C 840	6.2	36.5	23	17	AZ833407	AZ833407	C 913	6.2	36.5	25	17	BM400473
C 841	6.2	36.5	23	17	AZ833407	AZ833407	C 914	6.2	36.5	25	17	BM400473
C 842	6.2	36.5	23	17	AZ833407	AZ833407	C 915	6.2	36.5	25	17	BM400473
C 843	6.2	36.5	23	17	AZ833407	AZ833407	C 916	6.2	36.5	25	17	BM400473
C 844	6.2	36.5	23	17	AZ833407	AZ833407	C 917	6.2	36.5	25	17	BM400473
C 845	6.2	36.5	23	17	AZ833407	AZ833407	C 918	6.2	36.5	25	17	BM400473
C 846	6.2	36.5	23	17	AZ833407	AZ833407	C 919	6.2	36.5	25	17	BM400473
C 847	6.2	36.5	23	17	AZ833407	AZ833407	C 920	6.2	36.5	25	17	BM400473
C 848	6.2	36.5	23	17	AZ833407	AZ833407	C 921	6.2	36.5	25	17	BM400473
C 849	6.2	36.5	23	17	AZ833407	AZ833407	C 922	6.2	36.5	25	17	BM400473
C 850	6.2	36.5	23	17	AZ833407	AZ833407	C 923	6.2	36.5	25	17	BM400473
C 851	6.2	36.5	23	17	AZ833407	AZ833407	C 924	6.2	36.5	25	17	BM400473
C 852	6.2	36.5	23	17	AZ833407	AZ833407	C 925	6.2	36.5	25	17	BM400473
C 853	6.2	36.5	23	17	AZ833407	AZ833407	C 926	6.2	36.5	25	17	BM400473
C 854	6.2	36.5	23	17	AZ833407	AZ833407	C 927	6.2	36.5	25	17	BM400473
C 855	6.2	36.5	23	17	AZ833407	AZ833407	C 928	6.2	36.5	25	17	BM400473
C 856	6.2	36.5	23	17	AZ833407	AZ833407	C 929	6.2	36.5	25	17	BM400473
C 857	6.2	36.5	23	17	AZ833407	AZ833407	C 930	6.2	36.5	25	17	BM400473
C 858	6.2	36.5	23	17	AZ833407	AZ833407	C 931	6.2	36.5	25	17	BM400473
C 859	6.2	36.5	23	17	AZ833407	AZ833407	C 932	6.2	36.5	25	17	BM400473
C 860	6.2	36.5	23	17	AZ833407	AZ833407	C 933	6.2	36.5	25	17	BM400473
C 861	6.2	36.5	23	17	AZ833407	AZ833407	C 934	6.2	36.5	25	17	BM400473
C 862	6.2	36.5	23	17	AZ833407	AZ833407	C 935	6.2	36.5	25	17	BM400473
C 863	6.2	36.5	23	17	AZ833407	AZ833407	C 936	6.2	36.5	25	17	BM400473
C 864	6.2	36.5	23	17	AZ833407	AZ833407	C 937	6.2	36.5	25	17	BM400473
C 865	6.2	36.5	23	17	AZ833407	AZ833407	C 938	6.2	36.5	25	17	BM400473
C 866	6.2	36.5	23	17	AZ833407	AZ833407	C 939	6.2	36.5	25	17	BM400473
C 867	6.2	36.5	23	17	AZ833407	AZ833407	C 940	6.2	36.5	25	17	BM400473
C 868	6.2	36.5	23	17	AZ833407	AZ833407	C 941	6.2	36.5	25	17	BM400473
C 869	6.2	36.5	23	17	AZ833407	AZ833407	C 942	6.2	36.5	25	17	BM400473
C 870	6.2	36.5	23	17	AZ833407	AZ833407	C 943	6.2	36.5	25	17	BM400473
C 871	6.2	36.5	23	17	AZ833407	AZ833407	C 944	6.2	36.5	25	17	BM400473
C 872	6.2	36.5	23	17	AZ833407	AZ833407	C 945	6.2	36.5	25	17	BM400473
C 873	6.2	36.5	23	17	AZ833407	AZ833407	C 946	6.2	36.5	25	17	BM400473
C 874	6.2	36.5	23	17	AZ833407	AZ833407	C 947	6.2	36.5	25	17	BM400473
C 875	6.2	36.5	23	17	AZ833407	AZ833407	C 948	6.2	36.5	25	17	BM400473
C 876	6.2	36.5	23	17	AZ833407	AZ833407	C 949	6.2	36.5	25	17	BM400473
C 877	6.2	36.5	23	17	AZ833407	AZ833407	C 950	6.2	36.5	25	17	BM400473
C 878	6.2	36.5	23	17	AZ833407	AZ833407	C 951	6.2	36.5	25	17	BM400473
C 879	6.2	36.5	23	17	AZ833407	AZ833407	C 952	6.2	36.5	25	17	BM400473
C 880	6.2	36.5	23	17	AZ833407	AZ833407	C 953	6.2	36.5	25	17	BM400473
C 881	6.2	36.5	23	17	AZ833407	AZ833407	C 954	6.2	36.5	25	17	BM400473
C 882	6.2	36.5	23	17	AZ833407	AZ833407	C 955	6.2	36.5	25	17	BM400473

[illegible]

ALIGNMENTS

XX	RESULT 1
XX	ABN99615
ID	ABN99615 standard; DNA; 25 BP.
XX	
AC	ABN99615;
XX	
DT	05-AUG-2002 (first entry)
XX	
DE	Fungi PCR primer SEQ ID NO 187.
XX	
KM	Fungus; bacteria; quantification; detection; infection; gastroenteritis;
XX	ulcer; asthma; allergy; sinusitis; PCR; primer; ss.
OS	Stachybotrys chartarum.
XX	
PN	US6387652-B1.
XX	
PD	14-MAY-2002.
XX	
PP	13-JUN-2000; 2000US-0593012.
XX	
PR	15-APR-1998; 98US-081773P.
XX	
PR	14-APR-1999; 99US-0250990.
XX	
PA	(USSI) US ENVIRONMENTAL PROTECTION AGENCY.
XX	

PI Haugland R., Vesper S;
xx
xx
XX WPI: 2002-462353/49.
DR
PT
PT
PT Detection and quantification of specific fungi or bacteria useful e.g.
in medical diagnosis and treatment of fungal and bacterial conditions,
by hybridizing and amplifying DNA using sequences unique to the species
or group of species -
PT
PS
PS Claim 62; Column 97; 55pp; English.
xx
xx
CC The invention relates to specific fungi or bacteria detected and
CC quantified in a sample by extracting and recovering DNA from the organism
CC in the sample and hybridising and amplifying the DNA sequence using
CC sequences unique to the species/group of species but common to all
CC isolates of the species/group of species. The method especially employs
CC sequences selected from 225 fungal and bacterial primer and probe
CC sequences (ABN93429-ABN9653) for detection of specified fungi/fungal
CC groups or specified bacteria. The method enables detection and
CC quantification of specific fungi or bacteria, or groups of
CC fungal/bacterial species, useful medically for diagnosis and treatment of
CC fungi or bacteria associated with health problems such as infections,
CC gastroenteritis, ulcers, asthma, allergies and sinusitis. It is also
CC useful to detect and/or quantify microorganisms in the environment e.g.
CC to establish the risk of adverse health effects (e.g. pulmonary
CC haemorrhage from levels of Stachybotrys chartarum in air samples in
CC houses).
Sequence 25 BP; 9 A; 5 C; 5 G; 6 T; 0 other;

Query Match	75.0%	Score 15	DB 24	Length 25
Best Local Similarity	100.0%	Pred. No. 2.9e+02		
Matches	15	Conservative	0	Mismatches 0
				Indels 0
				Gaps 0
Qy	6	GTTCGCACCTCAGAG	20	
Db	1	GTTCGCACCTCAGAG	15	

RESULT 2
 ID ABRK29212
 AC ABRK29212;
 DT 23-APR-2002 (first entry)
 DE Stachybotrys chartarum reverse PCR primer.
 KW Fungal detection; bacterial detection; probe; primer; ss.
 OS Stachybotrys chartarum.
 PN W0200196612-A2.
 PD 20-DEC-2001.
 PF 13-JUN-2001; 2001MO-US18892.
 PR 13-JUN-2000; 2000US-0593012.
 PA (USSI) US ENVIRONMENTAL PROTECTION AGENCY.
 PI Haugland R, Vesper SJ;
 DR WPI, 2002-098078/13.
 PT Detecting and quantifying fungi and bacteria, involves obtaining a
 PT sequence of the fungus, extracting the DNA from the sample, and
 PT subjecting the DNA to polymerase chain reaction and fluorescent probe
 analysis -
 XS Claim 62; Page 20; 110pp; English.

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCTTCGGCGGA 15
12 GCTTCGGCGGA 23

Db 12 GCTTCGGCGGA 23

RESULT 3
AZ307451/c 21 bp DNA linear GSS 29-SEP-2000

LOCUS AZ307451.1
DEFINITION 1M009509F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION UUGC1M0009509 F, DNA sequence.
VERSION AZ307451
KEYWORDS AZ307451.1 GI:10346464
SOURCE GSS.
ORGANISM house mouse.
MUS musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
CONTACT: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0009 row: E column: 09
Seq primer: CGTTGTAAACGACGCGCACT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1. 21
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0009509"
/clone_1ib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
/note="Vector: PMD42uv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF1207.1), a copy-number
inducible derivative of plasmid RI. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 5 a 8 c 6 g 2 t

ORIGIN

Query Match 58.8%; Score 10; DB 17; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCTTCGGCGG 13
12 GCTTCGGCGG 3

Db 12 GCTTCGGCGG 3

RESULT 4
A1421881/c 25 bp mRNA linear EST 30-MAR-1999

LOCUS A1421881.1
DEFINITION U55H03.X1 NCI CGAP Brn23 Homo sapiens cDNA IMAGE:2103221 3'
similar to TR:P93237 P93237 PROLINE-RICH PROTEIN PRP2 PRECURSOR.,
mRNA sequence.
ACCESSION A1421881
KEYWORDS A1421881.1 GI:4267812
SOURCE EST.
ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 25)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTCAP), Tumor Gene Index
Unpublished (1998)
CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILMW at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 764 Std Error: 0.00
Seq primer: -40UP from Glbco
High quality sequence stop: 1.
Location/Qualifiers
1. 25
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2103221"
/clone_1ib="NCI CGAP Brn23"
/tissue_type="Glioblastoma (pooled)"
/lab_host="DH10B"
/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer (5'
TGTTACCAATCTGAAGTGGAGCGCGCCGACATCTTTTCTTTTCTTTT
T 3'); double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M. Fatima Bonaldo."

BASE COUNT 8 a 13 c 3 g 1 t

ORIGIN

Query Match 57.6%; Score 9.8; DB 9; Length 25;
Best Local Similarity 84.6%; Pred. No. 4.9e+05;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGCTTCGGCGG 14
16 TTGCTTCGGCGG 4

Db 16 TTGCTTCGGCGG 4

RESULT 5
TNA16120

CC diagnosis, prevention and treatment of conditions associated with Nck-2
CC expression, such as leukaemia and breast cancer.
XX
SQ Sequence 20 BP; 7 A; 4 C; 7 G; 2 T; 0 other;
Query Match 69.0%; Score 13.8; DB 22; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
DY 1 TTGCGTTGCCACTCA 17
Db 19 TCTCGTTGCCACTCA 3
RESULT 5
AAZ59948
ID AAZ59948 standard; DNA; 21 BP.
XX
AC AAZ59948;
XX
XX 08-MAY-2000 (first entry)
DT
DE Human delta-like protein (DLK) PCR primer, SEQ ID NO:6.
XX
XX Drug exposure; drug abuse; gene expression; EST;
XX expressed sequence tag; identification; tolerance; addiction; therapy;
XX screening; cellular response; ethanol; expression analysis;
XX Northern blot; delta-like protein; DLK; reverse transcriptase-PCR;
XX RT-PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO9967267-A1.
XX
XX 29-DEC-1999.
XX PD
XX 22-JUN-1999; 99WO-US13639.
XX PE
XX 22-JUN-1998; 98US-0090268.
XX PR 21-JUN-1999; 99US-0337022.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Miles MF, Lai C, Lockhart DJ;
XX
XX MPI, 2000-147195/13.
XX
XX Novel methods for evaluating an organism's response to alcohol used to
XX evaluate drug treatment and identifying susceptibility to alcohol -
XX
XX Example 3; Page 69; 98pp; English.
XX
XX The invention relates the identification of genes whose expression
XX levels are altered by chronic exposure to one or more drugs of abuse
XX (e.g., ethanol, stimulants, opiates). The methods of the invention
XX monitor the response of a cell to a drug of abuse, and comprise
XX contacting the cell with the drug of abuse, and detecting the expression
XX of one or more of 218 expressed sequence tags (ESTs) via the use of
XX probes that specifically hybridize to the ESTs. The methods are used to
XX identify genes whose expression levels are altered by chronic or acute
XX exposure to one or more drugs of abuse. The identification of genes
XX whose regulation is altered in alcohol tolerance and/or addiction
XX provides a valuable tool to evaluate the response to one or more drugs of
XX abuse. Evaluation of the nature of this response provides information
XX useful in designing therapeutic and recovery regimens, and in evaluating
XX the susceptibility of an organism or patient to drugs in a medical
XX context. Monitoring the expression of identified genes and/or ESTs
XX provides a mechanism by which test agents can be screened for the ability
XX to alter or modulate the response of the organism to drugs of abuse.
XX Sequences AAZ59944-259951 represent reverse transcriptase-PCR (RT-PCR)
XX primers used to amplify 4 cDNA hybridisation probes from SH-SY5Y-A41861
XX human neuroblastoma cell total RNA. The probes were used in Northern
XX blot analysis of gene expression in control and ethanol-treated

CC SH-SY5Y-A41861 cells in an exemplification of the present invention. The
CC genes whose expression was analysed were dopamine beta-hydroxylase (DBH)
CC and sodium-dependent norepinephrine transporter (NET), both of which are
CC involved in norepinephrine metabolism; delta-like protein (DLK), and
CC monocyte chemoattractant peptide 1 (MCP-1). These genes are thought to
CC be important targets of ethanol. Primers AAZ59948-259949 were used to
CC generate the delta-like protein (DLK) probe.
XX
SQ Sequence 21 BP; 4 A; 6 C; 5 G; 6 T; 0 other;
Query Match 69.0%; Score 13.8; DB 21; Length 21;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
DY 2 TTGCGTTGCCACTCAG 18
Db 4 TTGCGTTGCCACTCAG 20
RESULT 6
AAO50799/C
ID AAO50799 standard; RNA; 17 BP.
XX
AC AAO50799;
XX
XX 26-MAY-1994 (first entry)
DT
DE HBV target sequence 25.
XX
XX RNA; enzyme; enzymatic RNA molecule; ERN; cleave; RNA; mRNA; HNRNA;
XX picornavirus; HIV; immunodeficiency virus; hepatitis B virus; HBV;
XX papilloma virus; HPV; Epstein-Barr virus; EBV; TGLV;
XX T-cell leukaemia virus; hepatitis C virus; HCV; cytomegalovirus;
XX influenza virus; HSV; herpes simplex virus; vector; immune response;
XX antibody; ribozyme; viral RNA; treatment; ss.
XX
XX Synthetic.
XX OS
XX WO9323569-A.
XX
XX 25-NOV-1993.
XX PD
XX 29-APR-1993; 93WO-US04020.
XX PE
XX 11-MAY-1992; 92US-0882689.
XX PR 14-MAY-1992; 92US-0882712.
XX PR 14-MAY-1992; 92US-0882713.
XX PR 14-MAY-1992; 92US-0882714.
XX PR 14-MAY-1992; 92US-0882823.
XX PR 14-MAY-1992; 92US-0882824.
XX PR 14-MAY-1992; 92US-0882886.
XX PR 14-MAY-1992; 92US-0882888.
XX PR 14-MAY-1992; 92US-0882889.
XX PR 14-MAY-1992; 92US-0882921.
XX PR 14-MAY-1992; 92US-0883823.
XX PR 14-MAY-1992; 92US-0883849.
XX PR 14-MAY-1992; 92US-0884073.
XX PR 14-MAY-1992; 92US-0884074.
XX PR 14-MAY-1992; 92US-0884333.
XX PR 14-MAY-1992; 92US-0884422.
XX PR 14-MAY-1992; 92US-0884431.
XX PR 14-MAY-1992; 92US-0884436.
XX PR 14-MAY-1992; 92US-0884451.
XX PR 31-JUL-1992; 92US-0923738.
XX PR 26-AUG-1992; 92US-0936086.
XX PR 18-SEP-1992; 92US-0948359.
XX PR 15-OCT-1992; 92US-0963322.
XX PR 07-DEC-1992; 92US-0967129.
XX PR 07-DEC-1992; 92US-0967130.
XX PR 07-DEC-1992; 92US-0967133.
XX
XX (RIBO-) RIBOZYME PHARM INC.

PT therapy methods -
XX
PS Disclosure; Page 14; 44pp; English.
XX

CC The present invention relates to a member of the family of proteins known
CC as ADAMTS (A Disintegrin And Metalloprotease Thrombospondin domain)
CC protein, the new member being designated ADAMTS-S1. The invention also
CC relates to polynucleotides encoding ADAMTS-S1, antibodies to ADAMTS-S1,
CC assays for studying the function of ADAMTS-S1, assays for determining
CC agonists or antagonists of ADAMTS-S1, and to the use of ADAMTS-S1
CC polypeptides or polynucleotides in diagnostic, biotherapeutic, or gene
CC therapy methods. ADAMTS proteins and ADAMTS protein agonists and
CC antagonists are useful in the manufacture of a medicament for treating
CC arthritis (osteoarthritis and rheumatoid arthritis), inflammatory bowel
CC disease, Crohn's disease, emphysema, acute respiratory distress syndrome,
CC asthma, chronic obstructive pulmonary disease, Alzheimer's disease, organ
CC transplant toxicity and rejection, cachexia, allergy, cancer (such as
CC solid tumour cancer including colon, breast, lung, prostate, brain, and
CC haematopoietic malignancies including leukaemia and lymphoma), tissue
CC ulcerations, restenosis, periodical disease, epidermolysis bullosa,
CC osteoporosis, loosening of artificial joint implants, atherosclerosis
CC (including atherosclerotic plaque rupture), aortic aneurysm (including
CC abdominal aortic and aneurysm), congestive heart failure, myocardial
CC infarction, stroke, cerebral ischemia, head trauma, spinal cord injury,
CC neurodegenerative diseases (acute and chronic), autoimmune disorders,
CC Huntington's disease, Parkinson's disease, migraine, depression,
CC peripheral neuropathy, pain, cerebral amyloid angiopathy, noctropic or
CC cognitive enhancement, amyotrophic lateral sclerosis, multiple sclerosis,
CC ocular angiogenesis, corneal injury, macular degeneration, abnormal wound
CC healing, burns, infertility or diabetic shock. This polynucleotide
CC sequence represents the antisense primer used for amplification of the
CC ADAMTS-S1 DNA of the invention. This amplification was involved in the
CC expression of ADAMTS-S1 in chondrocytes derived from osteoarthritis (OA)
CC cartilage and induction by proinflammatory cytokines.

SO Sequence 23 BP; 7 A; 7 C; 5 G; 4 T; 0 other;

Query Match 66.0%; Score 13.2; DB 24; Length 23;
Best Local Similarity 83.3%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TGGGTTGGCAGCTCAGAG 20
DB 19 TGGGTTTTCAGCTCAGTG 2

RESULT 9

AB183724/C
ID AB183724 standard; DNA; 24 BP.

AC AB183724;
XX

DT 15-FEB-2002 (first entry)

DE Capture oligonucleotide zip ID#664 oligo #1.

XX Human; K-ras; PCR primer; probe; capture probe; mutation detection;
XX ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
XX infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
XX cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
XX environmental monitoring; food industry; feed industry; ss.

OS Synthetic.
XX

PN W0200179548-A2.
XX

PD 25-OCT-2001.
XX

PF 04-APR-2001; 2001WO-US10958.
XX

PR 14-APR-2000; 2000US-197271P.
XX

PA (CORR) CORNELL RES FOUND INC.

XX Barany F, Zilvi M, Gerry NP, Favis R, Klaman R;
XX WPI, 2002-034366/04.
DR

PT Designing capture oligonucleotide probes for use on a support to which
PT complementary oligonucleotides hybridize with little mismatch -
PS Example 5; Fig 25; 300pp; English.
XX

CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridise with little mismatch, where:
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
CC medinensis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprised scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. AB182074 to
CC AB197546 represent oligonucleotide sequences used in the exemplification
CC of the present invention.

SO Sequence 24 BP; 3 A; 9 C; 6 G; 6 T; 0 other;

Query Match 64.0%; Score 12.8; DB 24; Length 24;
Best Local Similarity 87.5%; Pred. No. 3.9e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCGTTGGCAGCTCAGA 19
DB 16 GCGATTGCCACTCAGA 1

RESULT 10

AB183725
ID AB183725 standard; DNA; 24 BP.

AC AB183725;
XX

DT 15-FEB-2002 (first entry)

DE Capture oligonucleotide zip ID#664 oligo #2.

XX Human; K-ras; PCR primer; probe; capture probe; mutation detection;
XX ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
XX infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
XX cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
XX environmental monitoring; food industry; feed industry; ss.

OS Synthetic.
XX

PN W0200179548-A2.
XX

PD 25-OCT-2001.
XX

PF 04-APR-2001; 2001WO-US10958.
XX

PR 14-APR-2000; 2000US-197271P.
XX

PA (CORR) CORNELL RES FOUND INC.

```

sequence.
ACCESSION      BH854200
VERSION        BH854200.1
KEYWORDS       GI:21425071
SOURCE         GSS.
ORGANISM       chae crees.
                Arabidopsis thaliana
REFERENCE      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
                1 (bases 1 to 25)
AUTHORS        Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
                ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
                , Zimmerman,J. and Ecker,J.R.
TITLE          A Sequence-indexed Library of Insertion Mutations in the
                Arabidopsis Genome
JOURNAL        Unpublished (2001)
COMMENT        Contact: Joseph R. Ecker
                Salk Institute Genomic Analysis Laboratory (Signal)
                The Salk Institute for Biological Studies
                10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
                Tel: 858 453 4100 x1752
                Fax: 858 558 6379
                Email: ecker@salk.edu
                This is single pass sequence recovered from the left border of
                TDNA. This sequence lies within an annotated exon of Atg49990 and
                300 bases of the 3' end of Atg50000.
                Class: TDNA tagged.
FEATURES       Location/Qualifiers
                1..25
                /organism="Arabidopsis thaliana"
                /strain="Columbia 0"
                /db_xref="taxon:3702"
                /clone="SALK_078881.34.80.x"
                /note="PCR was performed on Arabidopsis thaliana lines
                each of which contains one or more TDNA insertion
                elements. The resultant fragment for each line was
                directly sequenced to determine the genomic sequence at
                the site of insertion. Details of the protocols used can
                be found at http://signal.salk.edu/tdna\_protocols.html"
BASE COUNT     5 a          5 c          5 g          10 t
ORIGIN
Query Match    54.1%; Score 9.2; DB 17; Length 25;
Best Local Similarity 78.6%; Pred. No. 1e+06;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY             3 TGCTTCGCGGGA 16
Db             9 TCCCTTCGCGGA 22

RESULT 13
ACCESSION      A2659612
LOCUS          A2659612
DEFINITION     20 bp DNA linear GSS 14-DEC-2000
                1M0537A07F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
                clone UUGCIM0537A07 F, DNA sequence.
ACCESSION      A2659612
VERSION        A2659612.1
KEYWORDS       GI:11796758
SOURCE         house mouse.
ORGANISM       Mus musculus
                Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                1 (bases 1 to 20)
REFERENCE      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
                Islam,H., Longacre,S., Mahmood,M., Meenen,B., Pedersen,T., Reilly
                ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                and Wright,D., Weis,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
                plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weis

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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetic.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0537 Row: A Column: 07
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
FEATURES       Location/Qualifiers
                1..20
                /organism="Mus musculus"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGCIM0537A07"
                /clone_lib="Mouse 10kb plasmid UUGCIM library"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                /note="Vector: PMD42ny; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adaptor DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of pMD42 (g1473214[gb|AF129072.1], a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adaptor mouse DNA was annealed to
                adaptor vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."
BASE COUNT     2 a          8 c          8 g          2 t
ORIGIN
Query Match    52.9%; Score 9; DB 17; Length 20;
Best Local Similarity 70.6%; Pred. No. 1.2e+06;
Matches 12; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY             1 GTTGCTTCGCGGGAAC 17
Db             4 GGTGCTTCGCGGAC 20

RESULT 14
ACCESSION      A2663981
LOCUS          A2663981
DEFINITION     21 bp DNA linear GSS 14-DEC-2000
                1M0543J22R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
                clone UUGCIM0543J22 R, DNA sequence.
ACCESSION      A2663981
VERSION        A2663981.1
KEYWORDS       GI:11801127
SOURCE         house mouse.
ORGANISM       Mus musculus
                Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                1 (bases 1 to 21)
REFERENCE      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
                Islam,H., Longacre,S., Mahmood,M., Meenen,B., Pedersen,T., Reilly
                ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                and Wright,D., Weis,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
                plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weis

```


was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

2 a 4 c 11 g 8 t

ORIGIN

Query Match 52.9%; Score 9; DB 17; Length 25;
Best local similarity 70.6%; Pred. No. 1.3e+06;
Matches 12; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGGAC 17

Db 4 GTTGCTTCGGCGGAC 20

RESULT 17
AZ339811/c 23 bp DNA linear GSS 29-SEP-2000
LOCUS 1M0071M19P Mouse 10kb plasmid UNGCM library Mus musculus genomic
DEFINITION clone UNGCM0071M19 F. DNA sequence.
ACCESSION AZ339811 GI:10414445
VERSION AZ339811.1 GI:10414445
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weis, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weis
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 2C S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0071 row: M column: 19
Seq primer: CGTGTAAACGACGCCACT
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers

FEATURES

source

1. 23
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UNGCM0071M19"
/clone_lib="Mouse 10kb plasmid UNGCM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

11 a 7 c 3 g 2 t

ORIGIN

Query Match 51.8%; Score 8.8; DB 17; Length 23;
Best local similarity 83.3%; Pred. No. 1.6e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGCTTCGGCGG 13

Db 17 TTGCTTCGTGAG 6

RESULT 18
TA106C010/c 23 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 106c01, reverse sequence.
DEFINITION genomic survey sequence.
ACCESSION AL461896 GI:11831493
VERSION AL461896.1 GI:11831493
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.

REFERENCE 1 (bases 1 to 23)
AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
TITLE Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA. E-mail: barrell@sanger.ac.uk and nh1@sanger.ac.uk
JOURNAL Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 CUTac 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + 1 method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsaye@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source

1. 23
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="106c01"
BASE COUNT 8 a 6 c 8 g 1 t
ORIGIN
Query Match 51.8%; Score 8.8; DB 17; Length 23;
Best local similarity 83.3%; Pred. No. 1.6e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GTTGCTTCGGCG 12
||||| |||||

CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NCO expression. The
CC present sequence is an amberzyme molecule of the invention.

50 Sequence 17 BP; 2 A; 6 C; 3 G; 6 U; 0 other;

Query Match	61.0%;	Score 12.2;	DB 23;	Length 17;
Best Local Similarity	53.9%;	Pred. No. 7.6e+03;		
Matches	9;	Conservative	5;	Mismatches 3;
				Indels 0;
				Gaps 0;

```

oy      1 TTGCGTTGCCACTCA 17
         : :| :| :| :| :| :|
Db      1 UCUGCUTUGGCCACUCA 17

```

RESULT 17
ABK17746/c
ID ABK17746 standard; RNA; 17 BP

AC ABK17746;
vv

DT. 09-APR-2002 (first entry)

DB Human ERG hammerhead ribozyme target sequence, Seq ID No 393.

KM Human hammerhead ribozyme; cytosolic; antitumour; antidiabetic;
KM opththalmologic; antirheumatic; antiproliferative; virucide; osteoprotic;
KM vulnary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
KM tumour angiogenesis; diabetic retinopathy; macular degeneration;
KM neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris
KM angiolipoma of tuberous sclerosis; port-wine stain; wound healing;
KM Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
KM Oster-Weber-Rednu syndrome; leukaemia; osteoporosis; DNasezyme; inozyme;
KM amberyzyme.

Homo sapiens.

PN WO200188124-A2.

PD 22-NOV-2001.

PF 16-MAY-2001; 2001WO-US15866.

PR 16-MAY-2000; 2000US-0572021.

PA (RIBO-) RIBOZYME PHARM INC.

2000

8

100

PT gene, useful for treating cancer, diabetic retinopathy, macular
PT degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber
PT syndrome

PS Claim 4; Page 65; 149pp; English.

CC The invention relates to a nucleic acid molecule (I) which down regulates
CC expression of an Ets-related gene (ERG). (I) is useful for treating
CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
CC vulgaris, angiolipoma of tubercous sclerosis, port-wine stains, Sturge
CC Weber syndrome, Kippel-Trenau-Werber syndrome, Osier-Weber-rendu
CC syndrome, leukaemia, osteoporosis and wound healing. (II) is useful for
CC treating a patient having a condition associated with the level of ERG,
CC by contacting cells of the patient with (I) under conditions suitable for
CC the treatment. The method comprises the use of one or more therapies
CC under conditions suitable for the treatment. Leukaemia or tumour
CC angiogenesis is treated by administering (I) to the patient in
CC conjunction with one or more of other therapies such as radiation or

chemotherapy treatment. (I) is useful for reducing ERG activity in a cell, by contacting the cell with (I). (i) is useful for cleaving RNA of ERG gene, by contacting (I) with RNA, in the presence of a divalent cation such as Mg²⁺. (I) is useful for diagnosis of conditions and diseases related to the expression of ERG, and as diagnostic tool to examine genetic drift and mutations within diseased cells or to detect the presence of ERG RNA in a cell. (I) is useful for specifically targeting genes that share homology with ERG gene or ERG fusion genes. ABK1754-ABK22719 represent nucleic acids, including antisense and enzymatic nucleic acid molecules which regulate expression of ERG, and related PCR primers of the invention.

5Q Sequence 17 BP; 3 A; 5 C; 5 G; 4 U; 0 other;

Query Match	61.0%	Score 12.2;	DB 24	Length 17;
Best Local Similarity	82.4%	Pred. No. 7	6e+03;	
Matches 14;	Conservative	0;	Mismatches 3;	Indels 0;
				Gaps .0

Oy 4 GCGTTGGCACTCAGAG 20
 |||||
 Db 17 GCGTTCGCGACTCAAG 1

RESULT 18
AAQ90138/c
ID AAQ90138 standard; DNA; 22 BP.

AC AAQ90138;

DT 05-JAN-1996 (first entry)

DE Transthyretin (TTR) gene exon 2 PCR primer 1791-1769.

KW Transthyretin; TTR; PCR primer 1791-1769; mutation Gly6-Ser6;

XX

[illegible]

XX

XX

XX

XX

1. \mathbb{R}^n is a vector space over \mathbb{R} .

XX

22

PT useful for diagnosis, prevention and treatment of amyloidosis
XX
PS Example 5; Page 32; 54pp; English.

CC AAQ90137 and AAQ90138 are a pair of

CC PCR-SSCP analysis for the identification of the TTR mutation Gly6
CC to Ser¹, this mutation, as a genetic marker for familial Alzheimer's
CC disease, is useful for identifying people at risk of developing
CC amyloidosis.

sq Sequence 22 BP; 8 A; 2 C; 10 G; 2 T; 0 other;

Query Match	61.0%	Score 12.2;	DB 16;	Length 22;
Best Local Similarity	82.4%;	Pred. No. 7.9e+03;		
Matches 14; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0

Qy	1	TTTGGCGTTGGCACTCA	17
Db	19	TTCCCGTTGGCCCTCA	3

Tissue Procurement: DCTD/BTP cDNA library Preparation: Ling Hong/Rubin Laboratory cDNA library Arrived by: The I.M.A.G.E. Consortium (LNUd) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNUd at: www.bio.1ln1.gov/bdrr/image/image.html Base Calling / Quality scores: PHRED from University of Washington Genome Center. Vector trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T identification: patmatch.pl from Berkeley Drosophila genome project. University of Washington Genome Center: <http://www.genome.washington.edu> low Quality Sequence: 9 contiguous PHRED high quality bases following vector sequence. Very low Quality Sequence: Trace file contained 22 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated. Short Insert: Based upon the presence of vector at both ends of the untrimmed sequence, this clone probably contains a cDNA insert of approximately 663 bases. Plate: LLCM4 row: F column: 6 High quality sequence, step: 9.

```

FEATURES
source
Location/Qualifiers
1..22
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2820485"
/clone_id="NH_MGC_7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pORF7; Site:1: XhoI, Site:2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

BASE COUNT	4	a	0	c	6	g	12	t			
ORIGIN											
Query Match	50.6%; Score 8.6; DB 10; Length 22;										
Best Local Similarity	73.3%; Pred. No. 2e+06;										
Matches	11;	Conservative.				Mismatches	4;	Indels	0;	Gaps	0;

QY	DB
2 TTGCTTCGGCGGGA 16	4 TTTTTCGGGGGGA 18

RESULT 22	
LOCUS	AZ780543/c
DEFINITION	AZ780543 23 bp DNA linear GSS 16-FEB-2001
ACCESSION	200018C03 Mouse 10kb plasmid UUCGM library Mus musculus genomic
VERSION	clone UUCG200018C03 F, DNA sequence.
KEYWORDS	AZ780543
SOURCE	AZ780543.1 GI:12912310
ORGANISM	GSS. house mouse. Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23)
REFERENCE	Dunn,D., Aoyagi,A., Barber,M., Baacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly, 'M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0018 row: C column: 03
Seq primer: CGTTGTTAAACACACGCGCACT
Class: plasmid ends
High quality sequence stop: 23.

```

FEATURES
SOURCE
location/Qualifiers
1. 23
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UBGCM0018C03"
/clone_lbe="Mouse 10kb plasmid library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMPD2 (gll4732114[gb|AF129072.1]) a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

BASE COUNT	8 a	8 c	1 g	6 t
ORIGIN				
Query Match		50.6%	Score 8.6;	DB 17;
Best Local Similarity		73.3%;	Pred. No. 2.1e+06;	length 23;
Matches 11;	Conservative	0;	Mismatches 4;	Indels 0;
				Gaps 0;

Qy	3	TGCTTCGGCGGGAC	17
Db	15	TGATTTTGAGGGAC	1

```

RESULT 23
AA034350/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE

```

AA034350 25 bp RNA linear EST 10-MAY-1997
Z220901.1 Soares, Pregnant_uterus_NbHPU Homo sapiens cDNA clone
IMAGE:471120 5' similar to PIR:A44125 A44125 high density
lipo-protein-binding protein, 110K - human ;, mRNA sequence.
AA034350
AA034350.1 GI:1506159
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 25)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiappelli, B.,
Chissee, S., Dietrich, N., Dubugue, T., Pavello, A., Gish, W., Hawkins
B., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore
M., Morris, M., Parsons, J., Prange, C., Rickin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierff-Mog, J., Treviski, B.,
Underwood, K., Wohlmann, F., Waterston, R., Wilson, R. and Watta, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)

XX 13-JUN-2000; 2000US-0593012.
 PR (USST) US ENVIRONMENTAL PROTECTION AGENCY.
 PA Haugland R, Vesper SJ,
 PI WPI; 2002-098078/13.
 XX
 DR Detecting and quantifying fungi and bacteria, involves obtaining a
 PT sequence of the fungus, extracting the DNA from the sample, and
 PT subjecting the DNA to polymerase chain reaction and fluorescent probe
 PT analysis.
 XX
 PS Claim 37; Page 14; 110pp; English.
 XX
 CC The invention relates to a method of detecting and quantifying fungi and
 CC bacteria, involving obtaining a sequence of the microorganism to be
 CC detected and quantified, extracting the DNA from the sample, and
 CC subjecting the DNA to polymerase chain reaction (PCR) and fluorescent
 CC probe analysis. The method is useful for identifying and quantifying
 CC specific fungi and bacteria using specific DNA sequences. The specific
 CC DNA sequences are useful for the real time detection of PCR products with
 CC a fluorogenic probe system or other molecular probes like hybridisation.
 CC ABK29026-ABK29474 represent fungal and bacterial PCR primers and probes
 CC used in the method of the invention.
 XX
 SQ Sequence 24 BP; 9 A; 4 C; 6 G; 5 T; 0 other;
 XX
 Query Match 61.0%; Score 12.2; DB 24; Length 24;
 Best Local Similarity 82.4%; Pred. No. 86+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 XX
 QY 4 GCCTTGGCCACTCAGAG 20
 Db 1 GCTTGTGCAACTCAGAG 17
 XX
 RESULT 22
 AAT92300/c
 ID AAT92300 standard; DNA; 25 BP.
 XX
 AC AAT92300;
 XX
 DT 20-JAN-1998 (first entry)
 XX
 DE Breast cancer tissue cDNA PCR primer from the IL-3R alpha gene.
 XX
 KW Breast cancer; PCR primer; cytokine; oncostatin M; prophylaxis;
 KW leukaemia inhibitory factor; agonist; cell morphology; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9716202-A1.
 XX
 PD 09-MAY-1997.
 XX
 PF 25-OCT-1996; 96WO-AU00676.
 XX
 PR 07-JUN-1996; 96AU-0000364.
 PR 27-OCT-1995; 95AU-0006242.
 PR 27-OCT-1995; 95AU-0006243.
 PR 27-MAR-1996; 96AU-0008966.
 XX
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 XX
 PI Begley CG, Douglas AM;
 XX
 DR WPI; 1997-271880/24.
 XX
 PT Use of cytokine(s), especially oncostatin M and leukaemia inhibitory
 PT factor or functional derivatives or agonists - for the treatment or

PT prophylaxis of breast cancer by ameliorating the effects of or
 PT delaying the onset of cancer.
 XX
 PS Example 3; Page 57; 83pp; English.
 XX
 CC A novel method has been developed for the treatment or prophylaxis of
 CC breast cancer in a mammal. The method involves administering one or
 CC more cytokines or functional derivatives or agonists of one or more
 CC cytokines for a time and under conditions to ameliorate the effects
 CC of or to delay onset of cancer. The present sequence represents a
 CC PCR primer which amplifies the cDNA from breast cancer tissue. The
 CC cytokines can inhibit the growth of breast cancer cells and also
 CC detrimentally affect cell morphology.
 XX
 SQ Sequence 25 BP; 5 A; 11 C; 5 G; 4 T; 0 other;
 XX
 Query Match 61.0%; Score 12.2; DB 18; Length 25;
 Best Local Similarity 82.4%; Pred. No. 86+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 XX
 QY 3 TGGCTTGGCCACTCAGA 19
 Db 20 TGGCTTGGCCACTCGGA 4
 XX
 RESULT 23
 AAV95070
 ID AAV95070 standard; RNA; 17 BP.
 XX
 AC AAV95070;
 XX
 DT 24-FEB-1999 (first entry)
 XX
 DE Canine IL-2 receptor g-chain substrate position 24.
 XX
 KW Human; IL-2 receptor g-chain; interleukin 2 receptor gamma chain;
 KW hammerhead ribozyme; hairpin ribozyme; substrate; expression; cancer;
 KW autoimmune disease; psoriasis; allergy; inflammatory disease;
 KW graft rejection; ss.
 XX
 OS Synthetic.
 OS Canis sp.
 XX
 PN WO9824913-A2.
 XX
 PD 11-JUN-1998.
 XX
 PF 02-DEC-1997; 97WO-US21748.
 XX
 PR 03-DEC-1996; 96US-0758306.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI McSwiggen JA, Stinchcomb DT;
 XX
 DR WPI; 1998-33332/29.
 XX
 PT Ribozymes targeted to interleukin 2 - useful for treating e.g.
 PT cancer, autoimmune disease and allergies
 XX
 PS Claim 4; Page 45; 61pp; English.
 XX
 CC The present sequence invention describes ribozymes targeted to modulate
 CC the synthesis and/or expression of interleukin (IL)-2R gamma encoded
 CC RNA. AAV93889 to AAV94574 represent specifically claimed ribozymes, and
 CC AAV94575 to AAV95260 represent specifically claimed substrate sequences
 CC from the present invention. The ribozymes can be used for the treatment
 CC of, e.g. graft rejection, autoimmune disease, cancer, psoriasis,
 CC allergy and other inflammatory conditions. The ribozymes are also used
 CC to induce tolerance in a recipient to alloantigen from a donor.
 XX
 SQ Sequence 17 BP; 3 A; 7 C; 2 G; 5 U; 0 other;

XX ABK02000;
 AC
 XX 12-MAR-2002 (first entry)
 DT
 XX
 DE Human NCOG Zinzyne #322.
 KM Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KM cerebroprotective; neuroprotective; antiparkinsonian;
 KM muscular; CD20; neurite growth inhibitor gene; NCOG; hammerhead ribozyme;
 KM DNazyme; Inozyme; G-cleaver; amberzyme; zinzyne; lymphoma; leukaemia;
 KM B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KM human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KM MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
 KM inflammatory arthropathy; central nervous system injury;
 KM cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KM chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KM Parkinson's disease; ataxia; Huntington's disease;
 KM Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 PN WO200159103-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US04273.
 XX
 PR 11-FEB-2000; 2000US-181797P.
 PR 18-FEB-2000; 2000US-18516P.
 PR 06-MAR-2000; 2000US-187128P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLATT) BLATT L.
 PA (MCSW) MCSWIGEN J.
 PA (CHOW) CHOWRIRA B M.
 PI Blact L, McSwigen J, Chowrira BM;
 DR WPI; 2001-607195/69.
 XX
 PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,
 PT and central nervous system injury -
 XX
 PS Claim 88; Page 101; 200pp; English.
 XX
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NCOG).
 CC The nucleic acids may be enzymatic nucleic acids (e.g., a ribozyme or a
 CC DNazyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN
 CC motif) or an amberyzyme (cleaving RNA with an NGN triplet), a zinzyne
 CC (cleaving RNA with a YGY motif). The CD20-targeting nucleic acid is used
 CC to cleave RNA of CD20 in the presence of a divalent cation that is
 CC preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce
 CC CD20 activity of the cell and treat a patient having a condition
 CC associated with the level of CD20. The treatment may further comprise the
 CC use of one or more therapies. In particular, the CD20 targeting
 CC nucleic acid may be used to treat lymphoma, leukaemia, B-cell
 CC lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky
 CC low-grade or follicular NHL, lymphocytic leukaemia, HIV (human
 CC immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL),
 CC immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune
 CC thrombocytopenia, and inflammatory arthropathy. The NCOG-targeting
 CC nucleic acid is used to cleave RNA of the NCOG gene in the presence of a
 CC divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid
 CC may be contacted with a cell to reduce NCOG activity of the cell and
 CC treat a patient having a condition associated with the level of NCOG. The
 CC treatment may further comprise the use of one or more therapies.

CC In particular, the NCOG-targeting nucleic acid may be used to treat
 CC central nervous system (CNS) injury and cerebrovascular accident (CVA,
 CC stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NCOG expression. The
 CC present sequence is a zinzyne molecule of the invention.
 XX
 SQ Sequence 17 BP; 3 A; 6 C; 3 G; 5 U; 0 other;
 XX
 QY Query Match 59.0%; Score 11.8; DB 23; Length 17;
 DB Best Local Similarity 60.0%; Pred. No. 1.2e+04;
 Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 3 TGCCTTGCACCTCA 17
 DB 2 UGCUUUGCCACUCA 16
 XX
 RESULT 27
 AAV3720/C
 ID AAV3720 standard; DNA; 20 BP.
 XX
 AC AAV3720;
 XX
 DT 20-AUG-1998 (first entry)
 XX
 DE PCR primer used in the course of the invention.
 XX
 KM Lipase; variant; improved wash performance; removal; lipid stain;
 KM reduced calcium dependence; one-cycle wash efficiency; detergent;
 KM cleaning composition; PCR primer; ss.
 XX
 OS Synthetic.
 OS Pseudomonas pseudocaligenes.
 XX
 PN W09808939-A1.
 PD 05-MAR-1998.
 XX
 PF 26-AUG-1997; 97WO-DK0345.
 XX
 PR 29-AUG-1996; 96US-0029190.
 PR 27-AUG-1996; 96DK-0000902.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 PA
 PI Okkels JS, Svendsen A;
 DR WPI; 1998-230259/20.
 XX
 PT Variants of lipase from Pseudomonas containing specific amino acid
 PT substitutions - deletions or additions, having improved wash
 PT performance in detergent formulations
 XX
 PS Disclosure; Page 74; 104pp; English.
 XX
 CC PCR primers AAV3717-23 were used during the course of the invention.
 CC The specification describes Pseudomonas pseudocaligenes lipase
 CC variants. The variant lipases described in the specification has have
 CC better wash performance than the original lipase. It has improved
 CC removal of lipid stains, reduced calcium dependence, better compatibility
 CC with detergents or their components, increased hydrophobicity, altered
 CC substrate specificity and better one-cycle wash efficiency. The variant
 CC lipase is used in detergent and cleaning compositions.
 XX
 SQ Sequence 20 BP; 8 A; 4 C; 7 G; 1 T; 0 other;
 XX
 QY Query Match 59.0%; Score 11.8; DB 19; Length 20;
 DB Best Local Similarity 86.7%; Pred. No. 1.2e+04;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0294 row: P column: 19
Seq primer: CACACAGGAAACAGCTATACC
Class: plasmid ends
High quality sequence stop: 22.

FEATURES
source
1..22
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0294P19"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42uv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|47321415b|AF1297.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN
7 a 8 c 3 g 4 t

Query Match 49.4%; Score 8.4; DB 17; Length 22;
Best Local Similarity 90.0%; Pred. No. 2.6e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CGCGCGGGAAC 17
|||
Db 22 CGGTGGGAAAC 13

RESULT 32
TA219C09P 22 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 219C09, forward sequence,
DEFINITION genomic survey sequence.
ACCESSION AL479371
VERSION AL479371.1 GI:11845122
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 22)
Hall, N., Bowman, S., Lennard, N. J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S. E., Rajandream, M. A. and Barrett, B. G.
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA. E-mail: barrell@sanger.ac.uk and

COMMENT nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J. C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source
1..22
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="219C09"

BASE COUNT
ORIGIN
3 a 8 c 4 g 7 t

Query Match 49.4%; Score 8.4; DB 17; Length 22;
Best Local Similarity 90.0%; Pred. No. 2.6e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTGCTTCGCG 11
|||
Db 10 TTGCTTCGCC 19

RESULT 33
A2475852 20 bp DNA linear GSS 04-OCT-2000
LOCUS 1M0294A18f Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0294A18 F, DNA sequence.
ACCESSION A2475852
VERSION A2475852.1 GI:10633977
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausen, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
CONTACT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0294 row: A column: 18
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.

FEATURES
source
1..20
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0294A18"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

```

PN      WO200055325-A2.
XX
XX      21-SEP-2000.
XX
XX      17-MAR-2000; 2000WO-US07392.
XX
XX      18-MAR-1999; 99US-0125219.
XX      01-APR-1999; 99US-0127409.
XX      18-MAY-1999; 99US-0134770.
XX      13-SEP-1999; 99US-0153584.
XX      17-SEP-1999; 99US-0154603.
XX
XX      (UYCH-) UNIV CHICAGO.
XX
XX      Preuss D, Copenhaver G, Keith K;
XX      WPI; 2000-587529/55.
XX
XX      Recombinant DNA construct comprising a plant centromere, useful for
XX      producing stably inherited chromosomes which can serve as vectors for
XX      the construction of transgenic plant and animal cells -
XX
XX      Disclosure; Page 279; 1449pp; English.
XX
XX      The present invention relates to a recombinant DNA construct of a plant
XX      (Arabidopsis thaliana) centromere. The constructs are useful for
XX      producing stably inherited chromosomes which can serve as vectors for
XX      the construction of transgenic plant and animal cells expressing
XX      selected proteins such as hormones, enzymes, interleukins, clotting
XX      factors, cytokines, antibodies, and growth factors.
XX
XX      Sequence 20 BP; 9 A; 4 C; 5 G; 2 T; 0 other;
XX
XX      Query Match      59.0%; Score 11.8; DB 21; Length 20;
XX      Best Local Similarity 86.7%; Pred. No. 1.2e+04;
XX      Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX      1 TTTCGCTTGCCTACT 15
XX      17 TTTCGCTTGCCTACT 3
XX
XX      Db
XX
XX      RESULT 31
XX      ABL44914
XX      ID ABL44914 standard; DNA; 20 BP.
XX      AC ABL44914;
XX      DT 11-APR-2002 (first entry)
XX      DE Human chromosome 1p36-35 PCR primer SEQ ID NO:1958.
XX      KW Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis;
XX      genome; PCR primer; ss.
XX      OS Homo sapiens.
XX      PN JP2001321190-A.
XX      PD 20-NOV-2001.
XX      PF 12-MAR-2001; 2001JP-0068285.
XX      PR 10-MAR-2000; 2000JP-0066716.
XX      PA (RIKA) RIKAGAKU KENKYUSHO.
XX      PA (GENO-) GENOTEX YG.
XX      DR WPI; 2002-144136/19.
XX      PT Arraying genome clones -
XX      PS Claim 4; Page 43; 528pp; Japanese.

```

```

XX
XX      The present invention describes a method of arraying genome clones. The
XX      method comprises: (a) clones of the genomic libraries contained in
XX      multowell plates numbered for discrimination are mixed in each of the
XX      multowell plates; (b) a primer designed based on the chromosome marker
XX      sequence is added to the mixture to carry out an amplification reaction;
XX      (c) a signal corresponding to the marker is detected from the resultant
XX      amplified product to specify the discrimination Nos. of the multowell
XX      plates containing the clones having said marker sequence; (d) the order
XX      of the markers is changed so that the same discrimination Nos. succeed to
XX      the maximum in the specified discrimination Nos. to array the multowell
XX      plates; (e) the clones in the multowell plates of the specified
XX      discrimination Nos. are mixed respectively in each well of longitudinal
XX      and lateral directions; (f) the mixed clones are cultured and the
XX      resultant cultures are amplified by using the above primer; (g) signals
XX      are detected from the amplified products; (h) the clones in the multowell
XX      plates are specified from the detected result; and (i) the clones are
XX      reconstituted as the positions on the chromosome and arrayed. The
XX      microarray is useful for gene analysis. ABL42957 to ABL45322 represent
XX      PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
XX      represent PCR primers for human chromosome 21q22.1, which are
XX      specifically claimed for use in the present invention.
XX
XX      Sequence 20 BP; 4 A; 8 C; 4 G; 4 T; 0 other;
XX
XX      Query Match      59.0%; Score 11.8; DB 24; Length 20;
XX      Best Local Similarity 86.7%; Pred. No. 1.2e+04;
XX      Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX      6 GTTTCGCTTGCCTAGAG 20
XX      1 GTTAGCCACTCCGAG 15
XX
XX      Db
XX
XX      RESULT 32
XX      AAH24199/c
XX      ID AAH24199 standard; DNA; 23 BP.
XX      AC AAH24199;
XX      DT 11-SEP-2001 (first entry)
XX      DE PCR primer, SEQ ID NO:10, used to isolate ageing inhibition-related DNA.
XX      KW Mouse; ageing inhibition-related DNA; ageing inhibitory protein;
XX      recombinant production; transgenic animal; detection; drug screening;
XX      ligand identification; ageing-related disorder; premature ageing;
XX      PCR primer; ss.
XX      OS Synthetic.
XX      PN WO200138529-A1.
XX      PD 31-MAY-2001.
XX      PF 17-NOV-2000; 2000WO-JP08121.
XX      PR 19-NOV-1999; 99JP-0329649.
XX      PA (KYOW) KYOWA HAKKO KOGYO KK.
XX      PI Shiraiishi N, Sekine S, Nabeshima Y, Fujimori T, Ito S;
XX      DR WPI; 2001-367689/38.
XX      PT Polypeptide for treatment of premature aging -
XX      PS Example 1; Page 89; 94pp; Japanese.
XX
XX      The invention relates to 3 novel mouse proteins which inhibit ageing
XX      CC (AAH23664-AAH23666) and to the nucleic acids encoding them (AAH24199-
XX      CC AAH24195). The invention also relates to recombinant vectors, host
XX      CC cells and transgenic non-human animals comprising DNA encoding a

```

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN
Query Match
Best Local Similarity 48.2%; Score 8.2; DB 17; Length 20;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTGCTTCGGCGG 14
DB 5 TTGCTTCGGTGTG 17

RESULT 36
LOCUS AZ355490 21 bp DNA GSS 02-OCT-2000
DEFINITION clone UGCGIM0095N14 F, DNA sequence.
ACCESSION AZ355490
VERSION AZ355490.1 GI:10468057
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islem,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weis,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0095 row: N column: 14
Seq primer: CTTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1..21
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0095N14"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, TI-resistant, F-"

FEATURES
source

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN
Query Match
Best Local Similarity 48.2%; Score 8.2; DB 17; Length 21;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTCTTCGGCGG 13
DB 4 GTTCTTCATAG 16

RESULT 37
LOCUS AA908627 22 bp mRNA EST 13-APR-1998
DEFINITION cg86e01.s1 NCI CGAP OVR Homo sapiens CDNA clone IMAGE:1455192 3' similar to SW:U1A6_HUMAN P30041 24 KD PROTEIN ;, mRNA sequence.
ACCESSION AA908627
VERSION AA908627.1 GI:3048032
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 22)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
unknown library type
Trace considered overall poor quality
Seq primer: -40m13 fwd. ET from Amerham
High quality sequence stop: 1.
Location/Qualifiers
1..22
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1455192"
/clone_lib="NCI CGAP_OVR"
/issue_type="serous adenocarcinoma"
/lab_host="DH10B"
/note="Organ: ovary; Vector: pCMV-SPORT4; Site: 1; SalI; Site: 2; NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.1 kb. Life Technologies catalog #: 10982-015"

BASE COUNT
ORIGIN
Query Match
Best Local Similarity 48.2%; Score 8.2; DB 9; Length 22;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

SQ Sequence 24 BP; 4 A; 7 C; 7 G; 6 T; 0 other;
 Query Match 59.0%; Score 11.8; DB 24; Length 24;
 Best Local Similarity 86.7%; Pred. No. 1.3e+04;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 5 CGTTGCCACTCAGA 19
 |||||
 Db 23 CGTTGCCAAGCAGCA 9

RESULT 35
 ABI88869
 ID ABI88869 standard; DNA; 24 BP.
 AC ABI88869;
 XX
 XX

DT 15-FEB-2002 (first entry)
 XX
 XX DE Capture oligonucleotide Zip ID#3236 oligo #2.
 XX

KM Human, K-ras; PCR primer; probe; capture probe; mutation detection;
 KM ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
 KM infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
 KM cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
 KM environmental monitoring; food industry; feed industry; ss.
 XX
 XX

OS Synthetic.
 XX

XX WO200179548-A2.
 XX

XX 25-OCT-2001.
 XX

XX 04-APR-2001; 2001WO-US10958.
 XX

XX 14-APR-2000; 2000US-197271P.
 XX

XX (CORR) CORNELL RES FOUND INC.
 XX

XX Barany F, Zilv M, Gerry NP, Favis R, Kliman R;
 XX

XX WPI; 2002-034366/04.
 XX

PT Designing capture oligonucleotide probes for use on a support to which
 XX complementary oligonucleotides hybridize with little mismatch -
 XX

XX Example 5; Fig 25; 300bp; English.
 XX

XX The present invention describes a method (M1) for designing capture
 CC oligonucleotide probes (I) for use on a support to which complementary
 CC oligonucleotide probes (II) will hybridize with little mismatch, where
 CC (I) have melting temperatures within a narrow range. The method is useful
 CC for detecting infectious diseases caused by bacterial infectious agents
 CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
 CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
 CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
 CC Epstein-Barr virus and polio virus, and parasitic infectious agents
 CC rejected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
 CC medineensis. The method is also useful for detecting genetic diseases such
 CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
 CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
 CC involved in DNA amplification, replication, recombination or repair, the
 CC cancer is specifically associated with a gene selected from BRCA1 gene,
 CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
 CC method is also used for environmental monitoring, forensics and the food
 CC and feed industry, detecting complex scanning (using e.g. a scanning
 CC electron microscope and infrared microscope) the support at the
 CC particular sites and identifying if ligation of the oligonucleotide probe
 CC occurs and correlating (using a computer) identified ligation to a
 CC presence or absence of the target nucleotide sequences. ABI2074 to
 CC ABI97546 represent oligonucleotide sequences used in the exemplification
 CC of the present invention.
 XX

SQ Sequence 24 BP; 6 A; 7 C; 7 G; 4 T; 0 other;
 Query Match 59.0%; Score 11.8; DB 24; Length 24;
 Best Local Similarity 86.7%; Pred. No. 1.3e+04;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 5 CGTTGCCACTCAGA 19
 |||||
 Db 2 CGTTGCCAAGCAGCA 16

RESULT 36
 AAQ34205/c
 ID AAQ34205 standard; DNA; 19 BP.
 AC AAQ34205;
 XX
 XX

DT 02-FEB-1993 (first entry)
 XX
 XX

DE Upstream PCR primer AGLA254UP1.
 XX

KM PCR; selection; microsatellite; OPTIPRM; breeding; cattle; parentage;
 KM genetic mapping; traits; amplification; ss.
 XX
 XX

OS Bos taurus.
 XX

XX WO9211102-A.
 XX

XX 06-AUG-1992.
 XX

XX 15-JAN-1992; 92WO-US00340.
 XX

XX 15-JAN-1991; 91US-0642342.
 XX

XX (GENM-) GENMARK.
 XX

XX Georges M, Massey JM;
 XX

XX WPI; 1992-284684/34.
 XX

PT Polymorphic bovine DNA markers - used in genetic identification,
 XX gene mapping, and selective breeding
 XX

XX Table 8; Page 413; 517bp; English.
 XX

XX The sequence shows an upstream PCR primer for in vitro amplification
 CC of bovine microsatellite sequences obtained by screening library of
 CC bovine MboI DNA fragments of between 250 and 500 bp with an (AC)15
 CC and a (TC)15 oligonucleotide probe. One out of 50 clones cross-
 CC hybridized. Assuming independent distribution of microsatellites
 CC and MboI sites, the frequency of (16)n > 9 microsatellites in the
 CC bovine genome is estimated at >100,000. The sequence information
 CC for ca. 230 such bovine microsatellites is summarised in the
 CC specification and indexed herein (see below). For each such
 CC microsatellite sequence sufficient information was obtained to
 CC generate the required PCR primers for in vitro amplification of
 CC the corresp. microsatellite (using the program OPTIPRM).
 CC The microsatellites may be used to identify individuals, for
 CC parentage testing, and in the genetic mapping of economic trait loci,
 CC or genes involved in the determination of economically important
 CC traits esp. in cattle, to allow selective breeding.
 CC See also AAQ33501-34440.
 CC

XX Sequence 19 BP; 5 A; 5 C; 6 G; 3 T; 0 other;
 XX

SQ Query Match 58.0%; Score 11.6; DB 13; Length 19;
 Best Local Similarity 77.8%; Pred. No. 1.6e+04;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Oy 1 TTTCGTTGCCACTCAG 18
 |||||
 Db 19 TTTCGTTGCCAAGCAG 2

SOURCE
house mouse.

ORGANISM
Mus musculus

REFERENCE
Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)

AUTHORS
Dunn,D., Royagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
'M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A.
and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 1000 Std Error: 0.00
Plate: 0028 row: H column: 03
Seq primer: CACACAGGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.

FEATURES
location/Qualifiers

source
1..23
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0028H03"
/clone_1lb="Mouse 10kb plasmid UUCG1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42n; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT
4 a 3 c 12 g 4 t

ORIGIN

Query Match
Best Local Similarity 48.2%; Score 8.2; DB 17; Length 23;
Best Local Similarity 76.9%; Pred. No. 3.3e+06;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY
4 GCTTGGCGCGGA 16
||| ||| ||| |||
10 GCTGAGGGGGGA 22

DB

Search completed: June 7, 2003, 09:43:43
Job time : 1020.33 secs

```

XX OS Naja naja siamensis.
XX PN WO200170173-A2.
XX PD 27-SEP-2001.
XX PF 14-MAR-2001; 2001WO-US08150.
XX PR 23-MAR-2000; 2000US-0533454.
XX PA (PHYL-) PHYLAMED CORP.
XX PI Mundschchenk DD, Reid PF;
XX DR WPI; 2001-616350/71.
XX PT Composition for preventing HIV infection of mammalian cells comprises
XX PT an anti-immunodeficiency virus immunokine capable of binding to a
XX PT cellular protein by which HIV infection of the cell is prevented.
XX PS Example 1; Page 30; 54pp; English.
XX CC The present invention relates to a composition for preventing HIV
XX CC infection of mammalian cells. The composition comprises an
XX CC anti-immunodeficiency virus immunokine (a neurotoxin) capable of binding
XX CC to a cellular protein in a manner that prevents HIV infection of the
XX CC cell. One such neurotoxin is alpha-cobratoxin from Naja naja siamensis
XX CC (Thailand cobra). The present sequence is a PCR primer which was used to
XX CC amplify alpha-cobratoxin cDNA for use in the present invention.
SQ Sequence 21 BP; 4 A; 6 C; 3 G; 8 T; 0 other;
QY Query Match 58.0%; Score 11.6; DB 22; Length 21;
Best Local Similarity 77.8%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Db 1 TTTGCGTTGGCAGTCAG 18
2 TTTTCATTCGCCATTCAG 19
RESULT 40
ABL43246
ID ABL43246 standard; DNA; 21 BP.
XX AC ABL43246;
XX DT 11-APR-2002 (first entry)
XX DE Human chromosome 1p36-35 PCR primer SEQ ID NO:230.
XX KW Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis;
XX KW genome; PCR primer; se.
XX OS Homo sapiens.
XX PN JP2001321190-A.
XX PD 20-NOV-2001.
XX PF 12-MAR-2001; 2001JP-0068285.
XX PR 10-MAR-2000; 2000JP-0066716.
XX PA (RIKA) RIKAGAKU KENKUSHO.
XX PA (GENO-) GENOTEX YG.
XX DR WPI; 2002-144136/19.
XX PT Arraying genome clones
XX PS Claim 4; Page 10; 528pp; Japanese.

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XX CC The present invention describes a method of arraying genome clones. The
XX CC method comprises: (a) clones of the genomic libraries contained in
XX CC multiwell plates numbered for discrimination are mixed in each of the
XX CC multiwell plates; (b) a primer designed based on the chromosome marker
XX CC sequence is added to the mixture to carry out an amplification reaction;
XX CC (c) a signal corresponding to the marker is detected from the resultant
XX CC amplified product to specify the discrimination Nos. of the multiwell
XX CC plates containing the clones having said marker sequence; (d) the order
XX CC of the markers is changed so that the same discrimination Nos. succeed to
XX CC the maximum in the specified discrimination Nos. to array the multiwell
XX CC plates; (e) the clones in the multiwell plates of the specified
XX CC discrimination Nos. are mixed respectively in each wells of longitudinal
XX CC and lateral directions; (f) the mixed clones are cultured and the
XX CC resultant cultures are amplified by using the above primer; (g) signals
XX CC are detected from the amplified products; (h) the clones in the multiwell
XX CC plates are specified from the detected result; and (i) the clones are
XX CC reconstituted as the positions on the chromosome and arrayed. The
XX CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent
XX CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
XX CC represent PCR primers for human chromosome 21q22.1, which are
XX CC specifically claimed for use in the present invention.
SQ Sequence 21 BP; 3 A; 9 C; 1 G; 8 T; 0 other;
QY Query Match 58.0%; Score 11.6; DB 24; Length 21;
Best Local Similarity 77.8%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Db 1 TTTGCGTTGGCAGTCAG 18
2 TTTACATTCCTCTCAG 18

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Search completed: June 7, 2003, 08:30:37
Job time : 180.727 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Comphen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 7, 2003, 07:18:59 / Search time 164.727 Seconds
(without alignments)
273.421 Million cell updates/sec

Title: US-10-080-959a-2

Perfect score: 20
Sequence: 1 ttgcgcttcgcacccagag 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 1698378

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15.0	25	24	ABN99615	Fungi PCR primer S
2	15	25	24	ABK29212	Stachybotrys chart
3	14.4	24	22	AAH56097	Human SCNA3 PCR-SS
4	13.8	20	22	AAK2656	Human NCK-2 phosph
5	13.8	21	21	AAQ59948	Human delta-like p
6	13.4	17	14	AAQ50799	HBV target sequenc
7	13.4	24	19	AAV5581	STS probe GV10 gen
8	13.2	23	24	AAK98779	Antisense primer f
9	12.8	24	24	AB183724	Capture oligonucle

10	12.8	64.0	24	AB183725	Capture oligonucle
11	12.8	64.0	25	AAD07981	M. mycoides LppQ 5
12	12.8	64.0	25	AAD07982	M. mycoides LppQ 5
13	12.6	63.0	20	ABK41539	Human CTNNA3 exon-
14	12.6	63.0	21	AAK67562	Alzheimer's disease
15	12.6	63.0	21	AAQ58843	Human NBNH virus primer
16	12.2	61.0	17	ABK02611	Human NOGO Amberry
17	12.2	61.0	17	ABK17746	Human ERG hammerhe
18	12.2	61.0	22	AAQ90138	Transhyretin (TTR
19	12.2	61.0	24	AAZ30442	Degenerate primer
20	12.2	61.0	24	ABN99536	Fungi PCR primer S
21	12.2	61.0	24	ABK29133	Paecilomyces lilac
22	12.2	61.0	25	AAK92300	Breast cancer tlas
23	12.2	61.0	17	AAV95070	Canine IL-2 recept
24	12.2	61.0	21	AAK64985	Rat OB receptor PC
25	12	60.0	23	AAK21460	Human NOGO Zinzyme
26	11.8	59.0	17	ABK02000	PCR primer used in
27	11.8	59.0	20	AAV23720	PCR primer used to
28	11.8	59.0	20	AAK95488	PCR primer #7. Sy
29	11.8	59.0	20	AAK02576	Arabidopsis thalia
30	11.8	59.0	20	AAK23122	Human chromosome 1
31	11.8	59.0	20	ABL44914	Human chromosome 1
32	11.8	59.0	23	AAH24199	PCR primer, SEQ ID
33	11.8	59.0	24	ABK49704	Human kinase uridy
34	11.8	59.0	24	AB188868	Capture oligonucle
35	11.8	59.0	24	AB188869	Capture oligonucle
36	11.6	58.0	19	AAQ34205	Upstream PCR prime
37	11.6	58.0	20	AAI66253	a-Cobaloxin gene
38	11.6	58.0	21	AAI69969	alpha-cobaloxin p
39	11.6	58.0	21	AAI69969	Human chromosome 1
40	11.6	58.0	21	ABL43246	Sequence upstream
41	11.6	58.0	22	AAQ33559	Oligonucleotide ch
42	11.6	58.0	24	AAV05057	Oligonucleotide ad
43	11.6	58.0	24	ABQ02241	Oligonucleotide ad
44	11.6	58.0	24	ABQ08433	Oligonucleotide ad
45	11.6	58.0	24	ABQ08433	Oligonucleotide ad
46	11.6	58.0	25	AAH59820	Primer for JNK2 nu
47	11.6	58.0	25	AAH41862	JNK2 gene PCR prim
48	11.6	58.0	25	AAH39055	SNP specific SNR
49	11.4	57.0	15	ABK63990	Human Bf gene alle
50	11.4	57.0	17	AAK07448	Hammerhead ribozym
51	11.4	57.0	20	AAK08249	p22, PCR primer f
52	11.4	57.0	16	AAK08249	Binary vector back
53	11.4	57.0	21	AAK05684	Primer FPCRPROR fo
54	11.4	57.0	24	AAQ21129	PCR primer 2 used
55	11.4	57.0	24	AAH25008	Nucleotide sequenc
56	11.4	57.0	25	AAK71006	Single nucleotide
57	11.4	57.0	25	AAK82988	HHV6 detecting pro
58	11.4	57.0	25	AAK90744	Human secretory pr
59	11.2	56.0	25	ABK66421	Human gene specific
60	11.2	56.0	17	ABK00505	Human NOGO Hammerh
61	11.2	56.0	17	ABK18676	Human ERG G-cleave
62	11.2	56.0	19	AAQ13541	Probe JFL329 to co
63	11.2	56.0	19	AAK44568	Antisense oligo HU
64	11.2	56.0	19	AAH80607	Oligonucleotide IS
65	11.2	56.0	19	AAZ59338	Human STR2 inton
66	11.2	56.0	19	AAK00702	Sequencing primer
67	11.2	56.0	19	AAK38170	NOV2 gene specific
68	11.2	56.0	20	AAQ13447	Probe to mutant co
69	11.2	56.0	20	AAK06902	Modified oligonuc
70	11.2	56.0	20	AAZ00682	Human GPC3 exon 9
71	11.2	56.0	20	AAZ00604	Human GPC3 exon 7B
72	11.2	56.0	20	AAK06128	Human Sema7A codin
73	11.2	56.0	20	AB196581	Capture oligonucle
74	11.2	56.0	21	AAK58076	ICM-1 antisense o
75	11.2	56.0	21	AAV38612	Human ICM-1, E-se
76	11.2	56.0	21	AAV17884	Human albumin forw
77	11.2	56.0	22	AAV57864	Human chromosome 1
78	11.2	56.0	24	AB189732	Capture oligonucle
79	11.2	56.0	24	AB189733	Capture oligonucle
80	11.2	56.0	24	AAK67163	Human ATM gene exo
81	11	55.0	20	AAQ97421	Interferon regulat
82	11	55.0	20	AAK95546	PCR primer used to

Capture oligonucle
M. mycoides LppQ 5
M. mycoides LppQ 5
Human CTNNA3 exon-
Alzheimer's disease
Human NBNH virus primer
Human NOGO Amberry
Human ERG hammerhe
Transhyretin (TTR
Degenerate primer
Fungi PCR primer S
Paecilomyces lilac
Breast cancer tlas
Canine IL-2 recept
Rat OB receptor PC
Human NOGO Zinzyme
PCR primer used in
PCR primer used to
PCR primer #7. Sy
Arabidopsis thalia
Human chromosome 1
PCR primer, SEQ ID
Human kinase uridy
Capture oligonucle
Upstream PCR prime
a-Cobaloxin gene
alpha-cobaloxin p
Human chromosome 1
Sequence upstream
Oligonucleotide ch
Oligonucleotide ad
Oligonucleotide ad
Oligonucleotide ad
Primer for JNK2 nu
JNK2 gene PCR prim
SNP specific SNR
Human Bf gene alle
Hammerhead ribozym
p22, PCR primer f
Binary vector back
Primer FPCRPROR fo
PCR primer 2 used
Nucleotide sequenc
Single nucleotide
HHV6 detecting pro
Human secretory pr
Human gene specific
Human NOGO Hammerh
Human ERG G-cleave
Probe JFL329 to co
Antisense oligo HU
Oligonucleotide IS
Human STR2 inton
Sequencing primer
NOV2 gene specific
Probe to mutant co
Modified oligonuc
Human GPC3 exon 9
Human GPC3 exon 7B
Human Sema7A codin
Capture oligonucle
ICM-1 antisense o
Human ICM-1, E-se
Human albumin forw
Human chromosome 1
Capture oligonucle
Capture oligonucle
Human ATM gene exo
Interferon regulat
PCR primer used to

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C 81	7.6	44.7	19	17	A2361152	A2361152	1M0104A16	C 154	7.4	43.5	25	13	BM400880	BM400880
C 82	7.6	44.7	19	17	A2480905	A2480905	1M0302N22	C 155	7.4	43.5	25	13	BM437385	BM437385
C 83	7.6	44.7	19	17	A2586436	A2586436	1M0392016	C 156	7.4	43.5	25	17	A2766960	A2766960
C 84	7.6	44.7	20	13	BM397553	BM397553	5009-0-34	C 157	7.4	43.5	25	17	A27969075	A27969075
C 85	7.6	44.7	20	13	BM396892	BM396892	5009-0-50	C 158	7.2	42.4	15	13	BM396834	BM396834
C 86	7.6	44.7	20	13	BM399755	BM399755	5009-0-60	C 159	7.2	42.4	16	9	AA936037	AA936037
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C 89	7.6	44.7	20	17	A2946089	A2946089	2M0207A13	C 162	7.2	42.4	19	17	A2646801	A2646801
C 90	7.6	44.7	21	17	A2309054	A2309054	1M0012A18	C 163	7.2	42.4	19	17	A2805995	A2805995
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C 93	7.6	44.7	22	17	A2583690	A2583690	1M0378E16	C 166	7.2	42.4	20	17	A2530963	A2530963
C 94	7.6	44.7	22	17	A2589849	A2589849	1M0399A09	C 167	7.2	42.4	20	17	A2514414	A2514414
C 95	7.6	44.7	23	13	BM398474	BM398474	5009-0-45	C 168	7.2	42.4	20	17	A2810573	A2810573
C 96	7.6	44.7	23	13	BM398474	BM398474	5009-0-45	C 169	7.2	42.4	21	17	A2359241	A2359241
C 97	7.6	44.7	23	17	A2374746	A2374746	1M0137D15	C 170	7.2	42.4	21	17	A2765535	A2765535
C 98	7.6	44.7	23	17	A2443442	A2443442	1M0238E16	C 171	7.2	42.4	21	17	A2792515	A2792515
C 99	7.6	44.7	23	17	A2779607	A2779607	2M0016E18	C 172	7.2	42.4	21	17	BM758186	BM758186
C 100	7.6	44.7	23	17	A2784648	A2784648	2M0027P11	C 173	7.2	42.4	22	9	AA931331	AA931331
C 101	7.6	44.7	23	17	A2823400	A2823400	2M0097K24	C 174	7.2	42.4	22	13	BM396732	BM396732
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C 103	7.6	44.7	24	17	A2650143	A2650143	1M0520I11	C 176	7.2	42.4	22	17	TA47810P	TA47810P
C 104	7.6	44.7	24	17	TA238D04	TA238D04	AL481302 T. brucei	C 177	7.2	42.4	23	17	A2328328	A2328328
C 105	7.6	44.7	25	9	AL1000280	AL1000280	ov10e04.s	C 178	7.2	42.4	23	17	A2350054	A2350054
C 106	7.6	44.7	25	9	AL1049424	AL1049424	ub33f08.r	C 179	7.2	42.4	23	17	A2430197	A2430197
C 107	7.6	44.7	25	9	AL1471696	AL1471696	c199f05.x	C 180	7.2	42.4	23	17	A2456925	A2456925
C 108	7.6	44.7												

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C 262	10.4	52.0	24	24	ABO10541	Oligonucleotide ad
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C 266	10.4	52.0	25	16	AA099098	Extension/ligation
C 267	10.4	52.0	25	16	AA099101	Ligation primer us
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C 280	10.4	52.0	25	24	ABO12077	Oligonucleotide ad
C 281	10.4	52.0	25	24	ABA92545	Adenovirus 5 relat
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C 283	10.2	51.0	15	19	AAV59274	Avocado sunblotch
C 284	10.2	51.0	15	19	AAV58740	Insertion sequence
C 285	10.2	51.0	15	19	AAV38618	Human ICAM-1, E-se
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C 288	10.2	51.0	15	22	AAFA5737	IGFBP2 oligonucleo
C 289	10.2	51.0	15	22	AAFA7735	IGFBP3 oligonucleo
C 290	10.2	51.0	17	16	AAI53616	Rat ICAM hammerhea
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C 298	10.2	51.0	17	23	ABK18852	Human ERG DNaseyme
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C 302	10.2	51.0	18	21	AAZ71686	Human biallelic ma
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C 304	10.2	51.0	18	22	AAZ88854	Human HLA-B27 alle
C 305	10.2	51.0	18	22	AAZ88855	Human HLA-B27 alle
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C 307	10.2	51.0	19	19	AAI10201	Human biallelic po
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C 309	10.2	51.0	19	21	AAAB3849	Cyclin A2 ribozyme
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C 320	10.2	51.0	19	22	AAAB3860	Cyclin A2 ribozyme
C 321	10.2	51.0	19	22	AAAB3861	Cyclin A2 ribozyme
C 322	10.2	51.0	19	22	AAAB3862	Cyclin A2 ribozyme
C 323	10.2	51.0	19	22	AAAB3863	Cyclin A2 ribozyme
C 324	10.2	51.0	19	22	AAAB3864	Cyclin A2 ribozyme
C 325	10.2	51.0	19	22	AAAB3865	Cyclin A2 ribozyme
C 326	10.2	51.0	19	22	AAAB3866	Cyclin A2 ribozyme
C 327	10.2	51.0	19	22	AAAB3867	Cyclin A2 ribozyme
C 328	10.2	51.0	19	22	AAAB3868	Cyclin A2 ribozyme
C 329	10.2	51.0	19	22	AAAB3869	Cyclin A2 ribozyme
C 330	10.2	51.0	19	22	AAAB3870	Cyclin A2 ribozyme
C 331	10.2	51.0	19	22	AAAB3871	Cyclin A2 ribozyme
C 332	10.2	51.0	19	22	AAAB3872	Cyclin A2 ribozyme
C 333	10.2	51.0	19	22	AAAB3873	Cyclin A2 ribozyme
C 334	10.2	51.0	19	22	AAAB3874	Cyclin A2 ribozyme
C 335	10.2	51.0	19	22	AAAB3875	Cyclin A2 ribozyme
C 336	10.2	51.0	19	22	AAAB3876	Cyclin A2 ribozyme
C 337	10.2	51.0	19	22	AAAB3877	Cyclin A2 ribozyme
C 338	10.2	51.0	19	22	AAAB3878	Cyclin A2 ribozyme
C 339	10.2	51.0	19	22	AAAB3879	Cyclin A2 ribozyme
C 340	10.2	51.0	19	22	AAAB3880	Cyclin A2 ribozyme
C 341	10.2	51.0	19	22	AAAB3881	Cyclin A2 ribozyme
C 342	10.2	51.0	19	22	AAAB3882	Cyclin A2 ribozyme
C 343	10.2	51.0	19	22	AAAB3883	Cyclin A2 ribozyme
C 344	10.2	51.0	19	22	AAAB3884	Cyclin A2 ribozyme
C 345	10.2	51.0	19	22	AAAB3885	Cyclin A2 ribozyme
C 346	10.2	51.0	19	22	AAAB3886	Cyclin A2 ribozyme
C 347	10.2	51.0	19	22	AAAB3887	Cyclin A2 ribozyme
C 348	10.2	51.0	19	22	AAAB3888	Cyclin A2 ribozyme
C 349	10.2	51.0	19	22	AAAB3889	Cyclin A2 ribozyme
C 350	10.2	51.0	19	22	AAAB3890	Cyclin A2 ribozyme
C 351	10.2	51.0	19	22	AAAB3891	Cyclin A2 ribozyme
C 352	10.2	51.0	19	22	AAAB3892	Cyclin A2 ribozyme
C 353	10.2	51.0	19	22	AAAB3893	Cyclin A2 ribozyme
C 354	10.2	51.0	19	22	AAAB3894	Cyclin A2 ribozyme
C 355	10.2	51.0	19	22	AAAB3895	Cyclin A2 ribozyme
C 356	10.2	51.0	19	22	AAAB3896	Cyclin A2 ribozyme
C 357	10.2	51.0	19	22	AAAB3897	Cyclin A2 ribozyme
C 358	10.2	51.0	19	22	AAAB3898	Cyclin A2 ribozyme
C 359	10.2	51.0	19	22	AAAB3899	Cyclin A2 ribozyme
C 360	10.2	51.0	19	22	AAAB3900	Cyclin A2 ribozyme
C 361	10.2	51.0	19	22	AAAB3901	Cyclin A2 ribozyme
C 362	10.2	51.0	19	22	AAAB3902	Cyclin A2 ribozyme
C 363	10.2	51.0	19	22	AAAB3903	Cyclin A2 ribozyme
C 364	10.2	51.0	19	22	AAAB3904	Cyclin A2 ribozyme
C 365	10.2	51.0	19	22	AAAB3905	Cyclin A2 ribozyme
C 366	10.2	51.0	19	22	AAAB3906	Cyclin A2 ribozyme
C 367	10.2	51.0	19	22	AAAB3907	Cyclin A2 ribozyme
C 368	10.2	51.0	19	22	AAAB3908	Cyclin A2 ribozyme
C 369	10.2	51.0	19	22	AAAB3909	Cyclin A2 ribozyme
C 370	10.2	51.0	19	22	AAAB3910	Cyclin A2 ribozyme
C 371	10.2	51.0	19	22	AAAB3911	Cyclin A2 ribozyme
C 372	10.2	51.0	19	22	AAAB3912	Cyclin A2 ribozyme
C 373	10.2	51.0	19	22	AAAB3913	Cyclin A2 ribozyme
C 374	10.2	51.0	19	22	AAAB3914	Cyclin A2 ribozyme

C 521	10	50.0	20	24	ABN89238	Human Talin antisense	594	9.8	49.0	17	21	AAFP04367	Hammerhead ribozym
C 522	10	50.0	20	24	AAI38332	Interacting domain	595	9.8	49.0	17	21	AAFP04814	Hammerhead ribozym
C 523	10	50.0	20	24	ABK85195	Rat PTPB1 antisense	596	9.8	49.0	17	21	AAFP04815	Hammerhead ribozym
C 524	10	50.0	20	24	ABK85340	Human PTPB1 antisense	597	9.8	49.0	17	21	AAAG94160	Adenovirus 5 E2/E3
C 525	10	50.0	20	24	ABD34771	Human MEXK3 CDNA t	598	9.8	49.0	17	21	AAA65534	Human genomic SNP
C 526	10	50.0	20	24	ABK71111	Mouse HyPLIP1 locu	C 599	9.8	49.0	17	21	AAA25028	Oestrogen receptor
C 527	10	50.0	20	24	ABK68207	Mouse HyPLIP1 locu	600	9.8	49.0	17	21	AAA25516	Oestrogen receptor
C 528	10	50.0	20	24	ABK37364	Rat PTPB1 mRNA lev	601	9.8	49.0	17	21	AAA25517	Oestrogen receptor
C 529	10	50.0	20	24	AB193553	Capture oligonucle	602	9.8	49.0	17	21	AAA25518	Oestrogen receptor
C 530	10	50.0	20	24	AB193884	Capture oligonucle	C 603	9.8	49.0	17	22	ABAA75518	Retinoblastoma mut
C 531	10	50.0	20	24	AB195521	Capture oligonucle	604	9.8	49.0	17	22	ABAA77785	Retinoblastoma mut
C 532	10	50.0	21	19	AAV02959	Hepatitis GB virus	C 605	9.8	49.0	17	22	AAAB0177	Oligonucleotide by
C 533	10	50.0	21	21	AAAC69195	Human ABC1 gene ex	C 606	9.8	49.0	17	22	AAAB0178	Oligonucleotide by
C 534	10	50.0	21	21	AAAT74014	Reverse PCR primer	C 607	9.8	49.0	17	22	AAAB0179	Oligonucleotide by
C 535	10	50.0	21	22	AAFP66395	Human gene single	C 608	9.8	49.0	17	22	AAAB0180	Oligonucleotide by
C 536	10	50.0	21	22	AAFP66430	Human gene single	C 609	9.8	49.0	17	23	ABK01367	Human NOGO Inozyme
C 537	10	50.0	21	22	AAFP66433	Human gene single	C 610	9.8	49.0	17	24	ABN07422	Human GDMLP-1 17-m
C 538	10	50.0	21	22	AAFP97300	Human gene single	C 611	9.8	49.0	17	24	ABN07423	Human GDMLP-1 17-m
C 539	10	50.0	21	22	AAFP97529	Human gene single	C 612	9.8	49.0	17	24	ABN07424	Human GDMLP-1 17-m
C 540	10	50.0	21	23	ABD21805	Human ATM RB fragm	C 613	9.8	49.0	17	24	ABN07425	Human GDMLP-1 17-m
C 541	10	50.0	21	24	ABK54280	Nucleic acid seletc	C 614	9.8	49.0	17	24	ABN07426	Human GDMLP-1 17-m
C 542	10	50.0	21	24	ABK14157	Chlorinated ethyle	C 615	9.8	49.0	17	24	ABK17747	Human ERG hammethe
C 543	10	50.0	22	22	AAH22273	OX40 reverse PCR p	616	9.8	49.0	17	24	ABK17748	Human ERG hammethe
C 544	10	50.0	22	24	ABK51325	Human NOV2 protei	617	9.8	49.0	17	24	ABK18893	Human ERG DNAzyme
C 545	10	50.0	23	20	AAAX01739	Human GDMPR-beta c	C 618	9.8	49.0	18	16	AAQ91469	Mouse cyclooxygena
C 546	10	50.0	23	21	AAZ45300	Oligonucleotide us	C 619	9.8	49.0	18	17	AAI44572	Antisense oligo HU
C 547	10	50.0	23	21	ABAP90582	Lactococcus lactis	C 620	9.8	49.0	18	20	AAZ27846	PCR primer for hum
C 548	10	50.0	24	14	AAQ43318	Sequence of sense	C 621	9.8	49.0	18	22	AAAD21087	Dishevelled-2 PCR p
C 549	10	50.0	24	19	AAV29173	Ciliary neurotroph	C 622	9.8	49.0	18	22	AAAD21088	Mammalian PAC93.1
C 550	10	50.0	24	20	AAZ23722	M. foexilis Cytb p	C 623	9.8	49.0	18	22	AAAT1687	Human Survivin ant
C 551	10	50.0	24	21	AAAT9357	Primer for cloning	C 624	9.8	49.0	18	22	AAAT79616	Human Akt-3 antisense
C 552	10	50.0	24	22	AAH19015	Reverse primer use	C 625	9.8	49.0	19	18	AAAT7275	Capped RNA based o
C 553	10	50.0	24	22	AAAT91265	GLAV-5 nucleotide	C 626	9.8	49.0	19	18	AAAT7275	Capped RNA based o
C 554	10	50.0	24	22	ABN84058	Gene highly expres	C 627	9.8	49.0	19	19	AAV0474	Cantine beta-3 adre
C 555	10	50.0	24	24	AB183676	Capture oligonucle	628	9.8	49.0	19	21	AAAB2753	Cdk3 ribozyme bind
C 556	10	50.0	24	24	AB183677	Capture oligonucle	629	9.8	49.0	19	21	AAAB4364	Cyclin D2 ribozyme
C 557	10	50.0	24	24	AB184330	Capture oligonucle	630	9.8	49.0	19	21	AAAB4365	Cyclin D2 ribozyme
C 558	10	50.0	24	24	AB184331	Capture oligonucle	C 631	9.8	49.0	19	21	AAAB4366	Cyclin D2 ribozyme
C 559	10	50.0	24	24	AB184338	Capture oligonucle	C 632	9.8	49.0	19	21	AAAB4367	Cyclin D2 ribozyme
C 560	10	50.0	24	24	AB184339	Capture oligonucle	633	9.8	49.0	19	22	AAH57915	Cell-cycle depende
C 561	10	50.0	24	24	AB186726	Capture oligonucle	634	9.8	49.0	19	22	AAH59526	Cyclin D2 ribozyme
C 562	10	50.0	24	24	AB186727	Capture oligonucle	635	9.8	49.0	19	22	AAH59527	Cyclin D2 ribozyme
C 563	10	50.0	24	24	AB187280	Capture oligonucle	636	9.8	49.0	19	22	AAH59528	Cyclin D2 ribozyme
C 564	10	50.0	24	24	AB187281	Capture oligonucle	C 637	9.8	49.0	19	22	AAAD08001	Cyclin D2 ribozyme
C 565	10	50.0	24	24	AB187282	Capture oligonucle	638	9.8	49.0	19	24	ABN81123	Cyclin D2 ribozyme
C 566	10	50.0	24	24	AB187612	Capture oligonucle	C 639	9.8	49.0	19	24	ABN81123	Cyclin D2 ribozyme
C 567	10	50.0	25	13	AAQ23152	Capture oligonucle	C 640	9.8	49.0	19	24	ABN80409	Primer PHE-04 used
C 568	10	50.0	25	15	AAQ73520	HPV 11 specific pr	641	9.8	49.0	19	24	ABN80411	Cell-cycle depende
C 569	10	50.0	25	16	AAQ80579	AlpHa-adducin cDNA	C 642	9.8	49.0	20	12	ABL88854	Cyclin D2 ribozyme
C 570	10	50.0	25	16	AAQ75393	M. tuberculosis IS6	C 643	9.8	49.0	20	14	AAQ47770	Cyclin D2 ribozyme
C 571	10	50.0	25	17	AAQ75393	M. tuberculosis IS6	C 644	9.8	49.0	20	14	AAQ47770	Cyclin D2 ribozyme
C 572	10	50.0	25	17	AAQ75393	M. tuberculosis IS6	C 645	9.8	49.0	20	14	AAQ47770	Cyclin D2 ribozyme
C 573	10	50.0	25	19	AAV36478	Human papillomavir	C 646	9.8	49.0	20	16	AAQ84860	Urea-plasma uealyti
C 574	10	50.0	25	19	AAV36478	Human papillomavir	C 647	9.8	49.0	20	16	AAQ84860	Urea-plasma uealyti
C 575	10	50.0	25	21	AAAC96261	Nucleotide sequenc	C 648	9.8	49.0	20	16	AAQ84860	Urea-plasma uealyti
C 576	10	50.0	25	21	AAAC96262	HLA DPAl gene PCR	C 649	9.8	49.0	20	17	AAAT16444	PCR primer TAP98
C 577	10	50.0	25	21	AAZ40619	Human vWF gene spe	C 650	9.8	49.0	20	18	AAAT16444	PCR primer TAP98
C 578	10	50.0	25	22	AAI62267	Soybean 318013 reg	C 651	9.8	49.0	20	18	AAAT16444	PCR primer TAP98
C 579	10	50.0	25	22	AAAD03599	IAF-like protein-3	C 652	9.8	49.0	20	20	AAZ03157	PCR primer used to
C 580	10	50.0	25	22	AAAC92017	PCR primer OLI03	C 653	9.8	49.0	20	20	AAZ03157	PCR primer used to
C 581	10	50.0	25	24	ABK97188	Human P53 #1-s-5'B	C 654	9.8	49.0	20	20	AAZ03157	PCR primer used to
C 582	10	50.0	25	24	ABK97188	Human P53 #1-s-5'B	C 655	9.8	49.0	20	20	AAZ03157	PCR primer used to
C 583	10	50.0	25	24	ABK97188	Human P53 #1-s-5'B	C 656	9.8	49.0	20	20	AAZ03157	PCR primer used to
C 584	10	50.0	25	24	ABK97188	Human P53 #1-s-5'B	C 657	9.8	49.0	20	20	AAZ03157	PCR primer used to
C 585	9.8	49.0	13	23	ABK46416	Brevibacterium fla	C 658	9.8	49.0	20	21	AAAC62719	Human OB gene sequ
C 586	9.8	49.0	13	23	ABK46416	Oligonucleotide SE	C 659	9.8	49.0	20	21	AAAC62719	Human OB gene sequ
C 587	9.8	49.0	15	16	AAAT54209	Oligonucleotide SE	C 660	9.8	49.0	20	21	AAAC62719	Human OB gene sequ
C 588	9.8	49.0	15	16	AAAT54209	Human IL-5 hamme	C 661	9.8	49.0	20	21	AAAC62719	Human OB gene sequ
C 589	9.8	49.0	17	15	AAQ57189	Human IGRB allele	C 662	9.8	49.0	20	21	AAAC62719	Human OB gene sequ
C 590	9.8	49.0	17	17	AAAT81639	Enzymatic RNA mole	C 663	9.8	49.0	20	22	AAAF82429	Human OB gene sequ
C 591	9.8	49.0	17	17	AAAT81639	Human c-myb hamme	C 664	9.8	49.0	20	22	AAAF82429	Human OB gene sequ
C 592	9.8	49.0	17	21	AAFP02720	Human c-myb hamme	C 665	9.8	49.0	20	22	AAAF82429	Human OB gene sequ
C 593	9.8	49.0	17	21	AAFP02721	Hammerhead ribozym	C 666	9.8	49.0	20	24	ABAS5150	Hammerhead ribozym
C 594	9.8	49.0	17	21	AAFP04366	Hammerhead ribozym	C 667	9.8	49.0	20	24	ABAS5150	Hammerhead ribozym

C 664	6.4	37.6	25	9	A1287960	QV01A07..x	C 737	6.2	36.5	19	17	A2816318	A2816318	2M0085E05
C 665	6.4	37.6	25	9	A1307712	LB36D07..x	738	6.2	36.5	19	17	A2826361	A2826361	2M0102H04
C 666	6.4	37.6	25	9	A1361952	QY37E02..x	739	6.2	36.5	19	17	A2839642	A2839642	2M0335C23
C 667	6.4	37.6	25	9	A1363940	QW34B12..x	740	6.2	36.5	19	17	A2854647	A2854647	2M0158B15
C 668	6.4	37.6	25	9	A1469251	EM07D09..x	741	6.2	36.5	19	17	A2864599	A2864599	2M0174G17
C 669	6.4	37.6	25	9	A1471126	LF90E05..x	742	6.2	36.5	19	17	A2991317	A2991317	2M0275K24
C 670	6.4	37.6	25	9	A1521520	LO64D05..x	743	6.2	36.5	20	13	BM395725	BM395725	5009-0-10
C 671	6.4	37.6	25	9	A1527253	UJ50E07..x	744	6.2	36.5	20	13	BM396970	BM396970	5009-0-27
C 672	6.4	37.6	25	9	A1559609	LF58C02..x	745	6.2	36.5	20	13	BM398685	BM398685	5009-0-48
C 673	6.4	37.6	25	9	A1555893	LF93G08..x	746	6.2	36.5	20	13	BM399285	BM399285	5009-0-56
C 674	6.4	37.6	25	9	A1565902	LF93H08..x	747	6.2	36.5	20	13	BM400059	BM400059	5009-0-65
C 675	6.4	37.6	25	9	A1569102	LF93H08..x	748	6.2	36.5	20	14	C01581	C01581	HTMG5000858
C 676	6.4	37.6	25	9	A1664044	UE73E05..x	749	6.2	36.5	20	17	A2307483	A2307483	1M0009P10
C 677	6.4	37.6	25	9	A1669456	LY32H08..x	750	6.2	36.5	20	17	A2339930	A2339930	1M0071E07
C 678	6.4	37.6	25	9	A1744919	LF17B09..x	751	6.2	36.5	20	17	A2391065	A2391065	1M0152H20
C 679	6.4	37.6	25	12	BM399263	BM399263	752	6.2	36.5	20	17	A2489135	A2489135	1M0315B15
C 680	6.4	37.6	25	13	BM399181	BM399181	753	6.2	36.5	20	17	A2491509	A2491509	1M0325B09
C 681	6.4	37.6	25	14	H41677	H41677	754	6.2	36.5	20	17	A2626475	A2626475	1M0466E16
C 682	6.4	37.6	25	17	A2329925	A2329925	755	6.2	36.5	20	17	A2764505	A2764505	1M0560M06
C 683	6.4	37.6	25	17	A2335705	A2335705	756	6.2	36.5	20	17	A2793050	A2793050	2M0045M15
C 684	6.4	37.6	25	17	A2357277	A2357277	757	6.2	36.5	20	17	A2822878	A2822878	2M0096E02
C 685	6.4	37.6	25	17	A2414090	A2414090	758	6.2	36.5	20	17	A2827842	A2827842	2M0104F03
C 686	6.4	37.6	25	17	A2471181	IM0285H11	759	6.2	36.5	20	17	A2830285	A2830285	2M0109N22
C 687	6.4	37.6	25	17	A2510562	IM0355F11	760	6.2	36.5	20	17	A2864535	A2864535	2M0174J12
C 688	6.4	37.6	25	17	A2513486	IM0359A04	761	6.2	36.5	20	17	BSM00478	BSM00478	2M0288C21
C 689	6.4	37.6	25	17	A2515233	IM0055A14	762	6.2	36.5	21	2	HSM003692	HSM003692	2M0288C21
C 690	6.4	37.6	25	17	A2566311	IM0428G09	763	6.2	36.5	21	9	AU255698	AU255698	2M0288C21
C 691	6.4	37.6	25	17	A2606311	IM0428G09	764	6.2	36.5	21	9	AU255698	AU255698	2M0288C21
C 692	6.4	37.6	25	17	A2610030	IM0435A10	765	6.2	36.5	21	9	AU256158	AU256158	2M0288C21
C 693	6.4	37.6	25	17	A2621312	IM0454P19	766	6.2	36.5	21	13	BM399877	BM399877	5009-0-51
C 694	6.4	37.6	25	17	A2769533	IM0570D22	767	6.2	36.5	21	13	BM399877	BM399877	5009-0-51
C 695	6.4	37.6	25	17	A2782317	2M0032E01	768	6.2	36.5	21	17	A2309344	A2309344	1M0013A20
C 696	6.4	37.6	25	17	A2789794	2M0037J21	769	6.2	36.5	21	17	A2309732	A2309732	1M016K01
C 697	6.4	37.6	25	17	A2805210	2M0066D23	770	6.2	36.5	21	17	A2342046	A2342046	1M0074F23
C 698	6.4	37.6	25	17	A2807605	2M0070L05	771	6.2	36.5	21	17	A2387187	A2387187	1M0146L22
C 699	6.4	37.6	25	17	A2837511	2M0132N17	772	6.2	36.5	21	17	A2405188	A2405188	1M0173G15
C 700	6.4	37.6	25	17	A2843703	2M0142L09	773	6.2	36.5	21	17	A2766315	A2766315	1M0563K14
C 701	6.4	37.6	25	17	A2943422	2M0204P06	774	6.2	36.5	21	17	A2801236	A2801236	2M0059C12
C 702	6.4	37.6	25	17	A2958306	2M0225H23	775	6.2	36.5	21	17	A2802584	A2802584	2M0061I05
C 703	6.4	37.6	25	17	A2976143	2M0251F21	776	6.2	36.5	21	17	A2831993	A2831993	2M0112M01
C 704	6.4	37.6	25	17	A2979740	2M0256I01	777	6.2	36.5	21	17	A2967090	A2967090	2M0237D24
C 705	6.4	37.6	25	17	BH851787	BH851787	778	6.2	36.5	21	17	A1285579	A1285579	2M0237D24
C 706	6.4	37.6	25	17	BH857067	SAK 0735	779	6.2	36.5	22	9	A1285579	A1285579	2M0237D24
C 707	6.4	37.6	25	17	TA114E04P	TA114E04P	780	6.2	36.5	22	9	A1285579	A1285579	2M0237D24
C 708	6.4	37.6	25	17	TA207E09P	TA207E09P	781	6.2	36.5	22	9	A1285579	A1285579	2M0237D24
C 709	6.4	37.6	25	17	TA261003Q	TA261003Q	782	6.2	36.5	22	10	AW250395	AW250395	2M0237D24
C 710	6.4	37.6	25	17	TA296802Q	TA296802Q	783	6.2	36.5	22	12	BF979698	BF979698	602288551
C 711	6.4	37.6	25	17	TA324F07P	TA324F07P	784	6.2	36.5	22	13	BM395131	BM395131	50072-2-7
C 712	6.4	37.6	25	17	TA330H09Q	TA330H09Q	785	6.2	36.5	22	13	BM396056	BM396056	5009-0-16
C 713	6.4	37.6	25	17	TA376H10	TA376H10	786	6.2	36.5	22	13	BM398285	BM398285	5009-0-43
C 714	6.4	37.6	25	17	TA383N06P	TA383N06P	787	6.2	36.5	22	13	BM400906	BM400906	5009-0-80
C 715	6.4	37.6	25	17	TA3G07P	TA3G07P	788	6.2	36.5	22	13	BM401082	BM401082	5009-0-82
C 716	6.4	37.6	25	17	TA48G07Q	TA48G07Q	789	6.2	36.5	22	17	A2323601	A2323601	1M0045C11
C 717	6.2	36.5	14	13	BM398341	5009-0-44	790	6.2	36.5	22	17	A2323922	A2323922	1M0045D10
C 718	6.2	36.5	14	13	BM398814	5009-0-5-	791	6.2	36.5	22	17	A2330582	A2330582	1M0056F05
C 719	6.2	36.5	15	10	BM400407	5009-0-72	792	6.2	36.5	22	17	A2331565	A2331565	1M0059M06
C 720	6.2	36.5	16	13	BM400077	5009-0-28	793	6.2	36.5	22	17	A2343245	A2343245	1M0063K01
C 721	6.2	36.5	17	13	BM396959	5009-0-42	794	6.2	36.5	22	17	A2453635	A2453635	1M0238008
C 722	6.2	36.5	18	13	BM398259	5009-0-85	795	6.2	36.5	22	17	A2452777	A2452777	1M0252N14
C 723	6.2	36.5	18	13	BM401885	5009-0-85	796	6.2	36.5	22	17	A2462641	A2462641	1M0269M08
C 724	6.2	36.5	18	13	BM401332	5009-0-85	797	6.2	36.5	22	17	A2468023	A2468023	1M0279L15
C 725	6.2	36.5	18	14	BM675715	TOH602767	798	6.2	36.5	22	17	A2492512	A2492512	1M0326K08
C 726	6.2	36.5	19	9	A1251781	QU76501..x	799	6.2	36.5	22	17	A2581821	A2581821	1M0370L16
C 727	6.2	36.5	19	9	A1433460	AL61650	800	6.2	36.5	22	17	A2595064	A2595064	1M0407L23
C 728	6.2	36.5	19	9	A1641650	BM396264	801	6.2	36.5	22	17	A2666085	A2666085	1M0547G21
C 729	6.2	36.5	19	13	BM399863	5009-0-19	802	6.2	36.5	22	17	A2774731	A2774731	2M0004M18
C 730	6.2	36.5	19	13	BM399863	5009-0-62	803	6.2	36.5	22	17	A2797063	A2797063	2M0053M03
C 731	6.2	36.5	19	17	A2307864	1M0010P16	804	6.2	36.5	22	17	A2798235	A2798235	2M0054O19
C 732	6.2	36.5	19	17	A2358153	1M0100L23	805	6.2	36.5	22	17	A2801946	A2801946	2M0060E07
C 733	6.2	36.5	19	17	A2452087	1M0251F18	806	6.2	36.5	22	17	A2831937	A2831937	2M0111P22
C 734	6.2	36.5	19	17	A2482658	1M0307L16	807	6.2	36.5	22	17	A2953028	A2953028	2M0225U03
C 735	6.2	36.5	19	17	A2591563	1M0402P23	808	6.2	36.5	22	17	A2958390	A2958390	2M0225U07
C 736	6.2	36.5	19	17	A2651870	1M0522M15	809	6.2	36.5	22	17	TA160D07Q	TA160D07Q	2M0225U07

C 813	9.8	49.0	25	24	ABN12319	Human GDM1P-1 25-m	886	9.6	48.0	20	21	AAA55777	Human DNA methyl
C 814	9.8	49.0	25	24	ABN12320	Human GDM1P-1 25-m	887	9.6	48.0	20	21	AAA55778	Human DNA methyl
C 815	9.8	49.0	25	24	ABN12321	Human GDM1P-1 25-m	888	9.6	48.0	20	21	AAA55779	Human DNA methyl
C 816	9.8	49.0	25	24	ABN12322	Human GDM1P-1 25-m	889	9.6	48.0	20	21	AAA40906	Human TNFalpha ant
C 817	9.8	49.0	25	24	ABN12323	Human GDM1P-1 25-m	890	9.6	48.0	20	21	AAA40907	Human TNFalpha ant
C 818	9.8	49.0	25	24	ABN12324	Human GDM1P-1 25-m	891	9.6	48.0	20	21	AAA40908	Human TNFalpha ant
C 819	9.8	49.0	25	24	ABN12325	Human GDM1P-1 25-m	892	9.6	48.0	20	21	AAA40909	Human TNFalpha ant
C 820	9.8	49.0	25	24	ABN12326	Human GDM1P-1 25-m	893	9.6	48.0	20	21	AAA40910	Human TNFalpha ant
C 821	9.6	48.0	13	23	ABC48216	Oligonucleotide SE	894	9.6	48.0	20	22	AAH14793	Human glycogen bsn
C 822	9.6	48.0	13	23	ABC48217	Oligonucleotide SE	895	9.6	48.0	20	22	AAH42643	PCR primer and pro
C 823	9.6	48.0	13	23	ABC58176	Oligonucleotide SE	896	9.6	48.0	20	22	AAH81076	Oligonucleotide hy
C 824	9.6	48.0	13	23	ABC58177	Oligonucleotide SE	897	9.6	48.0	20	22	AAH81081	Oligonucleotide hy
C 825	9.6	48.0	17	18	AAH74549	Mouse flt-1 VEGF r	898	9.6	48.0	20	22	AAH08874	C. glutamicum bnf
C 826	9.6	48.0	17	18	AAH74550	Mouse flt-1 VEGF r	899	9.6	48.0	20	22	AAH21118	C. glutamicum bnf
C 827	9.6	48.0	17	18	AAH74492	Mouse flt-1 VEGF r	900	9.6	48.0	20	22	AAH25250	Antisense oligonuc
C 828	9.6	48.0	17	18	AAH74493	Mouse flt-1 VEGF r	901	9.6	48.0	20	22	AAH61241	C. glutamicum tran
C 829	9.6	48.0	17	18	AAH68743	Human flt1 VEGF re	902	9.6	48.0	20	22	AAH81142	Primer used for se
C 830	9.6	48.0	17	18	AAH68744	Human flt1 VEGF re	903	9.6	48.0	20	22	AAH16543	Gaeric acid produ
C 831	9.6	48.0	17	18	AAH68745	Human flt1 VEGF re	904	9.6	48.0	20	22	AAH16534	Gaeric acid produ
C 832	9.6	48.0	18	20	AAH201230	PCR primer for pgl	905	9.6	48.0	20	22	AAH49334	C. glutamicum ATCC
C 833	9.6	48.0	18	20	AAH58775	Primer NZArandom u	906	9.6	48.0	20	24	AAH43466	Human tissue kall
C 834	9.6	48.0	18	21	AAH40925	Human TNFalpha ant	907	9.6	48.0	20	24	ABK40363	Forward PCR primer
C 835	9.6	48.0	18	21	AAH40926	Human TNFalpha ant	908	9.6	48.0	20	24	AAH3198	DRbeta gene, DRB1
C 836	9.6	48.0	18	21	AAH40927	Human TNFalpha ant	909	9.6	48.0	20	24	AAH59633	Telemetase reverse
C 837	9.6	48.0	18	22	AAH59336	Sample member clus	910	9.6	48.0	20	24	AAH05857	Corynebacterium th
C 838	9.6	48.0	18	24	AAH57627	Mouse G protein-co	911	9.6	48.0	20	24	AAH23891	Human transferrin
C 839	9.6	48.0	19	12	AAH13538	Probe JFL326 to co	912	9.6	48.0	20	24	ABH93378	Capture oligonucle
C 840	9.6	48.0	19	12	AAH13539	Probe JFL326 to co	913	9.6	48.0	20	24	ABH93378	Capture oligonucle
C 841	9.6	48.0	19	12	AAH13540	Probe JFL326 to co	914	9.6	48.0	20	24	ABH93380	Capture oligonucle
C 842	9.6	48.0	19	15	AAH071141	Merlin exon 12A pr	915	9.6	48.0	20	24	ABH94403	Capture oligonucle
C 843	9.6	48.0	19	18	AAH01327	S-antigen PCR prim	916	9.6	48.0	20	24	ABH95868	Human chromosome 1
C 844	9.6	48.0	19	21	AAH43390	Human biallelic ma	917	9.6	48.0	20	24	ABH45096	Human growth hormo
C 845	9.6	48.0	19	21	AAH43390	Cyclin D3 ribozyme	918	9.6	48.0	21	16	AAH01401	Human growth hormo
C 846	9.6	48.0	19	21	AAH43390	Hepatitis B virus	919	9.6	48.0	21	18	AAH12446	Growth hormone rec
C 847	9.6	48.0	19	22	AAH59552	Cyclin D3 ribozyme	920	9.6	48.0	21	19	AAH33840	Human growth hormo
C 848	9.6	48.0	19	24	ABH88864	HIV-1 related bind	921	9.6	48.0	21	19	AAH52697	Hepatocyte nuclear
C 849	9.6	48.0	19	24	ABH88864	HIV-1 related bind	922	9.6	48.0	21	19	AAH67344	Nucleotide fragmen
C 850	9.6	48.0	20	12	AAH13444	Probe to wild-type	923	9.6	48.0	21	21	AAH38264	Histocompatibility
C 851	9.6	48.0	20	12	AAH13444	Probe to mutant co	924	9.6	48.0	21	21	AAH299458	PCR primer 25182-2
C 852	9.6	48.0	20	12	AAH13446	Probe to mutant co	925	9.6	48.0	21	22	AAH23940	5. spilitivorum al
C 853	9.6	48.0	20	12	AAH13451	Probe to mutant co	926	9.6	48.0	21	22	AAH58829	Human gene single
C 854	9.6	48.0	20	12	AAH13452	Probe to mutant co	927	9.6	48.0	21	23	ABH10137	Tail primer #130 f
C 855	9.6	48.0	20	13	AAH24485	Oligonucleotide #1	928	9.6	48.0	21	24	ABH91965	Botulin toxin gene
C 856	9.6	48.0	20	13	AAH24485	Cruciferous promot	929	9.6	48.0	21	24	ABH83533	RXR-alpha PCR prim
C 857	9.6	48.0	20	16	AAH095410	Primer B (Group 2,	930	9.6	48.0	21	24	AAH030310	Human PDI gene mu
C 858	9.6	48.0	20	16	AAH095410	Primer A5 (Group 4	931	9.6	48.0	21	21	AAH005319	Probe to DNA encod
C 859	9.6	48.0	20	16	AAH095410	Primer A5 (Group 4	932	9.6	48.0	22	18	AAH89915	Human inflammatory
C 860	9.6	48.0	20	19	AAH57186	Human Notch-3 muta	933	9.6	48.0	22	22	AAH37494	SNP specific lower
C 861	9.6	48.0	20	19	AAH57186	Human Notch-3 muta	934	9.6	48.0	22	22	AAH01519	dhfrXV resistance
C 862	9.6	48.0	20	19	AAH57186	Human Notch-3 muta	935	9.6	48.0	22	22	AAH01519	Human nerve growth
C 863	9.6	48.0	20	19	AAH57186	Human Notch-3 muta	936	9.6	48.0	22	22	AAH01519	Human nerve growth
C 864	9.6	48.0	20	19	AAH57186	Human Notch-3 muta	937	9.6	48.0	22	22	AAH01519	Human nerve growth
C 865	9.6	48.0	20	20	AAH23613	C. rastoni hemoly	938	9.6	48.0	22	22	AAH74302	Canine interleukin
C 866	9.6	48.0	20	20	AAH23614	C. rastoni hemoly	939	9.6	48.0	22	22	AAH74302	Primer #11. Homo
C 867	9.6	48.0	20	20	AAH23614	Oligonucleotide #7	940	9.6	48.0	22	22	AAH74302	Human multi drug r
C 868	9.6	48.0	20	20	AAH23614	Oligonucleotide #7	941	9.6	48.0	22	22	AAH74302	GBV-B oligonucleot
C 869	9.6	48.0	20	20	AAH23614	Oligonucleotide #1	942	9.6	48.0	22	22	AAH74302	Gaeric acid produ
C 870	9.6	48.0	20	20	AAH23614	PCR primer used to	943	9.6	48.0	22	24	AAH42842	UFD-associatd PC
C 871	9.6	48.0	20	20	AAH23614	PCR primer used to	944	9.6	48.0	23	19	AAH40978	Plasmodium falcipar
C 872	9.6	48.0	20	20	AAH23614	PCR primer used to	945	9.6	48.0	23	19	AAH40978	Primer ALH1.391L23
C 873	9.6	48.0	20	20	AAH23614	PCR primer used to	946	9.6	48.0	23	19	AAH40978	Oligonucleotide W
C 874	9.6	48.0	20	20	AAH23614	PCR primer used to	947	9.6	48.0	23	20	AAH30245	PCR amplification
C 875	9.6	48.0	20	20	AAH23614	PCR primer used to	948	9.6	48.0	23	22	AAH16544	Gaeric acid produ
C 876	9.6	48.0	20	20	AAH23614	PCR primer used to	949	9.6	48.0	23	22	AAH16544	Btll PCR primer #3
C 877	9.6	48.0	20	20	AAH23614	PCR primer used to	950	9.6	48.0	23	24	AAH23614	Human ACE-2 exon 1
C 878	9.6	48.0	20	20	AAH23614	PCR primer used to	951	9.6	48.0	24	14	AAH23614	Non-coding strand
C 879	9.6	48.0	20	20	AAH23614	PCR primer used to	952	9.6	48.0	24	15	AAH23614	6-O-methyldeoxygua
C 880	9.6	48.0	20	20	AAH23614	PCR primer used to	953	9.6	48.0	24	16	AAH23614	PX amplification p
C 881	9.6	48.0	20	21	AAH23614	Human ras oncogene	954	9.6	48.0	24	16	AAH23614	Tumorinhibitory inh
C 882	9.6	48.0	20	21	AAH23614	Human biallelic ma	955	9.6	48.0	24	19	AAH23614	Presentin-2 alter
C 883	9.6	48.0	20	21	AAH23614	Lama2/APPA transge	956	9.6	48.0	24	20	AAH23614	Antisense oligonuc
C 884	9.6	48.0	20	21	AAH23614	Hepatitis B virus	957	9.6	48.0	24	20	AAH23614	Target sequence
C 885	9.6	48.0	20	21	AAH23614	Hepatitis B virus	958	9.6	48.0	24	21	AAH23614	Nucleotide sequenc

XX The invention relates to a method of detecting and quantifying fungi and
CC bacteria, involving obtaining a sequence of the microorganism to be
CC detected and quantified, extracting the DNA from the sample, and
CC subjecting the DNA to polymerase chain reaction (PCR) and fluorescent
CC probe analysis. The method is useful for identifying and quantifying
CC specific fungi and bacteria using specific DNA sequences. The specific
CC DNA sequences are useful for the real time detection of PCR products with
CC a fluorescent probe system or other molecular probes like hybridisation.
CC ABK29026-ABK29474 represent fungal and bacterial PCR primers and probes
CC used in the method of the invention.

XX Sequence 25 BP; 9 A; 5 C; 5 G; 6 T; 0 other;

Query Match 75.0%; Score 15; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GTTTGCCACTCAG 20
1 GTTTGCCACTCAG 15

RESULT 3

AAH56097 standard; DNA; 24 BP.

AAH56097;

04-SBP-2001 (first entry)

Human SCN3A PCR-SSCP PCR primer SEQ ID NO:341.

Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
anticonvulsant; neuroprotective; PCR primer; ss.

Homo sapiens.
Synthetic.

MO200135564-A2.

31-MAY-2001.

24-NOV-2000; 2000MO-CA01404.

26-NOV-1999; 99US-0167623.

(UYMC-) UNIV MCGILL.

Rouleau GA, LaFreniere RG, Rochefort D, Coesette F, Ragsdale D;

WPI; 2001-355945/37.

Determining a predisposition to epilepsy and/or development of epilepsy
PT comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a
PT DNA variant, equivalent, or mutation which shows a linkage
PT disequilibrium -

Example 5; Fig 6; 268pp; English.

XX The present invention describes a method (M1) of determining an
CC individual's predisposition to epilepsy and/or development of epilepsy,
CC as well as predicting the individual's response to medication. The
CC method comprises determining the genotype of at least one gene selected
CC from SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation
CC which shows a linkage disequilibrium. SCN1A, SCN2A and SCN3A are all
CC sodium channel genes located on chromosome 2. The idiopathic generalised
CC epilepsy (IGE) gene is more specifically localised on chromosome
CC 2q23-q31. Compounds identified as modulators of the biological activity
CC of SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating
CC epilepsy or other neurological disorders. They have anticonvulsant and
CC neuroprotective activities. AAH5763 to AAH56164 and AAB99674 to

CC AAB99679 represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR
CC primers, oligonucleotides and proteins given in the exemplification of
CC the present invention.

XX Sequence 24 BP; 6 A; 5 C; 2 G; 10 T; 1 other;

Query Match 72.0%; Score 14.4; DB 22; Length 24;
Best Local Similarity 83.3%; Pred. No. 5.9e+02;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTGCGTTTGCCTCAG 18
6 TTTGCTTTATCTCAG 23

RESULT 4

AAC92656/c standard; DNA; 20 BP.

AAC92656;

27-MAR-2001 (first entry)

Human Nck-2 phosphorothioate antisense oligonucleotide, SEQ ID NO:17.

Human Nck-2; adapter protein; Nck adapter protein; hNck-beta; Grb4;
signal transduction; SH2 domain; SH3 domain; src homology domain;
integrin signalling; receptor tyrosine kinase signalling;
growth factor receptor signalling; PINCH; v-Abl; Ras; Sos;
transcriptional activation; cancer; tumour; leukaemia; breast cancer;
expression inhibition; phosphorothioate; antisense oligonucleotide; ss.

Homo sapiens.

US6165728-A.

26-DEC-2000.

19-NOV-1999; 99US-0444053.

19-NOV-1999; 99US-0444053.

(ISIS-) ISIS PHARM INC.

Ward DT, Cowseert LM;

WPI; 2001-090480/10.

Novel antisense compound which inhibits expression of human nck-2
PT useful for treating disease or condition associated with expression of
PT nck-2, and as research reagents, kits and diagnostics -

Claim 1; Column 41-42; 38pp; English.

XX Sequences AAC92649-C92728 represent antisense oligonucleotides
CC targeted to the human Nck-2 gene, which inhibit its expression.
CC The antisense oligonucleotides were designed to target different
CC regions of the human Nck-2 mRNA, and were analysed for their effect on
CC Nck-2 mRNA levels by quantitative real-time PCR. Nck-2 (also known
CC as Nck adapter protein, hNck-beta and Grb4), contains both SH2 and SH3
CC src homology domains and functions as an adapter protein in
CC integrin-mediated and receptor tyrosine kinase-mediated signal
CC transduction, particularly in growth factor receptor signalling.
CC Moreover, Nck-2 participates in pathways that connect growth factor
CC receptor signalling and integrin signalling via its interaction with
CC PINCH, a LIM domain-containing adapter protein which is involved in
CC integrin, growth factor and Wnt signalling pathways. Nck-2 also
CC interacts with EGF (epidermal growth factor) and PDGF (platelet-derived
CC growth factor) receptors, inhibiting EGF- and PDGF-stimulated DNA
CC synthesis in an SH2-dependent manner. Nck-2 is also able to interact with
CC v-Abl, Ras and Sos proteins to induce transcriptional activation, and is
CC therefore implicated in the development of cancer, particularly leukaemia
CC and breast cancer. The oligonucleotides of the invention are useful for

LOCUS	22 bp	DNA	linear	GSS 13-DEC-2000
DEFINITION	T. brucei shared genomic DNA clone 114g12, reverse sequence,			
ACCESSION	AL462379			
VERSION	AL462379.1 GI:11832660			
KEYWORDS	GSS.			
SOURCE	Trypanosoma brucei.			
ORGANISM	Trypanosoma brucei Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae;			
REFERENCE	1 (bases 1 to 22)			
AUTHORS	Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.			
TITLE	Direct Submission			
JOURNAL	Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk			
COMMENT	Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + 1 method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999). Email: nelsayed@tigr.org Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/ .			
FEATURES	location/Qualifiers			
source	1..22 /organism="Trypanosoma brucei" /strain="TREU927" /db_xref="taxon:5691" /clone="114g12"			
BASE COUNT	6 a 5 c 7 g 4 t			
ORIGIN				
Query Match	56.5%; Score 9.6; DB 17; Length 22;			
Best Local Similarity	75.0%; Pred. No. 6, 1e+05;			
Matches	12; Conservative 0; Mismatches 4; Indels 0; Gaps 0			
Qy	1 GTTGCTTCGGCGGGA 16 			
Db	2 GTTGATCGGACAGAA 17			
RESULT 6				
A2786547	24 bp DNA linear GSS 16-FEB-2001			
LOCUS	2M0032B10F Mouse 10kb plasmid UGCM library Mus musculus genomic			
DEFINITION	clone UGCM2M0032B10 F, DNA sequence.			
ACCESSION	A2786547			
VERSION	A2786547.1 GI:12924417			
KEYWORDS	GSS.			
SOURCE	house mouse.			
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE	1 (bases 1 to 24)			
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,M., Meenen,B., Pedersen,T., Reilly, M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A. and Wright,D., Weiss,R.			
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts			
JOURNAL	Unpublished (2000)			
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT			

Balliz, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddum@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0032 row: B column: 10
 Seq primer: GTTGTAAACGACGGCAGCT
 Class: plasmid ends
 High quality sequence stop: 24.
 Location/Qualifiers
 1. 24
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UTGCM0032B10"
 /clone_1kb="Mouse 10kb plasmid uTGCIM library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g11473114[9b]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

PI Draper KG, Dudycz LW, Holeczek JJ, Macejak DG, Mamine JA;
 PI MeSwiggen JA;
 XX WPI, 1993-386599/48.
 XX
 PT Enzymatic RNA molecules - used to inhibit viral replication,
 PT infection and gene expression
 XX
 PS Claim 5, Fig 8, 287pp; English.
 CC The sequences (AA050775-99) and (AA052551-8) are pref. hepatitis B
 CC virus target sequences for enzymatic RNA molecules. The RNA
 CC molecules are complementary to a substrate binding region in the
 CC specified gene target. They also have enzymatic activity, in that
 CC they specifically cleave RNA in the target. The ERMs interfere with
 CC viral replication and therefore have anti-viral properties. They can
 CC be used to attenuate viruses to be used in vaccines.
 XX
 SQ Sequence 17 BP; 4 A; 6 C; 4 G; 3 U; 0 other;
 QY
 Query Match 67.0%; Score 13.4; DB 14; Length 17;
 Best Local Similarity 93.3%; Pred. No. 1.8e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 DB 4 GCCTTGCCACTCAG 18
 15 GAGTTGCCACTCAG 1
 RESULT 7
 ID AAV35581/c
 ID AAV35581 standard; DNA; 24 BP.
 AC AAV35581,
 DT 04-SEP-1998 (first entry)
 XX
 XX STS probe GVI0 generating lower primer.
 DE
 XX Hydronephrosis gene; HNG gene; USF2 gene; renal disease; renal aplasia;
 KW vesical-ureteral reflux; pelvi-ureteral junction obstruction;
 KW multicystic renal dysplasia; renal agenesis; hydronephrosis; MMD;
 KW Von Mayer-Rokitansky-Kuester disorder; bifid ureter; STS probe;
 KW sequence tagged site; PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN K09815650-A2.
 XX
 PD 16-APR-1998.
 XX
 PF 09-OCT-1997; 97MO-EP05583.
 XX
 PR 09-OCT-1996; 96EP-0202820.
 XX
 PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
 XX
 PI Frysne JPCJ, Groenen PMA, Van De Ven WJM;
 XX
 DR WPI, 1998-240833/21.
 XX
 PT Hydronephrosis gene - useful to treat or diagnose renal diseases and
 PT disorders, e.g. vesical-ureteral reflux, pelvi-ureteral junction
 PT obstruction, multicystic renal dysplasia or renal agenesis
 XX
 PS Example 3; Page 46, 73pp; English.
 CC This primer is used for the generation of sequence tagged sites (STS)
 CC probes used for pinpointing chromosome 6 breakpoint. This was used for
 CC isolating the human hydronephrosis (HNG) gene of the invention. A
 CC translocation partner to this HNG gene on chromosome 6 is the
 CC chromosome 19 USF2 gene. The HNG gene can be used as a starting point

CC to design suitable compounds or techniques for the treatment of renal
 CC diseases or disorders, or nucleotide probes for diagnosing cells
 CC involved in renal diseases or disorders. A protein or a fragment
 CC encoded by HNG gene can be used as a starting point for preparing
 CC suitable antibodies for diagnosing cells involved in renal diseases and
 CC disorders. The products and method can be used to treat or diagnose
 CC renal diseases and disorders selected from vesical-ureteral reflux,
 CC uni or bilateral pelvi-ureteral junction obstruction, multicystic renal
 CC dysplasia (MMD), renal agenesis, renal aplasia, hydronephrosis,
 CC Von Mayer-Rokitansky-Kuester disorder and bifid ureter.
 CC
 SQ Sequence 24 BP; 3 A; 6 C; 8 G; 7 T; 0 other;
 QY
 Query Match 67.0%; Score 13.4; DB 19; Length 24;
 Best Local Similarity 93.3%; Pred. No. 1.9e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 DB 6 GTTGGCCACTCAG 20
 23 GTTGGCCACTCAG 9
 RESULT 8
 ID AAK98779/c
 ID AAK98779 standard; DNA; 23 BP.
 AC AAK98779;
 DT 13-MAY-2002 (first entry)
 XX
 XX Antisense primer for amplification of ADAMTS-SI.
 DE
 XX
 KW Antiarthritic; osteopathic; antirheumatic; antiinflammatory; nocrotic;
 KW antiasthmatic; neuromodulator; cyostatic; vasotropic;
 KW antiallergic; dermatological; antiarteriosclerotic; cerebroprotective;
 KW cardiant; immunosuppressive; anticonvulsant; antiparkinsonian; analgesic;
 KW antimigraine; antidepressant; ophthalmological; vulnery; antidiabetic;
 KW antifertility; a disintegrin and metalloprotease thrombospondin domain;
 KW ADAMTS; ADAMTS-SI agonist; antagonist; bioregulatory; gene therapy;
 KW arthritis; inflammatory bowel disease; Crohn's disease; atherosclerosis;
 KW peridontal disease; emphysema; acute respiratory distress syndrome;
 KW asthma; chronic obstructive pulmonary disease; Alzheimer's disease;
 KW organ transplant toxicity; rejection; cachexia; allergy; restenosis;
 KW cancer; tissue ulcerations; epidermolysis bullosa; aortic aneurysm;
 KW osteoporosis; artificial joint implant; congestive heart failure; stroke;
 KW myocardial infarction; cerebral ischemia; head trauma; corneal injury;
 KW spinal cord injury; neurodegenerative disease; autoimmune disorder;
 KW Huntington's disease; Parkinson's disease; migraine; multiple sclerosis;
 KW depression; peripheral neuropathy; pain; cerebral amyloid angiopathy;
 KW nocrotic; cognition enhancement; amyotrophic lateral sclerosis;
 KW ocular angiogenesis; macular degeneration; abnormal wound healing; burn;
 KW infertility; diabetic shock; chondrocyte; osteoarthritis; OA; cartilage;
 KW proinflammatory cytokine; human; PCR; primer; ss.
 XX
 OS Homo sapiens.
 OS
 PN EP1136547-A2.
 XX
 PD 26-SEP-2001.
 XX
 PF 21-MAR-2001; 2001EP-0302634.
 XX
 PR 22-MAR-2000; 2000US-191382P.
 XX
 PA (PFIZ) PFIZER PROD INC.
 XX
 PI Buckbinder L, Mitchell PG, Schaefer JF, Walsh RT;
 XX
 DR WPI, 2002-229167/29.
 XX
 PT Novel isolated polynucleotide encoding A Disintegrin And
 PT Metalloprotease family of metalloproteases, containing thrombospondin
 PT domain, termed ADAMTS-SI, useful for diagnostic, bioregulatory or gene

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF19072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

0 a 5 c 11 g 4 t

Query Match 54.1%; Score 9.2; DB 17; Length 20;
Best Local Similarity 78.6%; Pred. No. 9.8e+05;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTGCTGCGCGG 14
|||
4 GTTGCTGCGCGG 17

RESULT 10
TAT5A030 24 bp DNA linear GSS 13-DEC-2000
LOCUS TAT5A030
DEFINITION T. brucei sheared genomic DNA clone 75a03, reverse sequence,
ACCESSION AL458585
VERSION AL458585.1 GI:11860119
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei.
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 24)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Alkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct SubMISSION
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhle@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nleay@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source
1. 24
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="75a03"

BASE COUNT

2 a 4 c 6 g 12 t

ORIGIN
Query Match 54.1%; Score 9.2; DB 17; Length 24;
Best Local Similarity 78.6%; Pred. No. 1e+06;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

BASE COUNT

1 GTTGCTGCGCGG 14
|||
5 GTTGCTGCGTAG 18

BASE COUNT

3 a 8 c 9 g 5 t

ORIGIN
Query Match 54.1%; Score 9.2; DB 9; Length 25;
Best Local Similarity 78.6%; Pred. No. 1e+06;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GTTGCGCGCGAAC 17
|||
7 GTTGCTGCTGGTAC 20

BASE COUNT

25 bp DNA linear GSS 13-JUN-2002

RESULT 12
BH854200 25 bp DNA linear GSS 13-JUN-2002
LOCUS BH854200
DEFINITION SALX 078881.34.80.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALX_078881.34.80.x, DNA

RESULT 11

A1594892 25 bp mRNA linear EST 21-APR-1999

LOCUS

A1594892
ve12c06.x1 Soares mouse NBMH Mus musculus cDNA clone IMAGE:817930
3' similar to SW:SWR_PAT 009429 SULFONYLUREA RECEPTOR. [1] ;, mRNA
sequence.

ACCESSION

A1594892
A1594892.1 GI:4603940

VERSION

A1594892
EST.
house mouse.
Mus musculus

KEYWORDS

house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 25)
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person
B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Rutter
E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999

UNPUBLISHED

Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

COMMENT

Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MG1:486210
This clone was previously sequenced on the 5' end only, this new
data is from the 3' end
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
High quality sequence stop: 1.

LOCATION/QUALIFIERS

1. 25
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:817930"
/clone_lib="Soares mouse NBMH"
/sex="male"
/tissue_type="heart"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Vector: pRT3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer (5'
TGTTACCAATCTGAGTGGAGCGCGCGCGCGCAAGTTTCTTTTCTTTT
3') ; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pRT3D vector. RNA
constructed by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Benito Soares and M. Patricia
Bonaldo."

BASE COUNT

3 a 8 c 9 g 5 t

ORIGIN

Query Match 54.1%; Score 9.2; DB 9; Length 25;
Best Local Similarity 78.6%; Pred. No. 1e+06;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

BASE COUNT

4 GTTGCGCGCGAAC 17
|||
7 GTTGCTGCTGGTAC 20

BASE COUNT

25 bp DNA linear GSS 13-JUN-2002

LOCUS

BH854200 25 bp DNA linear GSS 13-JUN-2002
LOCUS BH854200
DEFINITION SALX 078881.34.80.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALX_078881.34.80.x, DNA

DEFINITION

SALX 078881.34.80.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALX_078881.34.80.x, DNA

PI	Barany F., Zilvi M., Gerry NP., Favie R., Kloman R.
PX	WPI; 2002-034366/04.
XX	
DR	
PT	Designing capture oligonucleotide probes for use on a support to which
PT	complementary oligonucleotides hybridize with little mismatch -
PS	Example 5; Fig 25; 300bp; English.
XX	
CC	The present invention describes a method (M1) for designing capture
CC	oligonucleotide probes (I) for use on a support to which complementary
CC	oligonucleotide probes (II) will hybridise with little mismatch, where
CC	(I) have melting temperatures within a narrow range. This method is useful
CC	for detecting infectious diseases caused by bacterial infectious agents
CC	e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC	infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC	Aspergillus fumigatus, viruses e.g. T-cell lymphocyctotropic virus,
CC	Epsilon-Barr virus and polio virus, and parasitic infectious agents
CC	selected from Onchoverva volvulus, Entamoeba histolytica and Dracunculus
CC	medineae. The method is also useful for detecting genetic diseases such
CC	as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC	Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC	involved in DNA amplification, replication, recombination or repair, the
CC	cancer is specifically associated with a gene selected from BRCA1 gene,
CC	p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC	method is also used for environmental monitoring, forensics and the food
CC	and feed industry, detecting complex scanning (using e.g. a scanning
CC	electron microscope and infrared microscope) the support at the
CC	particular sites and identifying if ligation of the oligonucleotide probe
CC	sets occurred and correlating (using a computer) identified ligation to a
CC	presence or absence of the target nucleotide sequences. AB182074 to
CC	AB197346 represent oligonucleotide sequences used in the exemplification
CC	of the present invention.
XX	
SQ	Sequence 24 BP; 6 A; 6 C; 9 G; 3 T; 0 other;
OY	Query Match 64.0%; Score 12.8; DB 24; Length 24;
	Best Local Similarity 87.5%; Pred. No. 3.e+03;
Db	Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
	4 GCGTTGGCAGCTGAGA 19 9 GGATTGCCACTCAGA 24
RESULT 11	
AAD07981	
ID	AAD07981 standard; DNA; 25 BP.
AC	
XX	AAD07981;
DT	06-AUG-2001 (first entry)
XX	
DE	M. mycoides LppQ gene site directed mutagenesis PCR primer MMMLP482.
XX	
KM	Lipoprotein; LppQ; antibacterial; vaccine; Mycoplasma infection;
KV	bovine pleuropneumonia; CBPP; site directed mutagenesis; PCR primer; ss.
XX	
OS	Mycoplasma mycoides subsp. mycoides SC.
XX	
FH	Key Location/Qualifiers
FH	misc_feature 17
FT	/tag= a
FT	/note= "Nucleotide G is present at this location in the
FT	sequence shown in sequence listing of the specification"
PN	WO200140471-A1.
PD	07-JUN-2001.
PF	24-NOV-2000; 2000MO-EPI1798.
XX	

XX	DR	29-NOV-1999;	99EP-0123676.
XX	PA	(ALKU) AKZO NOBEL NV.	
XX	P1	Frey JJ, Nicolet JJ, Abdo EE;	
XX	DR	WPI; 2001-381385/40.	
XX	PS	Example 3; Page 26; 56pp; English.	
XX	CC	The present sequence is a PCR primer used for site directed mutagenesis	
XX	CC	(to exchange Mycoplasma specific UGATP codons to universal UGCATP	
XX	CC	codons) of lipoprotein LppQ gene from Mycoplasma mycoides subsp.	
XX	CC	mycoides SC (small colony type). LppQ is useful in a diagnostic method	
XX	CC	for the direct or indirect detection of M. mycoides subsp. mycoides SC,	
XX	CC	where the diagnostic method is an immunological method such as	
XX	CC	immunoblotting, serological tests or ELISA (enzyme linked immunosorbent	
XX	CC	assay). LppQ DNA and protein are useful for the preparation of a vaccine	
XX	CC	M. mycoides subsp. mycoides SC., where the detection method is selected	
XX	CC	from PCR and hybridisation. LppQ protein is useful for detecting	
XX	CC	antibodies directed to it in a body fluid such as serum or bronchial	
XX	CC	fluid from an animal. LppQ protein are also useful as a specific antigen	
XX	CC	for sero-detection of contagious bovine pleuropneumonia (CBPP).	
XX	SX	Sequence 25 BP; 2 A; 5 C; 3 G; 15 T; 0 other;	
XX	QQ		
XX	Query Match	64.0%; Score 12.8; DB 22; Length 25;	
XX	Best Local Similarity	87.5%; Pred. No. 3.9e+03;	
XX	Matches 14; Conservative	0; Mismatches 2; Indels 0; Gaps 0;	
OY	2 TTGGCTTGGCACTCA 17		
Db	3 TTGTTTTCACACTCA 18		
RESULT 12			
AAD07982/c			
ID	AAD07982 standard; DNA; 25 BP.		
XX	AAD07982;		
XX	06-AUG-2001 (first entry)		
DE	M. mycoides lppq gene site directed mutagenesis PCR primer MMMLP483.		
KW	Lipoprotein; LppQ; antibacterial; vaccine; Mycoplasma infection;		
XX	bovine pleuropneumonia; CBPP; site directed mutagenesis; PCR primer; ss.		
OS	Mycoplasma mycoides subsp. mycoides SC.		
FN	WO200140471-A1.		
PD	07-JUN-2001.		
PE	24-NOV-2000; 2000WO-EP11798.		
FR	29-NOV-1999; 99EP-0123676.		
PA	(ALKU) AKZO NOBEL NV.		
P1	Frey JJ, Nicolet JJ, Abdo EE;		
DR	WPI; 2001-381385/40.		

University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
 Plate: 0543 row: 3 column: 22
 Seq primer: CACACGAGAAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 21.

FEATURES

source

1..21
 Location/Qualifiers
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone_1ib="UUCG1M0543J22"
 /clone_1ib="Mouse 10kb plasmid UUCG1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

6 a 3 c 6 g 6 t

ORIGIN

Query Match 52.9%; Score 9; DB 17; Length 21;
 Best Local Similarity 70.6%; Pred. No. 1.3e+06;
 Matches 12; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTTGCTCGCGGAGAC 17
 |||||
 2 GGTGCTTCATGCGTAC 18

RESULT 15

BM399936 25 bp mRNA linear EST 17-JUN-2002

LOCUS

5009-0-63-D08.t.1 Chilcoat/Turkewitz CDNA (large fraction)

DEFINITION

Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION

BM399936

VERSION

BM399936.1 GI:18199989

KEYWORDS

EST.

SOURCE

ORGANISM

Tetrahymena thermophila.
 Tetrahymena thermophila
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
 Hymenostomatida; Tetrahymenina; Tetrahymena.

1 (bases 1 to 25)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Turkewitz, A.P., Karver, K.M., John, C., Orlas, E., Kirk, K.E., Frankel, J., and Klobutcher, L.
 EST from Tetrahymena thermophila, strain CUA23.1, growing cells
 Unpublished (2002)
 Contact: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apurkew@midway.uchicago.edu
 Seq primer: T3.

FEATURES

source

1..25
 Location/Qualifiers
 /organism="Tetrahymena thermophila"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_1ib="Chilcoat/Turkewitz CDNA (large fraction)"
 /note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT

2 a 8 c 11 g 4 t

ORIGIN

Query Match 52.9%; Score 9; DB 13; Length 25;
 Best Local Similarity 70.6%; Pred. No. 1.3e+06;
 Matches 12; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTTGCTCGCGGAGAC 17
 |||||
 8 GTGCGTGGCGCGTAC 24

RESULT 16

LOCUS

A2478429 25 bp DNA linear GSS 04-OCT-2000

DEFINITION

1M029806R Mouse 10kb plasmid UUCG1M library Mus musculus genomic

ACCESSION

A2478429

VERSION

A2478429.1 GI:10637259

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Mus musculus
 house mouse.
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sclurognathi; Muride; Murinae; Mus.
 1 (bases 1 to 25)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamli, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rilly,
 M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausen, A.,
 and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0298 row: C column: 06
 Seq primer: CACACGAGAAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 25.

FEATURES

source

1..25
 Location/Qualifiers
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone_1ib="UUCG1M029806"
 /clone_1ib="Mouse 10kb plasmid UUCG1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA

Query Match 63.0%; Score 12.6; DB 21; Length 21;
 Best Local Similarity 78.9%; Pred. No. 4.9e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 TTGCGTTTGGCACTCAGA 19
 |||||
 1 TTGAGTTTCTAGGACAGA 19

Db 1 TTGAGTTTCTAGGACAGA 19

RESULT 15
 AAQ58843 standard; CDNA; 25 BP.
 AAQ58843;
 AAQ58843;
 24-NOV-1994 (first entry)
 XX NANBH virus primer group C14-5, primer 14-17.
 XX
 XX Antigen; structural, non-structural; non A non B hepatitis virus;
 KM NANBHv, NANBH, patient; plasma; diagnosis; detection; carrier; PCR;
 KM polymerase chain reaction; amplify; primer; ss.
 XX
 XX Synthetic.
 OS
 XX JP6070778-A.
 XX
 XX 15-MAR-1994.
 XX
 XX 01-JUN-1993; 93JP-0156087.
 XX
 XX 10-JUL-1992; 92JP-0207391.
 XX
 XX (KOKU-) KOKUSAI SHIYAKU KK.
 PA (SANW) SANWA KAGAKU KENKYUSHO CO.
 PA (TOFU) TONEN CORP.
 PA (TKR-) 2H TOKYO RINGHO IGAKU SOGO KENKYUSHO.
 XX
 DR WPI; 1994-128677/16.

XX Nucleic acid fragment coding non-A non-B hepatitis virus antigen
 PT - useful in diagnosis of NANB patient and detection of virus
 PT carrier
 XX
 XX Disclosure; Page 10; 37pp; Japanese.
 XX
 XX The sequences given in AAQ58828-72 are primers which were used to
 CC amplify cDNA sequences encoding antigens of structural and non-
 CC structural regions of non A non B hepatitis virus (NANBHv). The
 CC amplified sequences were derived from the plasma of a NANBH patient by
 CC recombinant DNA techniques. The amplified fragments are useful for
 CC the diagnosis of NANBH patients and the detection of NANBHv carriers.
 XX

XX Sequence 25 BP; 5 A; 7 C; 8 G; 5 T; 0 other:
 SO

Query Match 63.0%; Score 12.6; DB 15; Length 25;
 Best Local Similarity 78.9%; Pred. No. 5e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 TTGCGTTTGGCACTCAGAG 20
 |||||
 1 TCGCGTATGCGCGCTCAGG 19

Db 1 TCGCGTATGCGCGCTCAGG 19

RESULT 16
 ABK02611 standard; RNA; 17 BP.
 ID ABK02611
 AC ABK02611;
 XX
 XX 12-MAR-2002 (first entry)
 XX

DE Human NOGO Amberyne #283.
 XX
 XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KM cerebroprotective; neurotrophic; neuroprotective; antiparkinsonian;
 KM muscular; CD20; neurite growth inhibitor gene; NOGO; hammetted ribozyme;
 KM DNazyme; Inozyme; G-cleaver; amberyne; zinzyme; lymphoma; leukaemia;
 KM B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukemia;
 KM human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KM MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
 KM inflammatory arthropathy; central nervous system injury;
 KM cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KM chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KM Parkinson's disease; ataxia; Huntington's disease;
 KM Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 XX Homo sapiens.
 OS
 OS Synthetic.
 XX
 XX W0200159103-A2.
 XX
 XX 16-AUG-2001.
 XX
 XX
 XX 09-FEB-2001; 2001WO-US04273.
 XX
 XX 11-FEB-2000; 2000US-181797P.
 PR 28-FEB-2000; 2000US-185516P.
 PR 06-MAR-2000; 2000US-187128P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 PI Blatt L, McSwiggen J, Chowrira BM;
 XX
 XX WPI; 2001-607195/69.
 DR
 XX
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,
 PT and central nervous system injury -
 XX
 PS Claim 88; Page 137; 200pp; English.

XX The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO).
 CC The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNazyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN
 CC motif) or an amberyne (cleaving RNA with an NGN triplet), a zinzyme
 CC (cleaving RNA with a YGY motif). The CD20-targeting nucleic acid is used
 CC to cleave RNA of CD20 in the presence of a divalent cation that is
 CC preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce
 CC CD20 activity of the cell and treat a patient having a condition
 CC associated with the level of CD20. The treatment may further comprise the
 CC use of one or more therapies. In particular, the CD20 targeting
 CC nucleic acid may be used to treat lymphoma, leukemia, B-cell
 CC lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky
 CC low-grade or follicular NHL, lymphocytic leukemia, HIV (human
 CC immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL),
 CC immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune
 CC thrombocytopenia, and inflammatory arthropathy. The NOGO-targeting
 CC nucleic acid is used to cleave RNA of the NOGO gene in the presence of a
 CC divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid
 CC may be contacted with a cell to reduce NOGO activity of the cell and
 CC treat a patient having a condition associated with the level of NOGO. The
 CC treatment may further comprise the use of one or more therapies.
 CC In particular, the NOGO-targeting nucleic acid may be used to treat
 CC central nervous system (CNS) injury and cerebrovascular accident (CVA,
 CC stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob

Db 16 GTTGCTGGGGC 5

RESULT 19
TA266D03P/c

LOCUS
DEFINITION T. brucei sheared genomic DNA clone 266d03, forward sequence,
genomic survey sequence.

ACCESSION
VERSION AL488313
KEYWORDS
SOURCE
ORGANISM
TRYPANOSOMA BRUCEI.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.

REFERENCE
AUTHORS 1 (bases 1 to 23)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nh@sanger.ac.uk
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers

FEATURES
source
1..23
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="266d03"

BASE COUNT
2 a 9 c 5 g 7 t

ORIGIN

Query Match 51.8%; Score 8.8; DB 17; Length 23;
Best Local Similarity 83.3%; Pred. No. 1.6e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 TTGGCGCGGAGC 17
|||||
Db 17 TTCAGGGGAGC 6

RESULT 20
AZ345583/c

LOCUS
DEFINITION 20 bp DNA linear GSS 29-SEP-2000
clone UUGC1M080L18 F, DNA sequence.

ACCESSION
VERSION AZ345583
KEYWORDS
SOURCE
ORGANISM
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Bascorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: 1 column: 18
Seq primer: CCGTGTAAACGACGCGCAT
Clase: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
source
1..20
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M080L18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMW42 (g1473214|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptor complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT
5 a 12 c 0 g 3 t

ORIGIN

Query Match 50.6%; Score 8.6; DB 17; Length 20;
Best Local Similarity 73.3%; Pred. No. 2e+06;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTTGCTGGCGGAGC 15
|||||
Db 16 GTTGCTGGCGGAGC 2

RESULT 21
AM247820

LOCUS
DEFINITION 22 bp mRNA linear EST 07-JAN-2000
NM00485, 5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820485 3',
mRNA sequence.

ACCESSION
VERSION AM247820
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 22)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2820485, 5prime
Contact: Robert Strauberg, Ph.D.
Email: cga@db-remail.nih.gov


```

XX RESULT 19
XX ID AA230442/C
XX AA230442 standard; DNA; 24 BP.
XX
XX AC AA230442;
XX
XX DT 21-DEC-1999 (first entry)
XX
XX DGenerate primer #2 for isolating Mlo fungal resistance genes.
XX
XX KM Consensus; resistance; fungus; pathogen; wheat; cell wall; apposition;
XX papilla; contact site; callose; carbohydrate; phenol; transgenic plant;
XX Mlo; Erysiphe graminis; powdery mildew; PCR; primer; amplification; ss.
XX
XX OS Arabidopsis thaliana.
XX Triticum sp.
XX
XX PD W09947552-A2.
XX
XX 23-SEP-1999.
XX
XX PR 17-MAR-1999; 99WO-EP01779.
XX
XX PR 17-MAR-1998; 98US-0042763.
XX
XX (NOVS ) NOVARTIS AG.
XX (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
XX PI Salmeron JM, Weislo LJ, Strawn LJ, Kramer CM;
XX WPI; 1999-571820/48.
XX
XX DR New proteins useful for generating transgenic plants resistant to
XX fungal infection
XX
XX PS Example 8; Page 35; 102pp; English.
XX
XX CC Primers AA230441-230442 are degenerate primers based on regions of
XX homology in the amino acid sequences of the Arabidopsis thaliana and
XX wheat (Triticum sp.) Mlo fungal resistance protein. The primers are
XX used to isolate further Mlo gene family members. The Mlo protein confers
XX resistance to fungal pathogens by stimulating the formation of large
XX cell wall appositions, designated papillae, at the contact site with
XX the fungal pathogen. These papillae mainly contain callose, but also
XX contain carbohydrate, phenols and proteins and are used to prevent
XX penetration of the fungal hyphae into the plant. The new Mlo sequences
XX are used to generate transgenic plants resistant to fungal pathogens,
XX especially Erysiphe graminis (powdery mildew).
XX
XX SQ Sequence 24 BP; 5 A; 6 C; 5 G; 4 T; 4 other;
XX
XX Query Match 61.0%; Score 12.2; DB 20; Length 24;
XX Best Local Similarity 68.4%; Pred. No. 86+03;
XX Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0
XX
XX 1 TTGGGTTTGCACATCAGA 19
XX : : : : :
XX 24 TAYGCVTHGTCATCACA 6
XX
XX RESULT 20
XX ID ABN99536
XX ABN99536 standard; DNA; 24 BP.
XX
XX AC ABN99536;
XX
XX DT 05-AUG-2002 (first entry)
XX
XX DE Fungal PCR primer SEQ ID NO 108.
XX
XX Fungus; bacteria; quantification; detection; infection; gastroenteritis;

```

KM ulcer; asthma; allergy; sinusitis; PCR; primer; ss.
 XX
 OS Paecilomyces lilacinus.
 XX
 PN US6387652-B1.
 XX
 PD 14-MAY-2002.
 XX
 PF 13-JUN-2000; 2000US-0593012.
 XX
 PR 15-APR-1998; 98US-081773P.
 PR 14-APR-1999; 99US-0290990.
 XX
 PA (USSI) US ENVIRONMENTAL PROTECTION AGENCY.
 XX
 PI Haugland R, Vesper S;
 DR WPI, 2002-462353/49.
 XX
 PT Detection and quantification of specific fungi or bacteria useful e.g.
 PT in medical diagnosis and treatment of fungal and bacterial conditions,
 PT by hybridizing and amplifying DNA using sequences unique to the species
 PT or group of species -
 XX
 PS Claim 37; Column 94; 55pp; English.
 XX
 CC The invention relates to specific fungi or bacteria detected and
 CC quantified in a sample by extracting and recovering DNA from the organism
 CC in the sample and hybridizing and amplifying the DNA sequence using
 CC sequences unique to the species/group of species but common to all
 CC isolates of the species/group of species. The method especially employs
 CC sequences selected from 225 fungal and bacterial primer and probe
 CC sequences (ABN99423-ABN99653) for detection of specified fungi/fungal
 CC groups or specified bacteria. The method enables detection and
 CC quantification of specific fungi or bacteria, or groups of
 CC fungal/bacterial species, useful medically for diagnosis and treatment of
 CC fungi or bacteria associated with health problems such as infections,
 CC gastroenteritis, ulcer, asthma, allergies and sinusitis. It is also
 CC useful to detect and/or quantify microorganisms in the environment e.g.
 CC to establish the risk of adverse health effects (e.g. pulmonary
 CC haemorrhage from levels of Stachybotrys chartarum in air samples in
 CC houses).
 CC
 SC Sequence 24 BP; 9 A; 4 C; 6 G; 5 T; 0 other;
 SQ
 Query Match 61.0%; Score 12.2; DB 24; Length 24;
 Best Local Similarity 82.4%; Pred. No. 8e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 4 GCGTTTGCACTCAGAG 20
 |||||
 DB 1 GCTGTGCACTCAGAG 17
 |||||
 RESULT 21
 ABK29133
 ID ABK29133 standard; DNA; 24 BP.
 XX
 AC ABK29133;
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE Paecilomyces lilacinus reverse PCR primer.
 XX
 KW Fungal detection; bacterial detection; probe; primer; ss.
 XX
 OS Paecilomyces lilacinus.
 XX
 PN WO200196612-A2.
 XX
 PD 20-DEC-2001.
 XX
 PF 13-JUN-2001; 2001WO-US18892.
 XX

Query Match 60.0%; Score 12; DB 19; Length 17;
 Best Local Similarity 75.0%; Pred. No. 9.9e+03;
 Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 8 TTGGCACTCAGA 19
 :
 DB 1 UUGCCACUCACAGA 12

RESULT 24
 AAT64985
 ID AAT64985 standard; DNA; 21 BP.
 XX AAT64985;
 AC AAT64985;

XX 23-FEB-1998 (first entry)
 XX DT
 XX DE Rat OB receptor PCR primer ROBR 27.
 XX Ob receptor; obesity; leptin; rat; rodent; animal model; ligand;
 KM fatty; fa mutation; therapy; PCR; primer; MspI; ss.
 XX OS Synthetic.
 OS Rattus sp.
 XX MO9731015-A1.
 XX 28-AUG-1997.
 XX PD
 XX 18-FEB-1997; 97WO-US023397.
 XX PP
 XX 25-APR-1996; 96GB-0008473.
 PR 22-FEB-1996; 96US-0090405.
 PR 22-MAR-1996; 96US-0013969.
 PA (MERI) MERCK & CO INC.
 XX PI
 PI Caskey CT, Hess JW, Liu Q, Phillips MS;
 DR WPI; 1997-435085/40.
 XX WP1; 1997-435085/40.
 XX Rat wild-type and mutant ob receptor protein - useful in
 PT identification of new ligands for prevention and treatment of
 PT obesity

XX Example 8; Page 15; 35pp; English.

XX This oligonucleotide comprises forward PCR primer ROBR 27. Its
 CC sequence corresponds to bases 796-816 of a rat ob receptor (OB-R).
 CC CDNA sequence (see AAT64985). It was used with rat OB-R reverse
 CC primer ROBR 28 (see AAT64985) to amplify 1.8 kb fragments of rat
 CC genomic DNA from lean and fa/fa (fatty) Zucker rats. Subsequent
 CC digestion of the PCR product from a homozygous lean rat using
 CC restriction endonuclease MspI yielded 2 fragments of 1100 bp and
 CC 700 bp. MspI digestion of the PCR product from a fa/fa rat yielded
 CC fragments of 950, 110 bp and 700 bp. The fa mutant OB-R gene
 CC (see AAT64985) contains an A to C transversion at bp 880 that creates
 CC an extra MspI site. This allows genotype analysis of lean and
 CC fa/fa rats.
 XX

SO Sequence 21 BP; 5 A; 3 C; 7 G; 6 T; 0 other;

Query Match 60.0%; Score 12; DB 18; Length 21;
 Best Local Similarity 75.0%; Pred. No. 9.9e+03;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 TTGGCTTGGCAGAG 20
 :
 DB 2 TTGGCTATGGAGTCAGG 21

RESULT 25
 AAD21460/c

ID AAD21460 standard; DNA; 23 BP.
 XX AC
 XX AAD21460;
 AC AAD21460;

XX 28-JAN-2002 (first entry)
 XX DT
 XX DE RT-PCR primer, 2323-70 to examine the expression of human agp-96614-a1.
 XX RT-PCR primer, 2323-70 to examine the expression of human agp-96614-a1.

XX Human; CD20/IGF-receptor like protein; immunoglobulin E; agp-96614-a1;
 KM agp-69406-a1; cancer; abnormal cell proliferation; autoimmune disease;
 KM ovarian cancer; brain cancer; arteriosclerosis; vascular restenosis;
 KM rheumatoid arthritis; multiple sclerosis; allergy; dermatitis; asthma;
 KM reproductive disease; diabetes; transplant rejection; endometriosis;
 KM infertility; gene therapy; reverse transcription PCR; RT-PCR primer; ss.
 XX OS Homo sapiens.
 OS WO200174903-A2.
 XX PN
 XX PD 11-OCT-2001.
 XX PF 29-MAR-2001; 2001WO-US10048.
 XX PR 30-MAR-2000; 2000US-193728P.
 PR 27-NOV-2000; 2000US-0723258.
 XX PA (AMGE-) AMGEN INC.
 XX PI
 PI Welcher AA, Calzone FJ;
 XX WP1; 2001-662968/76.
 XX DR

XX Novel CD20/IGF-receptor like polypeptides and polynucleotides,
 PT antagonists and antibodies of the polypeptide useful for treating
 PT ameliorating or preventing diseases associated with the polypeptide
 PT e.g. cancer, asthma

XX Example 3; Page 112; 145pp; English.

XX The invention relates to human CD20/immunoglobulin E (IGE)-receptor
 CC like polypeptides designated as agp-96614-a1 and agp-69406-a1 and
 CC nucleic acid molecules encoding such polypeptides. Polypeptides of
 CC the invention are useful for treating, preventing or ameliorating
 CC a disease, condition, or disorder which includes cancer such as
 CC brain cancer, ovarian cancer; abnormal cell proliferation such as
 CC arteriosclerosis, vascular restenosis; pathology from allergens
 CC such as allergies, asthma, dermatitis; dysfunction of immune system
 CC such as rheumatoid arthritis, autoimmune disease, multiple sclerosis,
 CC diabetes, transplant rejection and reproductive diseases such as
 CC infertility, preterm labour and delivery, endometriosis etc. They
 CC are also useful for identifying antagonists and as immunogens, for
 CC raising antibodies which may also be used to prevent, treat or
 CC diagnose a number of diseases and disorders. Polynucleotides of the
 CC invention are used to map the location of CD20/IGF-receptor like
 CC gene and related genes on chromosomes and as hybridisation probes.
 CC They are also useful in gene therapy. The present sequence is
 CC reverse transcription PCR (RT-PCR) primer used to examine the
 CC expression of human agp-96614-a1 sequence.
 XX

SO Sequence 23 BP; 7 A; 7 C; 4 G; 5 T; 0 other;

Query Match 60.0%; Score 12; DB 22; Length 23;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 TGGCACTCAGAG 20
 :
 DB 23 TGGCACTCAGAG 12

RESULT 26
 ABK02000
 ID ABK02000 standard; RNA; 17 BP.

FEATURES
source

Location/Qualifiers
1..22
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:1947009"
/clone_lib="NCI CGAP GC4"
/ribose_type="pooled germ cell tumors"
/lab_host="DH10B"
/note="Vector: pTR73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTR73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT
5 a 7 c 5 g 5 t

Query Match 49.4%; Score 8.4; DB 9; Length 22;
Best Local Similarity 90.0%; Pred. No. 2.6e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TTGGGCGGGA 15
21 TTGGGCGGGA 12

Db

RESULT 29
LOCUS AU006620 22 bp mRNA linear EST 31-JUL-1998
DEFINITION Schizosaccharomyces pombe late log phase cDNA
ACCESSION AU006620
VERSION AU006620
KEYWORDS GI:3343079
SOURCE fission yeast.
ORGANISM Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomycetes.
REFERENCE 1 (bases 1 to 22)
Moriyomo, M. and Mita, K.
AUTHORS Identification of expressed sequence tags of Schizosaccharomyces pombe
TITLE Unpublished (1998)
JOURNAL Contact: Mitsunori Moriyomo
COMMENT Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-Ku, Chiba 263-8555, Japan
Email: moriyomo@nirs.go.jp.

FEATURES
source

Location/Qualifiers
1..22
/organism="Schizosaccharomyces pombe"
/strain="972"
/db_xref="taxon:4896"
/clone_lib="spc00195"
/clone_lib="Schizosaccharomyces pombe late log phase cDNA"
/sex="h minus"
/note="Vector: M13mp19. The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"

BASE COUNT
3 a 2 c 6 g 11 t

Query Match 49.4%; Score 8.4; DB 9; Length 22;
Best Local Similarity 90.0%; Pred. No. 2.6e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCTTCGG 10
1 GTTCTTCGG 10

Db

RESULT 30
LOCUS AU006633 22 bp mRNA linear EST 31-JUL-1998
DEFINITION Schizosaccharomyces pombe late log phase cDNA
ACCESSION AU006633
VERSION AU006633
KEYWORDS GI:3343092
SOURCE fission yeast.
ORGANISM Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomycetes.
REFERENCE 1 (bases 1 to 22)
Moriyomo, M. and Mita, K.
AUTHORS Identification of expressed sequence tags of Schizosaccharomyces pombe
TITLE Unpublished (1998)
JOURNAL Contact: Mitsunori Moriyomo
COMMENT Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-Ku, Chiba 263-8555, Japan
Email: moriyomo@nirs.go.jp.

FEATURES
source

Location/Qualifiers
1..22
/organism="Schizosaccharomyces pombe"
/strain="972"
/db_xref="taxon:4896"
/clone_lib="spc00210"
/clone_lib="Schizosaccharomyces pombe late log phase cDNA"
/sex="h minus"
/note="Vector: M13mp19. The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"

BASE COUNT
3 a 2 c 6 g 11 t

Query Match 49.4%; Score 8.4; DB 9; Length 22;
Best Local Similarity 90.0%; Pred. No. 2.6e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCTTCGG 10
1 GTTCTTCGG 10

Db

RESULT 31
LOCUS AZ476310 22 bp DNA linear GSS 04-OCT-2000
DEFINITION IM029494P19R Mouse 10kb plasmid UGCGIM library Mus musculus genomic clone UGCGIM0294P19 R. cDNA sequence.
ACCESSION AZ476310
VERSION AZ476310
KEYWORDS GI:10634435
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiser, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)

```

QY      1 TTGGCTTGGCACT 15
      |||||
      16 TTGGCTTGGCGCT 2

RESULT 28
AAK95488
ID      AAK95488 standard; DNA; 20 BP.
XX
XX
AC      AAK95488;
XX
DT      13-SEP-1999 (first entry)
XX
DE      PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX
XX      Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KM      sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
KM      vaccine; neutralising epitope; PCR primer; ss.
XX
OS      Synthetic.
OS      Chlamydia pneumoniae.
XX
XX      WO927105-A2.
XX
XX      03-JUN-1999.
XX
XX      20-NOV-1998; 98WO-1B01890.
XX
XX      04-NOV-1998; 98US-0107078.
XX      21-NOV-1997; 97FR-0014673.
XX
XX      (GEST ) GENSET.
XX
XX      Griffiths R;
XX
XX      WPI; 1999-357842/30.
XX
XX      Genome sequence of Chlamydia pneumoniae
XX
XX      Page 1752; Disclosure; 191pp; English.
XX
XX      AAY91991-X97517 represent PCR primers used to amplify open reading
CC      frames and other nucleic acid sequences from the genome of
CC      Chlamydia pneumoniae (see AAY91990). C. pneumoniae causes respiratory
CC      disease such as pneumonia and bronchitis and is thought to be a
CC      contributing factor in heart disease, sarcoidosis, sinusitis, purulent
CC      otitis media, erythema nodosum or pharyngitis. The polypeptides encoded
CC      by the open reading frames of the C. pneumoniae genome (see AAY34584-
CC      AAY35879) can be used in immunogenic compositions as vaccines. Vectors
CC      containing C. pneumoniae nucleotide sequences can also be used as
CC      immunogenic compositions, especially where the vector directs the
CC      expression of a neutralising epitope of C. pneumoniae.
XX
XX      Sequence 20 BP; 6 A; 3 C; 7 G; 4 T; 0 other;
SQ
Query Match      59.0%; Score 11.8; DB 20; Length 20;
Best Local Similarity 86.7%; Pred. No. 1.2e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      6 GTTGGCACTCAGAG 20
      |||||
      2 GTTGGCACTCAGAG 16

RESULT 29
AAK02576/C
ID      AAK02576 standard; DNA; 20 BP.
XX
XX
AC      AAK02576;
XX
DT      07-MAY-1999 (first entry)
XX
XX      PCR primer #7.
DB

```

```

XX      Plant artificial chromosome; PLAC; foreign gene expression; trait; oil;
KM      herbicide; resistance; tolerance; insect; disease; stress; drought;
KM      heat; chilling; freezing; salt; moisture; oxidative; yield; food content;
KM      physical appearance; male sterility; drydown; standability; prolificacy;
KM      starch; detection; PCR primer; ss.
XX
XX      Synthetic.
OS      Arabidopsis thaliana.
XX
XX      WO985637-A1.
XX
XX      10-DEC-1998.
XX
XX      03-JUN-1998; 98WO-US11288.
XX
XX      05-FEB-1998; 98US-0073741.
XX      03-JUN-1997; 97US-0048451.
XX
XX      (ARCH-) ARCH DEV CORP.
XX
XX      Copenhagen G, Preuss D;
XX
XX      WPI; 1999-080832/07.
XX
XX      New isolated Arabidopsis thaliana centromeres - used for the
PT      production of plant artificial chromosomes for the production of
PT      transgenic plants having desirable agronomic traits
XX
XX      Disclosure; Page 77; 150pp; English.
XX
XX      This invention describes a recombinant DNA construct which comprises a
CC      functional Arabidopsis thaliana centromere. This centromeric region can
CC      be used for the production of plant artificial chromosomes (PLAC's)
CC      which can be used for the production of plants which can express
CC      foreign genes. PLACs can be used to provide desirable traits such as
CC      herbicide resistance or tolerance, insect resistance or tolerance,
CC      disease resistance or tolerance (viral, bacterial, fungal, nematode),
CC      stress tolerance and/or resistance, as exemplified by resistance or
CC      tolerance to drought, heat, chilling, freezing, excessive moisture, salt
CC      stress, oxidative stress, increased yields, food content and makeup,
CC      physical appearance, male sterility, drydown, standability, prolificacy,
CC      starch quantity and quality, oil quantity and quality, protein quality
CC      and quantity, or amino acid composition. The centromeric regions can
CC      also be used to detect the presence of similar centromeric regions in
CC      other plants or animals. This sequence is a PCR primer used in the
CC      method of the invention.
XX
XX      Sequence 20 BP; 9 A; 4 C; 5 G; 2 T; 0 other;
SQ
Query Match      59.0%; Score 11.8; DB 20; Length 20;
Best Local Similarity 86.7%; Pred. No. 1.2e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TTGGCTTGGCACT 15
      |||||
      17 TTGGCTTGGCGACT 3

RESULT 30
AAF22122/C
ID      AAF22122 standard; DNA; 20 BP.
XX
XX
AC      AAF22122;
XX
DT      20-MAR-2001 (first entry)
XX
XX      Arabidopsis thaliana chromosome centromere associated primer #6.
XX
XX      Centromere; microsome; vector; ds.
XX
XX      Arabidopsis thaliana.
OS

```

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G1|4732114|GB|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

1 a 3 c 12 g 4 t

Query Match 48.2%; Score 8.2; DB 17; Length 20;
Best Local Similarity 76.9%; Pred. No. 3.3e+06;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 TTGCTCGGCGGG 14
1 TTCTCTGGCGGG 13

Db 1 TTCTCTGGCGGG 13

RESULT 34

AZ511616 20 bp DNA linear GSS 05-OCT-2000
LOCUS 1M035B18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M035B18 F, DNA sequence.
ACCESSION AZ511616
VERSION
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A., and Wright, D., Weis, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL
COMMENT unpublished (2000)
CONTACT: Robert B. Weiss
UNIVERSITY of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0356 row: B column: 15
Seq primer: CACACGAGAAACAGCATACAC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. 20
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M035B18"
/clone_11b="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

FEATURES

source

1. 20
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M035B18"
/clone_11b="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G1|4732114|GB|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

1 a 1 c 9 g 9 t

Query Match 48.2%; Score 8.2; DB 17; Length 20;
Best Local Similarity 76.9%; Pred. No. 3.3e+06;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 TTGCTCGGCGGG 14
7 TTGTTTGGCGGG 19

Db 7 TTGTTTGGCGGG 19

RESULT 35

AZ789409 20 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0037H1F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0037H1 F, DNA sequence.
ACCESSION AZ789409
VERSION
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A., and Wright, D., Weis, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL
COMMENT unpublished (2000)
CONTACT: Robert B. Weiss
UNIVERSITY of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0037 row: H column: 11
Seq primer: CGTGTAAACAGCGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. 20
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0037H1F"
/clone_11b="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

FEATURES

source

1. 20
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0037H1F"
/clone_11b="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "phosphorothioate"
FEATURE:
NAME/KEY: -
LOCATION: 1..21
OTHER INFORMATION: /note = "885-905 primer"
US-08-974-549A-510

Query Match 63.5%; Score 10.8; DB 4; Length 21;
Best Local Similarity 85.7%; Pred. No. 3.1e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGCTTCGGCGG 14
Db 6 GCTTCTTCGGCGG 19

Search completed: June 7, 2003, 09:45:18
Job time : 48.8545 secs

CC mouse ageing inhibitory protein of the invention; the recombinant
 CC production of a mouse ageing inhibitory protein; antibodies against
 CC the ageing inhibitory proteins; methods for immunologically assaying
 CC the proteins; and methods for identifying ligands or other modulators
 CC of the ageing inhibitory proteins; and the ligands and modulators thus
 CC identified. The ageing inhibitory proteins, nucleic acids encoding
 CC them, and antibodies, ligands and modulators, may be used in the
 CC diagnosis and treatment of ageing (particularly premature ageing),
 CC and ageing-related disorders. Sequences AAH24198-AAH24199 represent
 CC PCR primers used in an exemplification of the invention to isolate a
 CC mouse ageing inhibition-related DNA sequence (AAH24197).

CC Sequence 23 BP; 8 A; 6 C; 5 G; 4 T; 0 other;

Query Match 59.0%; Score 11.8; DB 22; Length 23;

Best Local Similarity 86.7%; Pred. No. 1.3e+04; Mismatches 2; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 TTTGCGTTGGCACT 15
 |||||
 16 TTTGCTTTGGCACT 4

RESULT 33
 ID ABK49704/C
 ID ABK49704 standard; DNA; 24 BP.

AC ABK49704;

DT 15-JUL-2002 (first entry)

DE Human kinase uridylylate 12 protein, RT-PCR primer 2.

KM Human, kinase uridylylate 12; malignant neoplasm; tumour; haemopathy; HIV;
 KM human immunodeficiency virus infection; immunological disease; RT-PCR;
 KM inflammation; sterility; pregnancy pathology; growth disorder; primer;
 KM embryonic development disorder; hereditary disease;
 KM reverse transcriptase PCR; ss.

OS Homo sapiens.

PN WO200183726-A1.

PD 08-NOV-2001.

PF 28-APR-2001; 2001WO-CN00649.

PR 29-APR-2000; 2000CN-0115551.

PA (SHAN-) SHANGHAI BIOWINDOM GENE DEV INC.

PI Mao Y, Xie Y;

DR WPI; 2002-062122/08.

PT Human uridylylate kinase 12 and encoded polynucleotide, applicable in
 PT diagnosis and treatment of developmental disorders, malignant tumour,
 PT haemopathy, HIV infection, immunological diseases and various
 PT inflammations

PS Example 2; Page 17; 36pp; Chinese.

CC The present invention relates to a new polypeptide of human uridylylate
 CC kinase 12, its fragment, analogue or derivative. The polypeptide of the
 CC invention and its encoding polynucleotide are applicable in diagnosis
 CC and treatment of malignant neoplasm, haemopathy, human immunodeficiency
 CC virus (HIV) infection, immunological diseases, various inflammations,
 CC sterility, pregnancy pathology, embryonic development disorders, growth
 CC and development disorders and hereditary diseases. The present nucleic
 CC acid sequence represents reverse transcriptase (RT)-PCR primer 2 that
 CC was used in the methods of the invention to isolate the coding sequence
 CC of the human kinase uridylylate 12 protein.

SQ Sequence 24 BP; 10 A; 3 C; 3 G; 8 T; 0 other;

Query Match 59.0%; Score 11.8; DB 24; Length 24;

Best Local Similarity 86.7%; Pred. No. 1.3e+04; Mismatches 2; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 TTTGCGTTGGCACT 15
 |||||
 15 TTTGATTTGGCACT 1

RESULT 34
 ID AB188868/C
 ID AB188868 standard; DNA; 24 BP.

AC AB188868;

DT 15-FEB-2002 (first entry)

DE Capture oligonucleotide 21p ID#3236 oligo #1.

KM Human, K-ras; PCR primer; probe; capture probe; mutation detection;
 KM ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
 KM infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
 KM cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
 KM environmental monitoring; food industry; feed industry; ss.

OS Synthetic.

PN WO200179548-A2.

PD 25-OCT-2001.

PF 04-APR-2001; 2001WO-US10958.

PR 14-APR-2000; 2000US-197271P.

PA (CORR) CORNELL RES FOUND INC.

PI Barany F, Zilvi M, Gerry NP, Favis R, Klaman R;

DR WPI; 2002-034366/04.

PT Designing capture oligonucleotide probes for use on a support to which
 PT complementary oligonucleotides hybridize with little mismatch -

PS Example 5; Fig 25; 30pp; English.

CC The present invention describes a method (M1) for designing capture
 CC oligonucleotide probes (I) for use on a support to which complementary
 CC oligonucleotide probes (II) will hybridise with little mismatch, where
 CC (I) have melting temperatures within a narrow range. The method is useful
 CC for detecting infectious diseases caused by bacterial infectious agents
 CC e.g. Salmonella, listeria monocytogenes and Haemophilus influenza, fungal
 CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
 CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
 CC Epstein-Barr virus and polio virus, and parasitic infectious agents
 CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
 CC medinensis. The method is also useful for detecting genetic diseases such
 CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
 CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
 CC involved in DNA amplification, replication, recombination or repair, the
 CC cancer is specifically associated with a gene selected from BRCA1 gene,
 CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
 CC method is also used for environmental monitoring, forensics and the food
 CC and feed industry, detecting complex scanning (using e.g. a scanning
 CC electron microscope and infrared microscope) the support at the
 CC particular sites and identifying if ligation of the oligonucleotide probe
 CC sets occurred and correlating (using a computer) identified ligation to a
 CC presence or absence of the target nucleotide sequences. AB182074 to
 CC AB17546 represent oligonucleotide sequences used in the exemplification
 CC of the present invention.

Qy 5 CTTGGCGGCGGAC 17
 |||
 4 CTGGCGGCGGAC 16

RESULT 38
 A1721471/c
 LOCUS
 DEFINITION
 A1721471 22 bp mRNA linear EST 07-JUN-2001
 fc28b01.x1 zebrafish wahu mpimg EST Danio rerio cDNA clone
 IMAGE:3722665.3; similar to TR:039949 039949 HYDROXYPROLINE-RICH
 PROTEIN. ;contains element MSRI repetitive element ;, mRNA
 sequence.

ACCESSION
 A1721471
 A1721471.1 GI:5039800

VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 zebrafish.
 Danio rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes
 ; Cyprinidae; Danio.

REFERENCE
 AUTHORS
 1 (bases 1 to 22)
 Clark, M., Johnson, S.L., Lehnach, H., Lee, R., Li, F., Marra, M., Eddy
 'S., Hillier, L., Kucada, T., Martin, D., Beck, C., Wylie, T., Underwood
 'K., Stepcie, M., Theising, B., Allen, M., Bowers, Y., Pearson, B.,
 Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Riteer, E.,
 Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
 and Wilson, R.

TITLE
 JOURNAL
 COMMENT
 Wahu zebrafish EST Project 1998
 Unpublished (1998)
 Contact: Stephen L. Johnson
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: zbrafish@watson.wustl.edu
 cDNA library preparation: Matthew Clark. cDNA Library Arrayed by:
 Matthew Clark. DNA Sequencing by: Washington University Genome
 Sequencing Center distribution: Genome Systems, St. Louis,
 Missouri (web address: www.genomesystems.com) (email contact:
 info@genomesystems.com) and Research Genetics, Huntsville, Alabama
 (web address: www.resgen.com) (email contact: info@resgen.com) and
 Resourcenetz/UMPrimarDatenbank, Berlin, Germany (web address:
 www.rtpd.de)
 Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand
 Seq primer: T7 EF from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers
 1..22
 /organism="Danio rerio"
 /db_xref="taxon:7955"
 /clone="IMAGE:3722665"
 /clone_lib="Zebrafish Wahu MPIMG EST"
 /sex="mixed"
 /tissue_type="26 somite embryos, adult livers, shield
 stage embryos"
 /lab_host="XLI-blue MRF"
 /note="Vector: pSPORT1, Site_1: NotI, Site_2: SalI; 1st
 strand cDNA was primed with a Not I - 3150(dT)15 primer
 (5' GCACTAGTCTAGATCGGAGCGCGCCCTTTTCTTTT3');
 double-stranded cDNA was ligated to Sal I adaptors (BRL),
 digested with Not I and cloned into the Not I and Sal I
 sites of the pSPORT1 vector (BRL). Library was constructed
 by Matthew Clark (Lehnach lab), ICRF, London and Max Planck
 Institut fuer Molekulare Genetik, Berlin). cDNAs for EST
 analysis were selected following oligonucleotide
 hybridization fingerprinting of arrayed clones from
 zebrafish late somitogenesis (26 ss), adult liver or
 embryonic shield stage (5.6 h) libraries. Fingerprint
 data were used to computationally cluster cDNAs, and a
 single cDNA from each cluster was chosen for sequencing.
 In some cases multiple members of the same cluster were
 sequenced to assess clustering parameters or single clones

BASE COUNT 7 a 13 c 1 g 1 t
 ORIGIN
 Query Match 48.2%; Score 8.2; DB 9; Length 22;
 Best Local Similarity 76.9%; Pred. No. 3.3e+06;
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTTGCTTCGGCGG 13
 |||
 20 GTTTTTCGGGGG 8

RESULT 39
 TAI74D06Q
 LOCUS
 DEFINITION
 TAI74D06Q 22 bp DNA linear GSS 13-DEC-2000
 T. brucei sheared genomic DNA clone 174d06, reverse sequence,
 genomic survey sequence.

ACCESSION
 AL474520
 AL474520.1 GI:11839734

VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Trypanosoma brucei.
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.

REFERENCE
 AUTHORS
 1 (bases 1 to 22)
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.

TITLE
 JOURNAL
 COMMENT
 Direct Submission
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nhl@sanger.ac.uk
 Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
 SOURCE
 1..22
 /organism="Trypanosoma brucei"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="174d06"

BASE COUNT 2 a 2 c 9 g 9 t
 ORIGIN
 Query Match 48.2%; Score 8.2; DB 17; Length 22;
 Best Local Similarity 76.9%; Pred. No. 3.3e+06;
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 TGCTTCGGCGGGA 15
 |||
 2 TGTTCGTGGCGGA 14

RESULT 40
 A2785027
 LOCUS
 DEFINITION
 A2785027 23 bp DNA linear GSS 16-FEB-2001
 2M0028H03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0028H03 R, DNA sequence.

ACCESSION
 A2785027
 A2785027.1 GI:12921357

VERSION
 KEYWORDS
 GSS.

```

RESULT 37
AA166253/c
ID AA166253 standard; DNA; 20 BP.
XX
XX
AC AA166253;
XX
XX
DT 22-JAN-2002 (first entry)
XX
DE S cerevisiae potassium translocation gene mutagenic primer Kan-antisense.
XX
XX S. cerevisiae; yeast; potassium translocation system; TRK1; TRK2;
XX TOK1; human erg potassium ion channel; HERG; antiarrhythmic;
XX antiinflammatory; antifibrillatory; HERG modulator; mutagenic primer; ss.
XX
OS Saccharomyces cerevisiae.
XX
XX Synthetic.
XX
XX DE19953478-A1.
XX
XX 11-OCT-2001.
XX
XX 06-NOV-1999; 99DE-1053478.
XX
XX 06-NOV-1999; 99DE-1053478.
XX
XX (LICH/) LICHTENBERG-FRATTE H.
XX (LUDW/) LUDWIG J.
XX
XX Lichtenberg-Fratt H, Ludwig J;
XX
XX WPI; 2001-603577/69.
XX
XX Genetically modified yeast lacking endogenous potassium transport
XX activity; useful for identifying e.g. antiarrhythmic agents; includes a
XX functional human potassium channel
XX
XX Example 1; Fig 2; 40pp; German.
XX
XX The present invention relates to a genetically modified Saccharomyces
XX cerevisiae in which the endogenous potassium-translocation systems (TRK1,
XX TRK2 and TOK1) are specifically deleted and the human erg potassium ion
XX channel (HERG) is stably integrated and expressed. This can be used to
XX identify specific modulators of HERG, which are potentially useful as
XX antiarrhythmic, antifibrillatory and antiinflammatory agents. The present
XX sequence is a mutagenic primer used to disrupt the yeast TRK1 gene.
XX
XX Sequence 20 BP; 6 A; 7 C; 3 G; 4 T; 0 other;
XX
XX Query Match 58.0%; Score 11.6; DB 22; Length 20;
XX Best Local Similarity 77.8%; Pred. No. 1.6e+04;
XX Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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XX 1 TTGGCGTTTGGCCACTCAG 18
XX 19 TTAGGATTTCACACTGAG 2
XX
XX Db
XX
XX RESULT 38
XX AA169508
XX ID AA169508 standard; DNA; 21 BP.
XX
XX AA169508;
XX
XX 15-MAY-1998 (first entry)
XX
XX a-Cobratoxin gene amplifying primer LAS 3.
XX
XX a-cobratoxin; neurotoxin; inactivated bioactive polypeptide;
XX disulphide bridge; LAS 2; wound healing; toxin; PCR primer; ss.
XX
XX Synthetic.
XX
XX Naja naja siamensis.

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XX
XX PN WO9743407-A1.
XX
XX 20-NOV-1997.
XX
XX 08-MAY-1997; 97WO-US08074.
XX
XX 10-MAY-1996; 96US-0644399.
XX
XX (PHYL-) PHYLAMED CORP.
XX
XX Mundschenk DD, Smith LA;
XX
XX WPI; 1998-008876/01.
XX
XX Production of inactivated bioactive polypeptide(s), particularly
XX neurotoxin(s) - by expression of DNA encoding the polypeptide in
XX such a way that one or more disulphide bridges are not formed
XX
XX Example 1; Page 16; 32pp; English.
XX
XX This primer is used for the asymmetric PCR amplification of the gene
XX a-cobratoxin. A Naja naja siamensis cDNA is used as a template. This was
XX used for the DNA sequencing of a-cobratoxin. This was used in a novel
XX method for producing an inactivated neurotoxin with post translational
XX modifications. A novel method for preparing a composition comprising
XX an inactivated bioactive polypeptide comprises identifying a polypeptide
XX having a biological activity dependent on the presence of one or more
XX disulphide bridges in its tertiary structure, preparing a cDNA strand
XX encoding the polypeptide, expressing the cDNA under conditions in which
XX the polypeptide is recovered in an inactive form due to the failure to
XX form one or more disulphide bridges and recovering the inactive
XX polypeptide and formulating it into an aqueous composition. The
XX polypeptide can be treated with ozonated water under conditions to
XX oxidise any disulphide bonds in order to form corresponding pairs of
XX cysteine residues, and to then stabilise the resultant cysteine residues
XX and prevent the reformation of disulphide bonds. The method can be used
XX for producing bioactive polypeptides which are inactivated but still
XX retain other useful properties such as immunogenicity and antiviral,
XX anti-tumour or wound healing activity. They can be used with toxins
XX affecting the presynaptic neurojunction such as norexin, crotoxin,
XX beta-bungarotoxin, taipoxin, textilotoxin and a-latrotoxin, toxins
XX affecting the postsynaptic neurojunction such as a-conotoxins, ion
XX erabutoxin, a-cobratoxin and a-bungarotoxin, toxins affecting ion
XX channels such as dendrotoxins, scorpion toxins, m-conotoxins, and sea
XX anemone toxins, or cell membrane-damaging toxins such as mycotoxins,
XX cardiotoxins, melittin, and phospholipases. The inactivated neurotoxin
XX composition can be used for the study and treatment of viral and
XX neurological diseases.
XX
XX Sequence 21 BP; 4 A; 6 C; 3 G; 8 T; 0 other;
XX
XX Query Match 58.0%; Score 11.6; DB 19; Length 21;
XX Best Local Similarity 77.8%; Pred. No. 1.6e+04;
XX Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 1 TTGGCGTTTGGCCACTCAG 18
XX 2 TTTCATTGCCATTTCAG 19
XX
XX Db
XX
XX RESULT 39
XX AA169969
XX ID AA169969 standard; DNA; 21 BP.
XX
XX AA169969;
XX
XX 18-DEC-2001 (first entry)
XX
XX alpha-cobratoxin PCR primer, LAS 3.
XX
XX alpha-cobratoxin; PCR primer; anti-HIV; HIV infection; immunokine;
XX neurotoxin; Thailand cobra; ss.

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OM nucleic - nucleic search, using sw model

Run on: June 7, 2003, 08:19:34 ; Search time 42.1818 Seconds

(Without alignment)
145,407 Million cell updates/sec

Title: US-10-080-959A-2

Perfect score: 20

Sequence: 1 ttgttgctgcctcactagag 20

Scoring table: IDENTITY_NUC

Gapped 10.0, Gapped 1.0

Searched: 441362 seqs, 1533381 residues

Total number of hits satisfying chosen parameters: 364038

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

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3: /cgn2_6/prodata/2/ina/6A.COMB.seq.*

4: /cgn2_6/prodata/2/ina/6B.COMB.seq.*

5: /cgn2_6/prodata/2/ina/PCITUS.COMB.seq.*

6: /cgn2_6/prodata/2/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	13.4	67.0	17	3	US-08-193-627-25
4	12.2	61.0	22	1	US-08-148-117A-2
5	12.2	61.0	24	4	US-09-593-012-108
6	12	60.0	21	4	US-08-758-306-999
7	12	60.0	17	1	US-08-803-346-29
8	11.8	59.0	20	4	US-09-553-231-7
9	11.6	58.0	21	1	US-07-994-423-4
10	11.6	58.0	21	1	US-08-421-891-4
11	11.6	57.0	21	2	US-08-908-212A-3
12	11.4	57.0	25	2	US-08-859-998-509
13	11.4	56.0	25	4	US-09-225-928-509
14	11.4	56.0	19	1	US-08-164-200-9
15	11.2	56.0	19	1	US-08-327-363-7
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17	11.2	56.0	21	1	US-08-136-118-6
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22	11.1	55.0	22	3	US-09-064-864-17
23	11.1	55.0	23	1	US-08-821-119-21
24	11.1	55.0	23	1	US-08-821-118-4
25	11.1	55.0	23	2	US-08-481-335-18
26	11.1	55.0	24	1	US-08-574-763-6
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30	10.8	54.0	20	2	US-08-757-653-68	Sequence 68, Appl
31	10.8	54.0	20	2	US-08-117-952-652	Sequence 652, Appl
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33	10.8	54.0	20	4	US-09-428-696-29	Sequence 29, Appl
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35	10.8	54.0	20	4	US-08-520-946-68	Sequence 68, Appl
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156	10.2	51.0	20	4	US-09-485-549-9	Sequence 9, Appl1	C 230	9.8	49.0	17	4	US-09-021-701-143	Sequence 143, App
157	10.2	51.0	20	4	US-09-485-549-10	Sequence 10, Appl	C 231	9.8	49.0	17	4	US-09-021-701-144	Sequence 144, App
158	10.2	51.0	20	4	US-09-412-499A-10	Sequence 10, Appl	C 232	9.8	49.0	18	1	US-08-164-200-13	Sequence 13, Appl
159	10.2	51.0	20	4	US-09-633-659-17	Sequence 17, Appl	C 233	9.8	49.0	18	2	US-08-627-254C-3	Sequence 3, Appl1
160	10.2	51.0	20	4	US-09-689-964-11	Sequence 11, Appl	C 234	9.8	49.0	18	4	US-09-474-922A-24	Sequence 24, Appl
161	10.2	51.0	20	4	US-09-187-108-9	Sequence 9, Appl1	C 235	9.8	49.0	18	4	US-09-018-584A-16	Sequence 16, App
162	10.2	51.0	20	5	PCT-US91-05815-8	Sequence 8, Appl	C 236	9.8	49.0	18	4	US-09-496-694B-167	Sequence 167, App
163	10.2	51.0	20	5	PCT-US91-05815-25	Sequence 25, Appl	C 237	9.8	49.0	19	2	US-08-807-104-12	Sequence 12, Appl
164	10.2	51.0	20	5	PCT-US93-08101-84	Sequence 84, Appl	C 238	9.8	49.0	19	3	US-08-480-068-12	Sequence 12, Appl
165	10.2	51.0	20	5	PCT-US93-08367A-11	Sequence 11, Appl	C 239	9.8	49.0	19	4	US-08-973-137-12	Sequence 12, Appl
166	10.2	51.0	20	6	PCT-US95-05265-55	Sequence 55, Appl	C 240	9.8	49.0	20	1	US-08-060-822A-14	Sequence 14, Appl
167	10.2	51.0	20	6	546585-8	Patent No. 546585	C 241	9.8	49.0	20	1	US-08-112-816-12	Sequence 12, Appl
168	10.2	51.0	21	1	US-08-327-363-4	Sequence 4, Appl1	C 242	9.8	49.0	20	1	US-08-290-936-7	Sequence 7, Appl1
169	10.2	51.0	21	1	US-08-327-363-5	Sequence 5, Appl1	C 243	9.8	49.0	20	1	US-08-228-913-5	Sequence 5, Appl1
170	10.2	51.0	21	3	US-09-143-370-14	Sequence 14, Appl	C 244	9.8	49.0	20	2	US-08-117-952-290	Sequence 290, App
171	10.2	51.0	21	4	US-09-283-011-31	Sequence 31, Appl	C 245	9.8	49.0	20	2	US-08-227-180B-30	Sequence 30, Appl
172	10.2	51.0	21	4	US-09-450-083-14	Sequence 14, Appl	C 246	9.8	49.0	20	3	US-08-485-942A-91	Sequence 91, Appl

C 247	9.8	49.0	20	3	US-08-488-214A-91	Sequence 91, Appl	330	9.6	48.0	20	2	US-08-481-876-9	Sequence 9, Appl
C 248	9.8	49.0	20	3	US-08-488-214A-91	Sequence 91, Appl	331	9.6	48.0	20	2	US-08-481-876-10	Sequence 8, Appl
C 249	9.8	49.0	20	4	US-09-429-322-84	Sequence 84, Appl	332	9.6	48.0	20	2	US-08-856-141-8	Sequence 1, Appl
C 250	9.8	49.0	20	4	US-09-103-875-78	Sequence 78, Appl	333	9.6	48.0	20	3	US-09-185-437-1	Sequence 9, Appl
C 251	9.8	49.0	20	4	US-09-183-846A-9	Sequence 9, Appl	334	9.6	48.0	20	3	US-09-185-437-9	Sequence 10, Appl
C 252	9.8	49.0	20	4	US-09-662-249A-33	Sequence 33, Appl	335	9.6	48.0	20	3	US-09-185-437-7	Sequence 7, Appl
C 253	9.8	49.0	20	4	US-08-483-211A-91	Sequence 91, Appl	336	9.6	48.0	20	3	US-09-018-034-7	Sequence 10, Appl
C 254	9.8	49.0	20	4	US-08-488-223A-91	Sequence 91, Appl	337	9.6	48.0	20	3	US-09-018-034-14	Sequence 14, Appl
C 255	9.8	49.0	20	4	US-08-361-578C-9	Sequence 9, Appl	338	9.6	48.0	20	3	US-09-018-034-21	Sequence 21, Appl
C 256	9.8	49.0	20	4	US-08-438-431A-91	Sequence 91, Appl	339	9.6	48.0	20	3	US-09-166-186-147	Sequence 14, Appl
C 257	9.8	49.0	20	4	US-09-791-211-20	Sequence 20, Appl	340	9.6	48.0	20	3	US-09-166-186-148	Sequence 14, Appl
C 258	9.8	49.0	20	5	PCT-US94-05257-14	Sequence 14, Appl	341	9.6	48.0	20	4	US-09-166-186-149	Sequence 14, Appl
C 259	9.8	49.0	21	1	US-08-009-263C-38	Sequence 38, Appl	342	9.6	48.0	20	4	US-09-313-932-149	Sequence 149, Appl
C 260	9.8	49.0	21	1	US-08-598-591-41	Sequence 41, Appl	343	9.6	48.0	20	4	US-09-313-932-150	Sequence 150, Appl
C 261	9.8	49.0	21	1	US-08-798-691-45	Sequence 45, Appl	344	9.6	48.0	20	4	US-09-313-932-151	Sequence 151, Appl
C 262	9.8	49.0	21	2	US-08-332-766A-118	Sequence 118, Appl	345	9.6	48.0	20	4	US-09-021-701-1045	Sequence 1045, Appl
C 263	9.8	49.0	21	2	US-08-628-687-6	Sequence 6, Appl	346	9.6	48.0	20	4	US-09-488-857B-34	Sequence 34, Appl
C 264	9.8	49.0	21	2	US-08-628-687-6	Sequence 6, Appl	347	9.6	48.0	20	4	US-09-488-857B-35	Sequence 35, Appl
C 265	9.8	49.0	21	3	US-08-825-487A-45	Sequence 45, Appl	348	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 266	9.8	49.0	21	3	US-08-825-487A-83	Sequence 83, Appl	349	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 267	9.8	49.0	21	3	US-09-074-476-45	Sequence 45, Appl	350	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 268	9.8	49.0	21	3	US-08-838-715B-38	Sequence 38, Appl	351	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 269	9.8	49.0	21	3	US-09-253-025-30	Sequence 30, Appl	352	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 270	9.8	49.0	22	6	5231015-4	Sequence 30, Appl	353	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 271	9.8	49.0	23	2	US-08-687-372-3	Sequence 78, Appl	354	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 272	9.8	49.0	23	2	US-08-761-277A-78	Sequence 78, Appl	355	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 273	9.8	49.0	23	4	US-09-238-356-21	Sequence 21, Appl	356	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 274	9.8	49.0	23	6	5219727-40	Sequence 21, Appl	357	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 275	9.8	49.0	24	1	US-08-470-202-22	Sequence 22, Appl	358	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 276	9.8	49.0	24	1	US-08-471-770-22	Sequence 22, Appl	359	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 277	9.8	49.0	24	2	US-08-468-059-22	Sequence 22, Appl	360	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 278	9.8	49.0	24	2	US-08-723-726-3	Sequence 22, Appl	361	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 279	9.8	49.0	24	4	US-09-177-953-47	Sequence 47, Appl	362	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 280	9.8	49.0	24	4	US-09-109-916-22	Sequence 22, Appl	363	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 281	9.8	49.0	24	4	US-09-268-347-39	Sequence 39, Appl	364	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 282	9.8	49.0	24	4	US-09-425-638A-19	Sequence 19, Appl	365	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 283	9.8	49.0	24	4	US-09-543-004-19	Sequence 19, Appl	366	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 284	9.8	49.0	24	4	US-09-395-345-32	Sequence 32, Appl	367	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 285	9.8	49.0	24	4	US-09-560-587-25	Sequence 25, Appl	368	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 286	9.8	49.0	24	4	US-09-261-358A-25	Sequence 25, Appl	369	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 287	9.8	49.0	24	4	US-09-201-458-18	Sequence 18, Appl	370	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 288	9.8	49.0	25	1	US-08-316-293-32	Sequence 32, Appl	371	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 289	9.8	49.0	25	3	US-08-835-728D-216	Sequence 216, Appl	372	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 290	9.8	49.0	25	4	US-09-490-558-216	Sequence 216, Appl	373	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 291	9.8	49.0	25	4	US-09-340-323A-6	Sequence 216, Appl	374	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 292	9.8	49.0	25	4	US-09-538-709-451	Sequence 451, Appl	375	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 293	9.6	48.0	17	4	US-08-584-040-1493	Sequence 1493, Appl	376	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 294	9.6	48.0	17	4	US-08-584-040-1493	Sequence 1493, Appl	377	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 295	9.6	48.0	17	4	US-08-584-040-7243	Sequence 7243, Appl	378	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 296	9.6	48.0	17	4	US-08-584-040-7243	Sequence 7243, Appl	379	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 297	9.6	48.0	17	4	US-08-584-040-7243	Sequence 7243, Appl	380	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 298	9.6	48.0	17	4	US-08-584-040-7243	Sequence 7243, Appl	381	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 299	9.6	48.0	18	2	US-08-450-905B-92	Sequence 92, Appl	382	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 300	9.6	48.0	18	3	US-07-982-759F-92	Sequence 92, Appl	383	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 301	9.6	48.0	18	3	US-09-166-186-165	Sequence 166, Appl	384	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 302	9.6	48.0	18	3	US-09-166-186-167	Sequence 167, Appl	385	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 303	9.6	48.0	18	3	US-09-166-186-168	Sequence 168, Appl	386	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 304	9.6	48.0	18	4	US-08-969-815-20	Sequence 20, Appl	387	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 305	9.6	48.0	18	4	US-09-120-025-20	Sequence 20, Appl	388	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 306	9.6	48.0	18	4	US-09-313-932-166	Sequence 166, Appl	389	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 307	9.6	48.0	18	4	US-09-313-932-167	Sequence 167, Appl	390	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 308	9.6	48.0	18	4	US-09-313-932-168	Sequence 168, Appl	391	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 309	9.6	48.0	18	4	US-09-313-932-169	Sequence 169, Appl	392	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 310	9.6	48.0	18	4	US-09-313-932-170	Sequence 170, Appl	393	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 311	9.6	48.0	19	3	US-08-171-718-82	Sequence 82, Appl	394	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 312	9.6	48.0	19	3	US-08-478-087-82	Sequence 82, Appl	395	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 313	9.6	48.0	19	4	US-09-470-443-114	Sequence 114, Appl	396	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 314	9.6	48.0	20	1	US-07-847-055A-3	Sequence 3, Appl	397	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 315	9.6	48.0	20	1	US-08-161-673A-1	Sequence 1, Appl	398	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 316	9.6	48.0	20	1	US-08-161-673A-10	Sequence 10, Appl	399	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 317	9.6	48.0	20	1	US-08-161-673A-19	Sequence 19, Appl	400	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 318	9.6	48.0	20	1	US-08-161-673A-10	Sequence 10, Appl	401	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl
C 319	9.6	48.0	20	2	US-08-481-876-1	Sequence 1, Appl	402	9.6	48.0	20	4	US-09-457-708-23	Sequence 23, Appl

393	9.4	47.0	20	1	US-08-913-976-7	Sequence 7, Appl1	466	9.4	47.0	24	3	US-08-691-563C-23	Sequence 23, Appl1
394	9.4	47.0	20	1	US-08-913-976-13	Sequence 16, App	467	9.4	47.0	24	3	US-08-471-039-186	Sequence 2, Appl1
395	9.4	47.0	20	1	US-08-655-878-8	Sequence 8, Appl1	468	9.4	47.0	24	3	US-09-085-735-2	Sequence 2, Appl1
396	9.4	47.0	20	2	US-08-530-524A-4	Sequence 4, Appl1	469	9.4	47.0	24	3	US-09-085-442-2	Sequence 2, Appl1
397	9.4	47.0	20	2	US-08-899-514-8	Sequence 8, Appl1	470	9.4	47.0	24	4	US-08-062-023-39	Sequence 39, Appl1
398	9.4	47.0	20	3	US-09-289-267-155	Sequence 155, App	471	9.4	47.0	24	4	US-09-200-990-19	Sequence 19, Appl1
399	9.4	47.0	20	3	US-09-016-649-7	Sequence 7, Appl1	472	9.4	47.0	24	4	US-09-200-990-23	Sequence 23, Appl1
400	9.4	47.0	20	3	US-09-249-730-206	Sequence 206, App	473	9.4	47.0	24	4	US-09-453-702A-13	Sequence 13, Appl1
401	9.4	47.0	20	4	US-09-433-699-50	Sequence 50, Appl1	474	9.4	47.0	24	4	US-09-133-411-19	Sequence 19, Appl1
402	9.4	47.0	20	4	US-09-126-109-17	Sequence 17, Appl1	475	9.4	47.0	24	4	US-09-133-411-23	Sequence 23, Appl1
403	9.4	47.0	20	4	US-09-253-025-23	Sequence 23, Appl1	476	9.4	47.0	24	4	US-09-225-928-1319	Sequence 1319, App
404	9.4	47.0	20	4	US-09-021-701-1046	Sequence 1046, App	477	9.4	47.0	24	5	PCT-US93-11198-186	Sequence 186, App
405	9.4	47.0	20	4	US-09-021-701-1047	Sequence 1047, App	478	9.4	47.0	24	5	PCT-US94-10957-13	Sequence 13, Appl1
406	9.4	47.0	20	4	US-09-021-701-1048	Sequence 1048, App	479	9.4	47.0	25	1	US-08-227-689-7	Sequence 7, Appl1
407	9.4	47.0	20	4	US-09-021-701-1049	Sequence 1049, App	480	9.4	47.0	25	1	US-08-068-945A-57	Sequence 57, Appl1
408	9.4	47.0	20	4	US-09-021-701-1050	Sequence 1050, App	481	9.4	47.0	25	1	US-08-317-432A-47	Sequence 47, Appl1
409	9.4	47.0	20	4	US-09-180-437-227	Sequence 227, App	482	9.4	47.0	25	1	US-08-462-806-57	Sequence 57, Appl1
410	9.4	47.0	20	4	US-09-489-868A-61	Sequence 61, Appl1	483	9.4	47.0	25	1	US-08-977-818-16	Sequence 16, Appl1
411	9.4	47.0	20	4	US-09-254-733-34	Sequence 34, Appl1	484	9.4	47.0	25	2	US-08-670-374B-16	Sequence 16, Appl1
412	9.4	47.0	20	4	US-09-488-744A-67	Sequence 67, Appl1	485	9.4	47.0	25	2	US-08-447-430A-12	Sequence 12, Appl1
413	9.4	47.0	20	4	US-09-593-589-4	Sequence 4, Appl1	486	9.4	47.0	25	4	US-08-256-799-19	Sequence 19, Appl1
414	9.4	47.0	20	4	US-09-702-246-29	Sequence 29, Appl1	487	9.4	47.0	25	4	US-08-462-437-19	Sequence 19, Appl1
415	9.4	47.0	20	4	US-09-336-643A-87	Sequence 87, Appl1	488	9.4	47.0	25	4	US-09-146-187-16	Sequence 16, Appl1
416	9.4	47.0	20	4	US-09-907-843-24	Sequence 24, Appl1	489	9.4	47.0	25	4	US-09-368-169-7	Sequence 7, Appl1
417	9.4	47.0	20	4	US-09-675-610B-79	Sequence 79, Appl1	490	9.4	47.0	25	5	PCT-US93-10106-19	Sequence 19, Appl1
418	9.4	47.0	20	5	PCT-US91-03056-12	Sequence 12, Appl1	491	9.2	46.0	14	4	US-08-535-249-135	Sequence 135, App
419	9.4	47.0	20	5	PCT-US95-04858-7	Sequence 7, Appl1	492	9.2	46.0	14	4	US-09-531-000-68	Sequence 68, Appl1
420	9.4	47.0	21	1	US-08-317-432A-49	Sequence 49, Appl1	493	9.2	46.0	15	2	US-08-292-620A-12	Sequence 12, Appl1
421	9.4	47.0	21	1	US-08-873-479-48	Sequence 48, Appl1	494	9.2	46.0	15	2	US-08-292-620A-261	Sequence 261, App
422	9.4	47.0	21	2	US-08-973-661A-34	Sequence 34, Appl1	495	9.2	46.0	15	3	US-09-071-845-12	Sequence 12, Appl1
423	9.4	47.0	21	2	US-08-249-189-14	Sequence 14, Appl1	496	9.2	46.0	15	3	US-09-071-845-261	Sequence 261, App
424	9.4	47.0	21	2	US-08-484-624A-14	Sequence 14, Appl1	497	9.2	46.0	17	1	US-07-854-596B-23	Sequence 23, Appl1
425	9.4	47.0	21	2	US-08-477-733B-14	Sequence 14, Appl1	498	9.2	46.0	17	1	US-07-854-596B-23	Sequence 23, Appl1
426	9.4	47.0	21	3	US-08-750-145A-6	Sequence 6, Appl1	499	9.2	46.0	17	1	US-08-373-124A-2343	Sequence 2343, App
427	9.4	47.0	21	3	US-08-973-965-8	Sequence 8, Appl1	500	9.2	46.0	17	1	US-08-275-983B-12	Sequence 12, Appl1
428	9.4	47.0	21	3	US-09-088-913A-14	Sequence 14, Appl1	501	9.2	46.0	17	1	US-08-758-306-129	Sequence 129, App
429	9.4	47.0	21	3	US-09-157-177-15	Sequence 15, Appl1	502	9.2	46.0	17	1	US-08-435-628-2343	Sequence 2343, App
430	9.4	47.0	21	4	US-09-384-305-25	Sequence 25, Appl1	503	9.2	46.0	17	2	US-08-292-620A-1637	Sequence 1637, App
431	9.4	47.0	21	4	US-09-101-886B-23	Sequence 23, Appl1	504	9.2	46.0	17	2	US-08-292-620A-1955	Sequence 1955, App
432	9.4	47.0	21	4	US-08-793-660B-17	Sequence 17, Appl1	505	9.2	46.0	17	2	US-08-475-288A-643	Sequence 643, App
433	9.4	47.0	21	4	US-08-769-819-14	Sequence 14, Appl1	506	9.2	46.0	17	2	US-08-906-484-7	Sequence 7, Appl1
434	9.4	47.0	21	4	US-08-770-974-14	Sequence 14, Appl1	507	9.2	46.0	17	3	US-08-482-080A-643	Sequence 643, App
435	9.4	47.0	21	4	US-08-793-109-4	Sequence 4, Appl1	508	9.2	46.0	17	3	US-08-071-845-1697	Sequence 1697, App
436	9.4	47.0	21	4	US-08-770-981-14	Sequence 14, Appl1	509	9.2	46.0	17	3	US-08-071-845-1925	Sequence 1925, App
437	9.4	47.0	21	4	US-09-399-106-14	Sequence 14, Appl1	510	9.2	46.0	17	4	US-08-794-002-20	Sequence 20, Appl1
438	9.4	47.0	21	4	US-09-410-903-79	Sequence 79, Appl1	511	9.2	46.0	17	4	US-08-584-040-2151	Sequence 2151, App
439	9.4	47.0	22	1	US-08-379-078-705	Sequence 705, App	512	9.2	46.0	17	4	US-08-584-040-2152	Sequence 2152, App
440	9.4	47.0	22	1	US-09-240-918-8	Sequence 8, Appl1	513	9.2	46.0	17	4	US-08-584-040-2153	Sequence 2153, App
441	9.4	47.0	22	4	US-07-974-409C-267	Sequence 267, App	514	9.2	46.0	17	4	US-08-854-039B-20	Sequence 20, Appl1
442	9.4	47.0	22	4	US-09-593-012-8	Sequence 8, Appl1	515	9.2	46.0	18	1	US-08-275-983B-13	Sequence 13, Appl1
443	9.4	47.0	22	5	PCT-US93-00977-267	Sequence 267, App	516	9.2	46.0	18	1	US-08-153-848-30	Sequence 30, Appl1
444	9.4	47.0	23	1	US-08-912-976-16	Sequence 16, Appl1	517	9.2	46.0	18	1	US-08-758-306-521	Sequence 521, App
445	9.4	47.0	23	1	US-08-854-222-14	Sequence 14, Appl1	518	9.2	46.0	18	3	US-09-166-186-164	Sequence 164, App
446	9.4	47.0	23	3	US-09-222-817-16	Sequence 16, Appl1	519	9.2	46.0	18	3	US-09-166-186-165	Sequence 165, App
447	9.4	47.0	23	3	US-09-188-039-14	Sequence 14, Appl1	520	9.2	46.0	18	3	US-09-299-843A-30	Sequence 30, Appl1
448	9.4	47.0	23	4	US-09-063-733A-13	Sequence 13, Appl1	521	9.2	46.0	18	4	US-09-313-932-164	Sequence 164, App
449	9.4	47.0	23	4	US-09-710-200-9	Sequence 9, Appl1	522	9.2	46.0	18	4	US-09-313-932-165	Sequence 165, App
450	9.4	47.0	23	4	US-09-907-843-4	Sequence 4, Appl1	523	9.2	46.0	18	4	US-09-632-580A-54	Sequence 54, Appl1
451	9.4	47.0	24	1	US-08-495-743-39	Sequence 39, Appl1	524	9.2	46.0	18	4	US-09-316-447A-72	Sequence 72, Appl1
452	9.4	47.0	24	1	US-08-411-796-186	Sequence 186, App	525	9.2	46.0	18	4	US-08-794-002-21	Sequence 21, Appl1
453	9.4	47.0	24	1	US-08-495-739-39	Sequence 39, Appl1	526	9.2	46.0	18	4	US-08-584-040-3103	Sequence 8103, App
454	9.4	47.0	24	1	US-08-495-741-39	Sequence 39, Appl1	527	9.2	46.0	18	4	US-09-088-337B-30	Sequence 30, Appl1
455	9.4	47.0	24	1	US-08-471-724-19	Sequence 19, Appl1	528	9.2	46.0	18	4	US-08-854-039B-21	Sequence 21, Appl1
456	9.4	47.0	24	1	US-08-471-724-23	Sequence 23, Appl1	529	9.2	46.0	18	4	US-09-636-735A-30	Sequence 30, Appl1
457	9.4	47.0	24	2	US-08-471-969-19	Sequence 19, Appl1	530	9.2	46.0	18	5	PCT-US93-11153-30	Sequence 15, Appl1
458	9.4	47.0	24	2	US-08-471-969-23	Sequence 23, Appl1	531	9.2	46.0	20	1	US-08-142-678A-15	Sequence 15, Appl1
459	9.4	47.0	24	2	US-08-384-137-19	Sequence 19, Appl1	532	9.2	46.0	20	1	US-07-872-678A-13	Sequence 13, Appl1
460	9.4	47.0	24	2	US-08-384-137-23	Sequence 23, Appl1	533	9.2	46.0	20	1	US-08-152-313-9	Sequence 9, Appl1
461	9.4	47.0	24	2	US-08-447-430A-10	Sequence 10, Appl1	534	9.2	46.0	20	1	US-08-152-313-117	Sequence 117, App
462	9.4	47.0	24	2	US-08-470-006A-19	Sequence 19, Appl1	535	9.2	46.0	20	1	US-08-255-264-16	Sequence 16, Appl1
463	9.4	47.0	24	2	US-08-470-006A-23	Sequence 23, Appl1	536	9.2	46.0	20	1	US-08-555-394-9	Sequence 9, Appl1
464	9.4	47.0	24	2	US-08-859-998-1319	Sequence 1319, App	537	9.2	46.0	20	1	US-08-413-118-101	Sequence 101, App
465	9.4	47.0	24	3	US-08-691-563C-19	Sequence 19, Appl1	538	9.2	46.0	20	1	US-08-325-562-6	Sequence 6, Appl1

539	9.2	46.0	20	1	US-08-579-223-9	Sequence 9, Appl1	C 612	9.2	46.0	22	1	US-08-599-252-36	Sequence 36, Appl1
C 540	9.2	46.0	20	1	US-08-579-223-117	Sequence 117, App	613	9.2	46.0	22	3	US-08-857-464-3	Sequence 3, Appl1
541	9.2	46.0	20	1	US-08-437-795-6	Sequence 6, Appl1	614	9.2	46.0	22	3	US-08-937-063-26	Sequence 26, Appl1
542	9.2	46.0	20	1	US-08-201-118-28	Sequence 28, Appl1	615	9.2	46.0	22	4	US-08-928-465-3	Sequence 3, Appl1
C 543	9.2	46.0	20	2	US-08-117-952-121	Sequence 121, App	616	9.2	46.0	22	4	US-09-230-225B-14	Sequence 14, Appl1
C 544	9.2	46.0	20	2	US-08-117-952-417	Sequence 417, App	C 617	9.2	46.0	22	5	PCT-US96-06352-36	Sequence 36, Appl1
545	9.2	46.0	20	2	US-08-583-345B-3	Sequence 3, Appl1	C 618	9.2	46.0	22	5	PCT-US96-06383-36	Sequence 36, Appl1
546	9.2	46.0	20	2	US-08-587-312B-3	Sequence 3, Appl1	619	9.2	46.0	22	5	US-08-753-147-63	Sequence 63, Appl1
547	9.2	46.0	20	2	US-08-238-821B-28	Sequence 28, Appl1	620	9.2	46.0	23	4	US-09-376-781-29	Sequence 29, Appl1
C 548	9.2	46.0	20	2	US-08-822-445-18	Sequence 18, Appl1	C 621	9.2	46.0	23	4	US-09-318-907-172	Sequence 172, App
C 549	9.2	46.0	20	2	US-08-793-170-4	Sequence 4, Appl1	C 622	9.2	46.0	23	4	US-09-218-207-172	Sequence 172, App
550	9.2	46.0	20	3	US-08-473-446-101	Sequence 101, App	623	9.2	46.0	23	4	US-09-686-179A-3	Sequence 3, Appl1
551	9.2	46.0	20	3	US-08-483-746A-16	Sequence 16, Appl1	624	9.2	46.0	23	4	US-09-851-220-6	Sequence 6, Appl1
C 552	9.2	46.0	20	3	US-08-892-873-4	Sequence 4, Appl1	C 625	9.2	46.0	24	1	US-07-791-213D-98	Sequence 98, Appl1
C 553	9.2	46.0	20	3	US-08-745-892-9	Sequence 9, Appl1	626	9.2	46.0	24	1	US-08-447-313-3	Sequence 3, Appl1
C 554	9.2	46.0	20	3	US-08-857-464-5	Sequence 5, Appl1	C 627	9.2	46.0	24	1	US-08-293-150A-98	Sequence 98, Appl1
C 555	9.2	46.0	20	3	US-09-166-186-145	Sequence 145, App	C 628	9.2	46.0	24	1	US-08-727-003A-20	Sequence 20, Appl1
C 556	9.2	46.0	20	3	US-09-166-186-145	Sequence 145, App	C 629	9.2	46.0	24	1	US-08-545-562A-17	Sequence 17, Appl1
557	9.2	46.0	20	3	US-08-778-381-22	Sequence 22, Appl1	C 630	9.2	46.0	24	2	US-08-356-132-6	Sequence 6, Appl1
558	9.2	46.0	20	3	US-08-855-312B-83	Sequence 83, Appl1	631	9.2	46.0	24	2	US-08-887-434-3	Sequence 3, Appl1
C 559	9.2	46.0	20	3	US-09-418-640-52	Sequence 52, Appl1	C 632	9.2	46.0	24	2	US-08-346-832-18	Sequence 18, Appl1
C 560	9.2	46.0	20	4	US-09-280-805-167	Sequence 167, App	C 633	9.2	46.0	24	2	US-08-160-063-18	Sequence 18, Appl1
C 561	9.2	46.0	20	4	US-08-766-528-65	Sequence 65, Appl1	C 634	9.2	46.0	24	2	US-08-350-260A-20	Sequence 20, Appl1
C 562	9.2	46.0	20	4	US-09-313-932-145	Sequence 145, App	C 635	9.2	46.0	24	2	US-08-859-998-835	Sequence 835, App
C 563	9.2	46.0	20	4	US-09-313-932-146	Sequence 146, App	636	9.2	46.0	24	3	US-08-487-799-36	Sequence 36, Appl1
564	9.2	46.0	20	4	US-09-038-637-175	Sequence 175, App	C 637	9.2	46.0	24	3	US-08-473-313-18	Sequence 18, Appl1
C 565	9.2	46.0	20	4	US-09-038-637-183	Sequence 183, App	C 638	9.2	46.0	24	3	US-08-672-850-33	Sequence 33, Appl1
C 566	9.2	46.0	20	4	US-09-334-765A-4	Sequence 4, Appl1	C 639	9.2	46.0	24	4	US-08-321-543-8	Sequence 8, Appl1
C 567	9.2	46.0	20	4	US-09-021-701-1038	Sequence 1038, Ap	640	9.2	46.0	24	4	US-09-481-288-2	Sequence 2, Appl1
C 568	9.2	46.0	20	4	US-09-021-701-1039	Sequence 1039, Ap	C 641	9.2	46.0	24	4	US-09-021-701-1	Sequence 1, Appl1
569	9.2	46.0	20	4	US-09-657-81A-12	Sequence 12, Appl1	C 642	9.2	46.0	24	4	US-09-463-702A-24	Sequence 24, Appl1
C 570	9.2	46.0	20	4	US-09-356-575E-4	Sequence 4, Appl1	C 643	9.2	46.0	25	1	US-09-225-928-835	Sequence 835, App
C 571	9.2	46.0	20	4	US-09-721-822A-35	Sequence 35, Appl1	C 644	9.2	46.0	25	1	US-08-125-012-19	Sequence 19, Appl1
C 572	9.2	46.0	20	4	US-09-333-820-4	Sequence 4, Appl1	C 645	9.2	46.0	25	1	US-08-321-579A-13	Sequence 13, Appl1
573	9.2	46.0	20	4	US-09-049-714-1	Sequence 1, Appl1	C 646	9.2	46.0	25	1	US-08-783-818-19	Sequence 19, Appl1
C 574	9.2	46.0	20	4	US-09-336-540-18	Sequence 18, Appl1	C 647	9.2	46.0	25	2	US-08-453-349-19	Sequence 19, Appl1
C 575	9.2	46.0	20	4	US-09-326-186B-204	Sequence 204, App	C 648	9.2	46.0	25	2	US-08-756-506-11	Sequence 11, Appl1
C 576	9.2	46.0	20	4	US-09-358-036-43	Sequence 43, Appl1	C 649	9.2	46.0	25	2	US-08-704-707-13	Sequence 13, Appl1
577	9.2	46.0	20	4	US-08-985-492-20	Sequence 20, Appl1	C 650	9.2	46.0	25	2	US-08-979-385B-17	Sequence 17, Appl1
C 578	9.2	46.0	20	4	US-09-851-520-25	Sequence 25, Appl1	C 651	9.2	46.0	25	3	US-08-487-799-49	Sequence 49, Appl1
C 579	9.2	46.0	20	4	US-09-087-239-43	Sequence 43, Appl1	C 652	9.2	46.0	25	3	US-08-714-071-5	Sequence 5, Appl1
580	9.2	46.0	20	4	US-09-498-851-83	Sequence 83, Appl1	653	9.2	46.0	25	3	US-08-586-039B-6	Sequence 6, Appl1
581	9.2	46.0	20	4	US-09-746-694-25	Sequence 25, Appl1	C 654	9.2	46.0	25	4	US-09-321-461-13	Sequence 13, Appl1
C 582	9.2	46.0	20	4	US-08-469-260A-107	Sequence 107, App	C 655	9.2	46.0	25	4	US-08-943-731-310	Sequence 310, App
C 583	9.2	46.0	20	4	US-08-469-260A-162	Sequence 162, App	C 656	9.2	46.0	25	4	US-09-368-140-24	Sequence 24, Appl1
584	9.2	46.0	20	5	PCT-US94-12947A-9	Sequence 9, Appl1	C 657	9.2	46.0	25	4	US-08-357-398A-5	Sequence 5, Appl1
C 585	9.2	46.0	20	5	PCT-US94-12947A-117	Sequence 117, App	658	9.2	46.0	25	4	US-09-538-709-319	Sequence 319, App
586	9.2	46.0	20	5	PCT-US94-05744-28	Sequence 28, Appl1	C 659	9.2	46.0	25	4	US-08-880-576-19	Sequence 19, Appl1
587	9.2	46.0	21	1	US-08-009-263C-42	Sequence 42, Appl1	C 660	9.2	46.0	25	5	PCT-US95-16206A-5	Sequence 5, Appl1
588	9.2	46.0	21	1	US-08-377-687-53	Sequence 53, Appl1	C 661	9.2	46.0	12	4	US-09-281-418-168	Sequence 168, App
C 589	9.2	46.0	21	1	US-08-232-177A-335	Sequence 335, App	C 662	9.2	46.0	16	4	US-09-813-781-57	Sequence 57, Appl1
590	9.2	46.0	21	1	US-08-461-823-25	Sequence 25, Appl1	C 663	9.2	46.0	17	1	US-08-373-124A-476	Sequence 476, App
591	9.2	46.0	21	1	US-08-777-192-53	Sequence 53, Appl1	664	9.2	46.0	17	1	US-08-204-679-14	Sequence 14, Appl1
C 592	9.2	46.0	21	2	US-08-117-952-601	Sequence 601, App	C 665	9.2	46.0	17	1	US-08-435-628-476	Sequence 476, App
C 593	9.2	46.0	21	2	US-08-474-450A-43	Sequence 43, Appl1	666	9.2	46.0	17	2	US-08-744-332-14	Sequence 14, Appl1
C 594	9.2	46.0	21	2	US-08-403-888A-87	Sequence 87, Appl1	C 667	9.2	46.0	17	3	US-08-985-162-222	Sequence 222, App
C 595	9.2	46.0	21	2	US-08-928-692-62	Sequence 62, Appl1	C 668	9.2	46.0	17	3	US-08-985-162-384	Sequence 384, App
C 596	9.2	46.0	21	3	US-09-009-913-37	Sequence 37, Appl1	C 669	9.2	46.0	17	3	US-08-985-162-385	Sequence 385, App
C 597	9.2	46.0	21	3	US-09-009-913-118	Sequence 118, App	670	9.2	46.0	17	4	US-08-584-040-7593	Sequence 7593, Ap
598	9.2	46.0	21	3	US-08-733-360A-6	Sequence 6, Appl1	671	9.2	46.0	17	4	US-09-291-541-4	Sequence 4, Appl1
599	9.2	46.0	21	3	US-09-371-710-17	Sequence 17, Appl1	672	9.2	46.0	18	1	US-08-403-634-23	Sequence 23, Appl1
C 600	9.2	46.0	21	3	US-09-371-710-18	Sequence 18, Appl1	673	9.2	46.0	18	1	US-08-403-634-23	Sequence 23, Appl1
C 601	9.2	46.0	21	3	US-08-838-715B-42	Sequence 42, Appl1	C 674	9.2	46.0	18	2	US-08-951-648-19	Sequence 19, Appl1
602	9.2	46.0	21	4	US-08-971-982-53	Sequence 53, Appl1	C 675	9.2	46.0	18	2	US-08-788-892-6	Sequence 6, Appl1
603	9.2	46.0	21	4	US-08-916-935-6	Sequence 6, Appl1	C 676	9.2	46.0	18	3	US-08-072-064-17	Sequence 17, Appl1
C 604	9.2	46.0	21	4	US-09-116-032-23	Sequence 23, Appl1	C 677	9.2	46.0	18	3	US-09-255-911-29	Sequence 29, Appl1
605	9.2	46.0	21	4	US-08-963-466-74	Sequence 74, Appl1	C 678	9.2	46.0	18	3	US-08-181-664-37	Sequence 37, Appl1
606	9.2	46.0	21	4	US-08-943-731-221	Sequence 221, App	679	9.2	46.0	18	3	US-08-180-470-44	Sequence 44, Appl1
C 608	9.2	46.0	21	4	US-09-648-386-17	Sequence 17, Appl1	680	9.2	46.0	18	3	US-09-289-377-39	Sequence 39, Appl1
609	9.2	46.0	21	4	US-09-648-386-18	Sequence 18, Appl1	C 681	9.2	46.0	18	3	US-09-174-437-19	Sequence 19, Appl1
610	9.2	46.0	21	4	US-09-339-972-62	Sequence 62, Appl1	682	9.2	46.0	18	4	US-08-913-441B-23	Sequence 23, Appl1
611	9.2	46.0	22	1	US-08-744-481A-32	Sequence 32, Appl1	683	9.2	46.0	18	4	US-08-584-040-8296	Sequence 8296, Ap
611	9.2	46.0	22	1	US-08-255-892-97	Sequence 97, Appl1	C 684	9.2	46.0	18	4	US-09-340-475-6	Sequence 6, Appl1

685	9	45.0	18	4	US-09-373-953-6	Sequence 6, Appl	C 758	9	45.0	22	4	US-08-552-369-11	Sequence 11, Appl
686	9	45.0	19	4	US-09-177-249-321	Sequence 321, App	759	9	45.0	22	4	US-08-677-064-4	Sequence 4, Appl
687	9	45.0	20	1	US-07-747-785-5	Sequence 5, Appl	C 760	9	45.0	22	4	US-09-448-894-24	Sequence 24, Appl
688	9	45.0	20	1	US-08-271-942A-87	Sequence 87, Appl	C 761	9	45.0	22	4	US-09-291-541-16	Sequence 16, Appl
689	9	45.0	20	1	US-08-242-403A-68	Sequence 68, Appl	C 762	9	45.0	22	5	PCT-US95-08604-80	Sequence 80, Appl
690	9	45.0	20	1	US-08-774-128-68	Sequence 68, Appl	C 763	9	45.0	22	5	PCT-US95-16806A-17	Sequence 17, Appl
691	9	45.0	20	2	US-08-896-365-25	Sequence 25, Appl	C 764	9	45.0	23	1	US-08-531-556-73	Sequence 73, Appl
692	9	45.0	20	3	US-08-866-340-39	Sequence 39, Appl	C 765	9	45.0	23	1	US-08-644-664B-10	Sequence 10, Appl
693	9	45.0	20	3	US-09-289-267-85	Sequence 85, Appl	C 766	9	45.0	23	2	US-08-472-416-73	Sequence 73, Appl
694	9	45.0	20	3	US-09-289-267-106	Sequence 106, App	C 767	9	45.0	23	2	US-08-753-979A-27	Sequence 27, Appl
695	9	45.0	20	3	US-08-779-916A-87	Sequence 87, Appl	C 768	9	45.0	23	2	US-08-488-940-6	Sequence 6, Appl
696	9	45.0	20	3	US-09-166-186-81	Sequence 81, Appl	C 769	9	45.0	23	2	US-08-761-277A-10	Sequence 10, Appl
697	9	45.0	20	3	US-08-621-841-35	Sequence 35, Appl	C 770	9	45.0	23	2	US-08-859-998-740	Sequence 740, App
698	9	45.0	20	3	US-08-909-954-14	Sequence 6, Appl	C 771	9	45.0	23	3	US-08-691-563C-47	Sequence 47, Appl
699	9	45.0	20	3	US-08-909-954-14	Sequence 14, Appl	C 772	9	45.0	23	3	US-08-068-784-2	Sequence 2, Appl
700	9	45.0	20	3	US-09-418-641-22	Sequence 22, Appl	C 773	9	45.0	23	3	US-08-854-764-5	Sequence 5, Appl
701	9	45.0	20	3	US-09-358-384-13	Sequence 13, Appl	C 774	9	45.0	23	4	US-09-325-926-2	Sequence 2, Appl
702	9	45.0	20	3	US-08-621-700-13	Sequence 13, App	C 775	9	45.0	23	4	US-09-369-494-13	Sequence 13, Appl
703	9	45.0	20	4	US-08-687-421-329	Sequence 329, App	C 776	9	45.0	23	4	US-09-617-302-21	Sequence 21, Appl
704	9	45.0	20	4	US-09-429-322-86	Sequence 86, Appl	C 777	9	45.0	23	4	US-09-617-302-21	Sequence 101, App
705	9	45.0	20	4	US-09-103-875-45	Sequence 45, Appl	C 778	9	45.0	23	4	US-08-556-978B-101	Sequence 12, Appl
706	9	45.0	20	4	US-08-313-932-81	Sequence 81, Appl	C 779	9	45.0	23	5	US-08-518-223-7	Sequence 740, App
707	9	45.0	20	4	US-08-800-215C-7	Sequence 7, Appl	C 780	9	45.0	24	1	US-08-161-673A-6	Sequence 5, Appl
708	9	45.0	20	4	US-09-488-074-7	Sequence 6, Appl	C 781	9	45.0	24	1	US-08-791-849A-3	Sequence 6, Appl
709	9	45.0	20	4	US-09-323-472A-6	Sequence 50, Appl	C 782	9	45.0	24	2	US-08-859-998-1077	Sequence 1077, Ap
710	9	45.0	20	4	US-09-702-251-50	Sequence 81, Appl	C 783	9	45.0	24	2	US-08-481-876-6	Sequence 6, Appl
711	9	45.0	20	4	US-09-688-255C-31	Sequence 31, Appl	C 784	9	45.0	24	2	US-09-185-437-6	Sequence 13, Appl
712	9	45.0	20	4	US-09-824-634-145	Sequence 145, App	C 785	9	45.0	24	2	US-08-873-235B-13	Sequence 4, Appl
713	9	45.0	20	4	US-08-929-940-13	Sequence 13, Appl	C 786	9	45.0	24	3	US-09-217-609A-13	Sequence 11, Appl
714	9	45.0	20	4	US-09-702-327-61	Sequence 61, Appl	C 787	9	45.0	24	3	US-08-893-993-45	Sequence 45, Appl
715	9	45.0	20	4	US-09-457-066-25	Sequence 25, Appl	C 788	9	45.0	24	4	US-08-899-279-10	Sequence 10, Appl
716	9	45.0	20	4	US-09-517-467B-141	Sequence 341, App	C 789	9	45.0	24	4	US-08-102-821-11	Sequence 11, Appl
717	9	45.0	20	4	US-09-657-453A-13	Sequence 33, Appl	C 790	9	45.0	24	4	US-08-120-827-74	Sequence 74, Appl
718	9	45.0	20	5	PCT-US95-03940-13	Sequence 13, Appl	C 791	9	45.0	25	1	US-08-244-269-9	Sequence 9, Appl
719	9	45.0	20	5	PCT-US95-05602-68	Sequence 68, Appl	C 792	9	45.0	25	1	US-08-348-683-10	Sequence 10, Appl
720	9	45.0	20	5	PCT-US95-05816-68	Sequence 68, Appl	C 793	9	45.0	25	1	US-08-478-675-74	Sequence 74, Appl
721	9	45.0	20	5	PCT-US95-08604-87	Sequence 87, Appl	C 794	9	45.0	25	1	US-08-939-028-14	Sequence 14, Appl
722	9	45.0	21	1	US-08-240-547-41	Sequence 104, App	C 795	9	45.0	25	1	US-08-586-039B-6	Sequence 6, Appl
723	9	45.0	21	1	US-08-647-584-104	Sequence 31, Appl	C 796	9	45.0	25	1	US-08-182-968A-251	Sequence 251, App
724	9	45.0	21	1	US-08-891-463-31	Sequence 323, App	C 797	9	45.0	25	1	US-08-319-497B-20	Sequence 20, Appl
725	9	45.0	21	2	US-08-117-952-323	Sequence 28, Appl	C 798	9	45.0	25	1	US-08-291-932A-337	Sequence 337, App
726	9	45.0	21	2	US-08-837-190C-21	Sequence 21, Appl	C 799	9	45.0	25	1	US-08-291-932A-337	Sequence 338, App
727	9	45.0	21	2	US-09-081-180-28	Sequence 28, Appl	C 800	9	45.0	25	1	US-08-334-847-443	Sequence 443, App
728	9	45.0	21	3	US-09-040-786-28	Sequence 28, Appl	C 801	9	45.0	25	2	US-08-334-847-443	Sequence 443, App
729	9	45.0	21	3	US-09-024-020B-26	Sequence 26, Appl	C 802	9	45.0	25	2	US-08-334-847-443	Sequence 443, App
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733	9	45.0	21	4	US-09-237-712-74	Sequence 74, Appl	C 806	9	45.0	25	3	US-08-334-847-443	Sequence 443, App
734	9	45.0	21	4	US-09-416-050A-18	Sequence 18, Appl	C 807	9	45.0	25	3	US-08-334-847-443	Sequence 443, App
735	9	45.0	21	4	US-09-664-800-18	Sequence 18, Appl	C 808	9	45.0	25	3	US-08-334-847-443	Sequence 443, App
736	9	45.0	21	4	US-09-262-773-113	Sequence 113, App	C 809	9	45.0	25	3	US-08-334-847-443	Sequence 443, App
737	9	45.0	21	4	US-09-665-309-18	Sequence 18, Appl	C 810	9	45.0	25	3	US-08-334-847-443	Sequence 443, App
738	9	45.0	21	4	US-09-661-569-18	Sequence 18, Appl	C 811	9	45.0	25	3	US-08-334-847-443	Sequence 443, App
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744	9	45.0	21	4	US-09-293-505-24	Sequence 24, Appl	C 817	9	45.0	25	3	US-08-334-847-443	Sequence 443, App
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748	9	45.0	21	4	US-08-361-806A-17	Sequence 17, Appl	C 821	9	45.0	25	3	US-08-334-847-443	Sequence 443, App
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C 833	8.8	44.0	17	4	US-08-584-040-5365	Sequence 5365, Ap	C 906	8.8	44.0	20	4	US-09-268-140-30	Sequence 30, Appl
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C 845	8.8	44.0	18	1	US-08-099-868B-15	Sequence 15, Appl	C 918	8.8	44.0	20	4	US-09-791-211-13	Sequence 13, Appl
C 846	8.8	44.0	18	1	US-08-399-986B-28	Sequence 28, Appl	C 919	8.8	44.0	20	4	US-09-746-634-19	Sequence 19, Appl
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C 848	8.8	44.0	18	1	US-08-570-311-23	Sequence 23, Appl	C 921	8.8	44.0	20	4	US-09-780-173A-65	Sequence 65, Appl
C 849	8.8	44.0	18	2	US-08-676-279-19	Sequence 19, Appl	C 922	8.8	44.0	20	4	US-09-091-952A-77	Sequence 77, Appl
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C 853	8.8	44.0	18	3	US-09-255-911-23	Sequence 23, Appl	C 926	8.8	44.0	20	6	5219727-25	Sequence 25, Appl
C 854	8.8	44.0	18	3	US-08-577-081A-66	Sequence 66, Appl	C 927	8.8	44.0	21	1	US-07-701-935-17	Sequence 17, Appl
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C 856	8.8	44.0	18	4	US-09-167-109-155	Sequence 155, App	C 929	8.8	44.0	21	1	US-08-017-570-11	Sequence 11, Appl
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C 858	8.8	44.0	18	4	US-09-387-341-4	Sequence 4, Appl1	C 931	8.8	44.0	21	1	US-08-038-932B-2	Sequence 2, Appl1
C 859	8.8	44.0	18	4	US-09-803-951-26	Sequence 26, Appl	C 932	8.8	44.0	21	1	US-08-330-123A-25	Sequence 25, Appl
C 860	8.8	44.0	18	4	US-09-207-359B-45	Sequence 45, Appl	C 933	8.8	44.0	21	1	US-08-056-300-43	Sequence 43, Appl
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C 871	8.8	44.0	19	4	US-09-444-295-65	Sequence 65, Appl	C 944	8.8	44.0	21	3	US-08-520-550A-33	Sequence 33, Appl
C 872	8.8	44.0	19	4	US-09-597-732-65	Sequence 65, Appl	C 945	8.8	44.0	21	3	US-08-998-443-25	Sequence 25, Appl
C 873	8.8	44.0	19	5	PCT-US94-07430-40	Sequence 40, Appl	C 946	8.8	44.0	21	3	US-09-009-913-60	Sequence 60, Appl
C 874	8.8	44.0	20	1	US-07-696-793A-36	Sequence 36, Appl	C 947	8.8	44.0	21	3	US-09-009-913-125	Sequence 125, App
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C 876	8.8	44.0	20	1	US-08-457-176-7	Sequence 7, Appl1	C 949	8.8	44.0	21	4	US-09-060-523-25	Sequence 25, Appl
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C 880	8.8	44.0	20	1	US-08-457-175-14	Sequence 14, Appl	C 953	8.8	44.0	21	4	US-08-469-260A-157	Sequence 157, App
C 881	8.8	44.0	20	1	US-08-255-892-56	Sequence 56, Appl	C 954	8.8	44.0	21	5	PCT-US94-01709-10	Sequence 10, Appl
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C 884	8.8	44.0	20	1	US-08-225-444-4	Sequence 4, Appl1	C 957	8.8	44.0	22	1	US-08-133-711-19	Sequence 19, Appl
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C 896	8.8	44.0	20	3	US-09-428-584-78	Sequence 78, Appl	C 969	8.8	44.0	22	2	US-08-635-761-50	Sequence 50, Appl
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C 901	8.8	44.0	20	4	US-09-038-637-135	Sequence 135, App	C 974	8.8	44.0	22	3	US-08-716-190-16	Sequence 16, Appl
C 902	8.8	44.0	20	4	US-09-061-769A-19	Sequence 19, Appl	C 975	8.8	44.0	22	3	US-08-857-464-3	Sequence 3, Appl1
C 903	8.8	44.0	20	4	US-09-488-857B-47	Sequence 47, Appl	C 976	8.8	44.0	22	3	US-08-912-272-58	Sequence 58, Appl

Sequence 3, Appl1
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Sequence 3, Appl1
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US-08-482-090-7

ALIGNMENTS

RESULT 1
US-09-593-012-187 Application US/09593012

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ORGANISM: Stachybotrys chartarum
US-09-593-012-187

Query Match 75.0%; Score 15; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GTTGGCACTCAGAG 20
DB 1 GTTGGCACTCAGAG 15

RESULT 2
US-09-444-053-17/c
Sequence 17, Application US/09444053A
GENERAL INFORMATION:
APPLICANT: Donna T. Ward
APPLICANT: Lex M. Cowart
TITLE OF INVENTION: ANTISENSE MODULATION OF NCK-2 EXPRESSION
FILE REFERENCE: RTS-0122
CURRENT APPLICATION NUMBER: US/09/444,053A
CURRENT FILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 89

SEQ ID NO 17
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-444-053-17

Query Match 69.0%; Score 13.8; DB 4; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTGGTTGCACTCA 17
DB 19 TTTGGTTGCACTCA 3

RESULT 3
US-08-193-627-25/c
Sequence 25, Application US/08193627

Patent No. 6017756
GENERAL INFORMATION:
APPLICANT: KENNETH G. DRAPER
TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING HEPATITIS B VIRUS
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/193,627

FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/882,712

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Marbury, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 197/072
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440

TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:

LENGTH: 17
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-193-627-25

Query Match 67.0%; Score 13.4; DB 3; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCGTTGGCACTCAG 18
DB 15 GAGTTGGCACTCAG 1

RESULT 4
US-08-148-117A-2/c

Sequence 2, Application US/08148117A
Patent No. 5744368
GENERAL INFORMATION:
APPLICANT: GOLDBER, DMITRY, Y.;
APPLICANT: SCHMARZMAN, ALEXANDER, L.; EISENBERG-
APPLICANT: GR NEERG, MOISES.
TITLE OF INVENTION: METHOD OF PREVENTING
TITLE OF INVENTION: AGGREGATION OF AMYLOID - PROTEIN
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/148.117A
FILING DATE: 04-NOV-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KENNETH H. SONNENFELD
REGISTRATION NUMBER: 33,285
REFERENCE/DOCKET NUMBER: 0867-4113
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 22
TYPE: NUCLEOTIDE
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
US-08-148-117A-2

Query Match 61.0%; Score 12.2; DB 1; Length 22;
Best Local Similarity 82.4%; Pred. No. 8.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTGGCTTGCCTCA 17
DB 19 TTCCGTTGCCCTCA 3

RESULT 5
US-09-593-012-108
Sequence 108, Application US/09593012
Patent No. 6387652
GENERAL INFORMATION:
APPLICANT: HAUGLAND, Richard
APPLICANT: VESPER, Stephen
TITLE OF INVENTION: METHOD OF IDENTIFYING AND QUANTIFYING SPECIFIC FUNGI AND BACTERIA
FILE REFERENCE: HAUGLAND-1A
CURRENT APPLICATION NUMBER: US/09/593.012
CURRENT FILING DATE: 2000-06-13
PRIOR APPLICATION NUMBER: US 09/290.990
PRIOR FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: US 60/081.773
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 108
LENGTH: 24
TYPE: DNA
ORGANISM: Paecilomyces lilacinus
US-09-593-012-108

Query Match 61.0%; Score 12.2; DB 4; Length 24;
Best Local Similarity 82.4%; Pred. No. 8.4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GCGTTGGCCTCAGAG 20
DB 1 GCTTGCTCCTCAGAG 17

RESULT 6
US-08-758-306-999
Sequence 999, Application US/08758306
Patent No. 5807743
GENERAL INFORMATION:
APPLICANT: Scinccomb, Dan T.
APPLICANT: McSwiggen, James A.
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES
TITLE OF INVENTION: ASSOCIATED WITH
TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
NUMBER OF SEQUENCES: 1379
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: storage
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758.306
FILING DATE: December 3, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wardburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/132
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 999:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-758-306-999

Query Match 60.0%; Score 12; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 1e+03;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 TTGGCCTCAGAG 19
DB 1 TUGCCACUCAGAG 12

RESULT 7
US-08-803-346-29
Sequence 29, Application US/08803346
Patent No. 6281346
GENERAL INFORMATION:

APPLICANT: HESS, JOHN W.
APPLICANT: CASKEY, C. THOMAS
APPLICANT: LIU, QINGYUN
APPLICANT: PHILIPS, MICHAEL SEAN
TITLE OF INVENTION: RAT OB RECEPTORS AND NUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: JOANNE M. GIESSEY - MERCK & CO., INC.
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/803,346
FILING DATE: 20-FEB-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: GIESSEY, JOANNE M
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 19642Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-3046
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-803-346-29

Query Match 60.0%; Score 12; DB 4; Length 21;
Best Local Similarity 75.0%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TTGGGTTTGGCCACTCAGAG 20
DB 2 TTGGGTTTGGAGTCTCAG 21

RESULT 8
US-09-553-231-7/C
Sequence 7, Application US/09553231
Patent No. 6432647
GENERAL INFORMATION:
APPLICANT: PREUS, DAPHNE
APPLICANT: COENHAVER, GREGORY
TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
FILE REFERENCE: ARCD:257--2
CURRENT APPLICATION NUMBER: US/09/553,231
CURRENT FILING DATE: 2000-04-19
PRIOR APPLICATION NUMBER: 60/073,741
PRIOR FILING DATE: 1998-02-05
PRIOR APPLICATION NUMBER: 60/048,451
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 7
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Primer
US-09-553-231-7

Query Match 59.0%; Score 11.6; DB 4; Length 20;
Best Local Similarity 86.7%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTCGTTTGGCCACT 15
DB 17 TTTCGTTTGGCCACT 3

RESULT 9
US-07-994-423-4/C
Sequence 4, Application US/07994423
Patent No. 5432080
GENERAL INFORMATION:
APPLICANT: HAMMOND, Geoffrey L.
APPLICANT: AVAKUMOV, George V.
TITLE OF INVENTION: Variants of Corticosteroid Binding
TITLE OF INVENTION: Globulin
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/994,423
FILING DATE: 16-DEC-1992
CLASSIFICATION: 435
TELEFAX: (202) 672-5399
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16777/197/ALLE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-07-994-423-4

Query Match 58.0%; Score 11.6; DB 1; Length 21;
Best Local Similarity 77.8%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 TCGGTTTGGCCACTCAGAG 20
DB 20 TCGGTTTGGCCACTCAGT 3

RESULT 10
US-08-421-891-4/C
Sequence 4, Application US/08421891
Patent No. 5595969
GENERAL INFORMATION:
APPLICANT: HAMMOND, Geoffrey L.
APPLICANT: AVAKUMOV, George V.
TITLE OF INVENTION: Variants of Corticosteroid Binding
TITLE OF INVENTION: Globulin

NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/421,891
FILING DATE: 14-Apr-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/994,423
FILING DATE: 16-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16777/197/ALLE
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-421-891-4

Query Match 58.0%; Score 11.6; DB 1; Length 21;
Best Local Similarity 77.8%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 TGGCTTGGCCATTCAG 20
DB 20 TGGCTTGGCCATTCAG 3

RESULT 11
US-08-908-212A-3
Sequence 3, Application US/08908212A
Patent No. 5989857
GENERAL INFORMATION:
APPLICANT: Mundschien, David
APPLICANT: Smith, Leonard
TITLE OF INVENTION: Polypeptide Compositions and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fredrickson & Byron, P.A.
STREET: 900 Second Avenue South
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
ZIP: 55402-3397
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows-95
SOFTWARE: ASCII files
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/908,212A
FILING DATE: 07 August 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/644,399
FILING DATE: 10 May 1996
ATTORNEY/AGENT INFORMATION:

NAME: Goldman, Philip M.
REGISTRATION NUMBER: 31,162
REFERENCE/DOCKET NUMBER: 15050.1.2.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 347-7088
TELEFAX: (612) 347-7077
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-908-212A-3

Query Match 58.0%; Score 11.6; DB 2; Length 21;
Best Local Similarity 77.8%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTTGGCTTGGCCATTCAG 18
DB 2 TTTTCATTCGCAATTCAG 19

RESULT 12
US-08-859-998-509/c
Sequence 509, Application US/08859998
Patent No. 5994076
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Jekhadze, George
APPLICANT: Bibilashvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,998
FILING DATE: 21-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 509:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
US-08-859-998-509

Query Match 57.0%; Score 11.4; DB 2; Length 25;
Best Local Similarity 92.3%; Pred. No. 2.2e+03;

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TTGCCACTCAGAG 20
Db 17 TTGCCACTCTGAG 5

RESULT 13

US-09-225-928-509/C

Sequence 509, Application US/09225928

Patent No. 6352829

GENERAL INFORMATION:

APPLICANT: Chenchik, Alex

Biblashvili, Robert

Jokhadze, George

TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL

NUMBER OF SEQUENCES: 1375

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.

STREET: 2200 Sand Hill Road, Suite 100

CITY: Menlo Park

STATE: CA

COUNTRY: US

ZIP: 94025

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/225,928

FILING DATE: 05-Jan-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/859,998

FILING DATE: 21-MAY-1997

ATTORNEY/AGENT INFORMATION:

NAME: Field, Bret E.

REGISTRATION NUMBER: 37,620

REFERENCE/DOCKET NUMBER: 09096/002001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-322-5070

TELEFAX: 415-854-0875

INFORMATION FOR SEQ ID NO: 509:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

OTHER INFORMATION: oligonucleotide primer

SEQUENCE DESCRIPTION: SEQ ID NO: 509:

US-09-225-928-509

Query Match 57.0%; Score 11.4; DB 4; Length 25;

Best Local Similarity 92.3%; Pred. No. 2.2e+03;

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TTGCCACTCAGAG 20
Db 17 TTGCCACTCTGAG 5

RESULT 14

US-08-164-200-9/C

Sequence 9, Application US/08164200

Patent No. 5552390

GENERAL INFORMATION:

APPLICANT: Scholier, Eric M.

APPLICANT: Iversen, Patrick L.

TITLE OF INVENTION: Phosphorothioate Inhibitors of Metastatic

TITLE OF INVENTION: Breast Cancer

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Zarley, McKee, Thome, Voorhees, & Sease

STREET: 801 Grand Avenue Suite 3200

CITY: Des Moines

STATE: Iowa

COUNTRY: United States

ZIP: 50309

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/164,200

FILING DATE: December 9, 1993

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Nebel, Heidi Sease

REGISTRATION NUMBER: P-37,719

REFERENCE/DOCKET NUMBER: UMC #63054

TELECOMMUNICATION INFORMATION:

TELEPHONE: (515) 288-3667

TELEFAX: (515) 288-1338

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 19 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: mRNA

HYPOTHETICAL: NO

ANTI-SENSE: YES

US-08-164-200-9

Query Match 56.0%; Score 11.2; DB 1; Length 19;

Best Local Similarity 81.2%; Pred. No. 2.7e+03;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTGCGTTGCCACTCA 17
Db 19 TTGCGTTGCCACCCA 4

RESULT 15

US-08-327-363-7/C

Sequence 7, Application US/08327363

Patent No. 5643780

GENERAL INFORMATION:

APPLICANT: Isis Pharmaceuticals and

APPLICANT: Brenda Baker

TITLE OF INVENTION: Compositions and Methods for Modulating

TITLE OF INVENTION: RNA Activity Through Modification of the 5' Cap Structure of

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5643780

STREET: One Liberty Place - 46th floor

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: WORDPERFECT 5.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/327,363

FILING DATE: herewith

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 847,054
FILING DATE: April 3, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Kathryn Leary, Ph.D.
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: ISIS-1719
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 19
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-327-363-7

Query Match 56.0%; Score 11.2; DB 1; Length 19;
Best Local Similarity 81.2%; Pred. No. 2.7e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CGTTGCCACTCAGAG 20
DB 16 CCTCTGCTACTCAGAG 1

RESULT 16
US-09-328-174A-96
Sequence 96, Application US/09328174A
Patent No. 6448003
GENERAL INFORMATION:
APPLICANT: Guida, Marco
TITLE OF INVENTION: Genotyping Human Phenol Sulfotransferase
FILE REFERENCE: 4389-6 (formerly SEQ-16P)
CURRENT APPLICATION NUMBER: US/09/328,174A
PRIOR FILING DATE: 1999-06-08
PRIOR APPLICATION NUMBER: 09/328,174
NUMBER OF SEQ ID NOS: 110
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 96:
LENGTH: 19
TYPE: DNA
ORGANISM: H. sapiens
US-09-328-174A-96

Query Match 56.0%; Score 11.2; DB 4; Length 19;
Best Local Similarity 81.2%; Pred. No. 2.7e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CGTTGCCACTCAGAG 20
DB 1 CCTTGCACCAAGAG 16

RESULT 17
US-08-136-118-6/c
Sequence 6, Application US/08136118
Patent No. 5580969
GENERAL INFORMATION:
APPLICANT: HOKE, Glenn D
APPLICANT: BRADLEY, Matthews O
APPLICANT: WILLIAMS, Taffy J
APPLICANT: LEE, Che-Hung
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES DIRECTED
AGAINST HUMAN ICAM-1
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Naval Medical Res. & Dev. Cmd.
STREET: 8901 Wisconsin Ave.
CITY: Bethesda

STATE: Maryland
COUNTRY: USA
ZIP: 20889-5606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/136,118
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/918,259
FILING DATE: 24-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Spevack, A. David
REGISTRATION NUMBER: 24,743
REFERENCE/DOCKET NUMBER: N.C. 75,776
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 295-6759
TELEFAX: (202) 295-1022
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-136-118-6

Query Match 56.0%; Score 11.2; DB 1; Length 21;
Best Local Similarity 81.2%; Pred. No. 2.8e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CGTTGCCACTCAGAG 20
DB 16 CCTCTGCTACTCAGAG 1

RESULT 18
US-09-091-952A-83
Sequence 83, Application US/09091952A
Patent No. 6458532
GENERAL INFORMATION:
APPLICANT: DeGera-Wadleigh, Sevilla D.
Gershon, Elliot S.
Badner, Judith A.
Goldin, Lynn R.
Berrettini, Wade H.
Yoshikawa, Takeo
Sanders, Alan R.
Barelling, Lisa E.
TITLE OF INVENTION: Chromosomal Markers and Diagnostic
Tests for Manic-Depressive Illness
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,952A
FILING DATE: 19-APR-1999
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,278
FILING DATE: 28-OCT-1996
APPLICATION NUMBER: PCT/US97/19381
FILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 015280-297100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1...22
OTHER INFORMATION: DIS1066 forward primer
SEQUENCE DESCRIPTION: SEQ ID NO: 83:
US-09-091-952A-83

Query Match 56.0%; Score 11.2; DB 4; Length 22;
Best Local Similarity 81.2%; Pred. No. 2.8e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TTGGTTGGCACTCAG 18
DB 1 TGCTGTGCTCTCAG 16

RESULT 19
US-09-360-416-65
Sequence 65, Application US/09360416
Patent No. 6458536
GENERAL INFORMATION:
APPLICANT: Richard A. Gatti
TITLE OF INVENTION: METHODS FOR DETECTION OF ATAXIA
FILE REFERENCE: 510015-222
CURRENT APPLICATION NUMBER: US/09/360,416
CURRENT FILING DATE: 1999-07-23
NUMBER OF SEQ ID NOS: 143
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 65
LENGTH: 19
TYPE: DNA
ORGANISM: Human
US-09-360-416-65

Query Match 55.0%; Score 11; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGCCACTCAGA 19
DB 2 TGCCACTCAGA 12

RESULT 20
US-08-393-997-1
Sequence 1, Application US/08393997
Patent No. 5633729
GENERAL INFORMATION:
APPLICANT: Taniguchi, Tadatsugu
APPLICANT: Harada, Hisaaki
TITLE OF INVENTION: Methods for Diagnosing Cancer, Precancerous
TITLE OF INVENTION: State, or Susceptibility to Other Forms of

TITLE OF INVENTION: Diseases by Detecting an Acceleration of Exon
TITLE OF INVENTION: Skipping in IRE-1 mRNA
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA: US/08/393,997
APPLICATION NUMBER: US/08/393,997
FILING DATE: herewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 0652.1420000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-393-997-1

Query Match 55.0%; Score 11; DB 1; Length 20;
Best Local Similarity 73.7%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TTGGTTGGCACTCAG 20
DB 1 TTCCCTTCCTCCAG 19

RESULT 21
US-08-927-219-12/c
Sequence 12, Application US/08927219
Patent No. 6187533
GENERAL INFORMATION:
APPLICANT: Bell, Graeme I.
APPLICANT: Yamagata, Kazuya
APPLICANT: Oda, Naohisha
APPLICANT: Katsuki, Pamela J.
APPLICANT: Furuta, Hiroko
APPLICANT: Horikawa, Yukio
APPLICANT: Menzel, Stephen
TITLE OF INVENTION: MUTATIONS IN THE DIABETES SUSCEPTIBILITY
TITLE OF INVENTION: GENES HEPATOCYTE NUCLEAR FACTOR (HNF) 1 ALPHA, HNF-1BETA
TITLE OF INVENTION: AND HNF-4ALPHA
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/927,219
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,679
FILING DATE: 30-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,056
FILING DATE: 02-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/025,719
FILING DATE: 10-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:272
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/474-7577
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-927-219-12

Query Match 55.0%; Score 11; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTGCGTTGCC 12
15 TTGCGTTGCC 5

RESULT 22
US-09-064-964-17
Sequence 17, Application US/09064964
Patent No. 6080399
GENERAL INFORMATION:
APPLICANT: Gajewski, Thomas F.
TITLE OF INVENTION: VACCINE ADJUVANTS FOR IMMUNOTHERAPY OF
TITLE OF INVENTION: MELANOMA
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,964
FILING DATE: Concurrently Herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:280
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512)418-3000
TELEFAX: (512)474-7577
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
US-09-064-964-17

Query Match 55.0%; Score 11; DB 3; Length 22;
Best Local Similarity 73.7%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TTGCGTTGCCACTCAG 20
4 TAGCGATGCTCTCAAG 22

RESULT 23
US-08-821-119-21
Sequence 21, Application US/08821119
Patent No. 5821104
GENERAL INFORMATION:
APPLICANT: Holm, Kaj Andre
APPLICANT: Rasmussen, Grethe
APPLICANT: Haikier, Torden
APPLICANT: Lehmebeck, Jan
TITLE OF INVENTION: Tripeptidyl Aminopeptidase
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58211040 No. 5821104disk of No. 5821104th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,119
FILING DATE: 19-MAR-1997
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4107.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: CDNA
US-08-821-119-21

Query Match 55.0%; Score 11; DB 1; Length 23;
Best Local Similarity 64.7%; Pred. No. 3.5e+03;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTGCGTTGCCACTCAG 18
7 YTGRTTYTGCCAYTCG 23

RESULT 24
US-08-821-118-4
Sequence 4, Application US/08821118
Patent No. 5989889
GENERAL INFORMATION:
APPLICANT: Rey, Michael
APPLICANT: Golightly, Elizabeth

TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDES
TITLE OF INVENTION: HAVING TRIPEPTIDE AMINOPEPTIDASE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESSES:
ADDRESSSEE: No. 59898890 No. 59898890dsk of No. 59898890th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,118
FILING DATE: 19-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiria, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4107,400-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-821-118-4

Query Match 55.0%; Score 11; DB 2; Length 23;
Best Local Similarity 64.7%; Pred. No. 3.6e+03;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TTGCGTTGCCACTCAG 18
Db 7 YTGRTTYTGCCAYTCGG 23

RESULT 25
US-08-481-435-18
Sequence 18, Application US/08481435
Patent No. 6027906
GENERAL INFORMATION:
APPLICANT: Baigamesh, Tanjore S
TITLE OF INVENTION: No. 6027906el Polypeptides
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESSES:
ADDRESSSEE: White & Case
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,435
FILING DATE: 10-JUL-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IN 580/MAS/94

FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9404072-2
FILING DATE: 24-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-151
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid (synthetic DNA primer)
US-08-481-435-18

Query Match 55.0%; Score 11; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GCGTTGCCAC 14
Db 13 GCGTTGCCAC 23

RESULT 26
US-08-574-763-6/C
Sequence 6, Application US/08574763
Patent No. 5736376
GENERAL INFORMATION:
APPLICANT: Yanagisawa, Masashi
TITLE OF INVENTION: RECOMBINANT ENDOTHELIN CONVERTING
ENZYME-2 AND ITS USE IN ECG INHIBITOR SCREENING
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESSES:
ADDRESSSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/574,763
FILING DATE: Concurrently herewith
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Corder, Timothy S.
REGISTRATION NUMBER: 38,414
REFERENCE/DOCKET NUMBER: UTXD:472
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-574-763-6

Query Match 55.0%; Score 11; DB 1; Length 24;
Best Local Similarity 73.7%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

Qy      2 TTGCGTTGGCACTCAGAG 20
          |||||
Db      22 TAGCACTTGCCTCAGAG 4

```

RESULT 27
US-08-292-620A-10
Sequence 10, Application US/08292620A

Query Match	54.0%;	Score 10.8;	DB 2;	Length 15;
Best Local Similarity	64.3%;	Pred.No. 4.2e+03;		
Matches 9; Conservative	3;	Mismatches 2;	Indels 0;	Gaps 0

RESULT 28
US-09-071-845-10

; Sequence 10, Application US/09071845

Query Match	54.0%	Score	10.8	DB 3	Length	15			
Best Local Similarity	64.3%	Pred. No.	4.2e+03						
Matches	9	Conservative	3	Mismatches	2	Indels	0	Gaps	0

RESULT 29
US-08-484-956-66/c
Sequence 68, Application US/08484956
Patent No. 5843654

GENERAL INFORMATION:

APPLICANT: DAHLBERG, JAMES E.
APPLICANT: LAMICHEV, VICTOR I.
APPLICANT: BROW, MARY ANN D.
APPLICANT: OLDENBURG, MARY C.

APPLICANT: HEISLER, LAURA
TITLE OF INVENTION: DETECTION OF p53 MUTATIONS
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,956
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/402,601
FILING DATE: 09-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,164
FILING DATE: 09-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/254,359
FILING DATE: 06-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,384
FILING DATE: 04-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/986,330
FILING DATE: 07-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL J. PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-01801
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-484-956-68
Query Match 54.0%; Score 10.8; DB 2; Length 20;
Best Local Similarity 85.7%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 7 TTGGCCACTGAG 20
19 TTGGCCACTGAG 6
RESULT 30
US-08-757-653-68/c
Sequence 68, Application US/08/757653
Patent No. 5843669
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichay, Victor I.
APPLICANT: Lyamichay, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
NUMBER OF SEQUENCES: 190
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 190
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH:
TYPE:
STRANDEDNESS:
TOPOLOGY:
MOLECULE TYPE:
US-08-757-653-68

CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02565
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-653-68
Query Match 54.0%; Score 10.8; DB 2; Length 20;
Best Local Similarity 85.7%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 7 TTGGCCACTGAG 20
19 TTGGCCACTGAG 6
RESULT 31
US-08-117-952-652/c
Sequence 652, Application US/08/117952
Patent No. 5851760
GENERAL INFORMATION:
APPLICANT: Evans, Glen A.
APPLICANT: Smith, Michael W.
TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE
NUMBER OF SEQUENCES: 797
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,952
FILING DATE: 07-SEP-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/078,471
FILING DATE: 15-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9423
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737

TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 652:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Oligonucleotide
; HYPOTHEetical: NO
; ANTI-SENSE: NO
US-08-117-952-652

Query Match 54.0%; Score 10.8; DB 2; Length 20;
Best Local Similarity 85.7%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 TTGGCCACTCAG 20
Db 19 TTGGCCACTCAG 6

RESULT 32
US-09-358-685-23/c
; Sequence 23, Application US/09358685
; Patent No. 6121047
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowart
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHP-1 EXPRESSION
; FILE REFERENCE: RTS-0081
; CURRENT APPLICATION NUMBER: US/09/358,685
; CURRENT FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 23
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-358-685-23

Query Match 54.0%; Score 10.8; DB 3; Length 20;
Best Local Similarity 85.7%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GTTGCCACTCAGA 19
Db 14 GTTGCCACTCAGA 1

RESULT 33
US-09-428-696-29/c
; Sequence 29, Application US/09428696
; Patent No. 6165789
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowart
; TITLE OF INVENTION: ANTISENSE MODULATION OF HNRNP A1 EXPRESSION
; FILE REFERENCE: RTS-0111
; CURRENT APPLICATION NUMBER: US/09/428,696
; CURRENT FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 29
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-428-696-29

Query Match 54.0%; Score 10.8; DB 4; Length 20;
Best Local Similarity 85.7%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTGGCTTGGCAC 14
Db 18 TTGGCTTGGCAC 5

RESULT 34
US-09-270-933-2/c
; Sequence 2, Application US/09270933
; Patent No. 6365375
; GENERAL INFORMATION:
; APPLICANT: Dietmarer, Wolfgang
; APPLICANT: Ruschoff, Josef
; TITLE OF INVENTION: IMPROVED METHOD OF PRIMER-EXTENSION PREAMPLIFICATION
; TITLE OF INVENTION: PCR
; FILE REFERENCE: 4802
; CURRENT APPLICATION NUMBER: US/09/270,933
; CURRENT FILING DATE: 1999-03-16
; EARLIER APPLICATION NUMBER: DE 198 13 317.0
; EARLIER FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer for
US-09-270-933-2

Query Match 54.0%; Score 10.8; DB 4; Length 20;
Best Local Similarity 85.7%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 TTGGCCACTCAG 20
Db 19 TTGGCCACTCAG 6

RESULT 35
US-08-520-946-68/c
; Sequence 68, Application US/08520946
; Patent No. 6372424
; GENERAL INFORMATION:
; APPLICANT: BROW, MARY ANN D.
; APPLICANT: LYAMICHEV, VICTOR I.
; APPLICANT: OLIVE, DAVID M.
; TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,946
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: FORS-01756
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-520-946-68

Query Match 54.0%; Score 10.8; DB 4; Length 20;
Best Local Similarity 85.7%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 7 TTGCGCTTGCAG 20
Db 19 TTGCGCAGCTGAG 6

RESULT 36
US-08-415-818-8/c
Sequence 8, Application US/08415818
Patent No. 5621079
GENERAL INFORMATION:
APPLICANT: Cascleri, Margaret A.
APPLICANT: Linemeyer, David L.
APPLICANT: Macneil, Douglas J.
APPLICANT: Shiao, Lin-Lin
APPLICANT: Strader, Catherine D.
APPLICANT: Tan, Carina P.
APPLICANT: Weinberg, David H.
TITLE OF INVENTION: NEUROPEPTIDE Y RECEPTOR
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mary A. Appollina
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/415,818
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/383,746
FILING DATE: 03-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Appollina, Mary A.
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19390
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-4720
TELEFAX: 908-594-4720
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-415-818-8

Query Match 54.0%; Score 10.8; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 4.5e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 2 TTGCGTTGCAGT 15
Db 17 TTGCTCTTGCAGT 4

RESULT 37
US-08-894-236-8/c
Sequence 8, Application US/08894236
Patent No. 5939263
GENERAL INFORMATION:
APPLICANT: Cascleri, Margaret A.
APPLICANT: Linemeyer, David L.
APPLICANT: Macneil, Douglas J.
APPLICANT: Shiao, Lin-Lin
APPLICANT: Strader, Catherine D.
APPLICANT: Tan, Carina P.
APPLICANT: Weinberg, David H.
TITLE OF INVENTION: NEUROPEPTIDE Y RECEPTOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mary A. Appollina
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,236
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/383,746
FILING DATE: 03-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/415,818
FILING DATE: 03-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Appollina, Mary A.
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19390Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3462
TELEFAX: 908-594-4720
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-894-236-8

Query Match 54.0%; Score 10.8; DB 2; Length 21;
Best Local Similarity 85.7%; Pred. No. 4.5e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 2 TTGCGTTGCAGT 15
Db 17 TTGCTCTTGCAGT 4

RESULT 38
PCT-US96-01444-8/c
Sequence 8, Application PC/TUS9601444
GENERAL INFORMATION:
APPLICANT: Cascleri, Margaret A.
APPLICANT: Linemeyer, David L.

APPLICANT: MacNeil, Douglas J.
APPLICANT: Shiao, Lin-Lin
APPLICANT: Strader, Catherine D.
APPLICANT: Tan, Carina P.
APPLICANT: Weidner, David H.
TITLE OF INVENTION: NEUROPEPTIDE Y RECEPTOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mary A. Appollina
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/01444
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/383,746
FILING DATE: 03-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/415,818
FILING DATE: 03-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Appollina, Mary A.
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19390Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3462
TELEFAX: 908-594-4720
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US96-01444-8

Query Match 54.0%; Score 10.8; DB 5; Length 21;
Best Local Similarity 85.7%; Pred. No. 4.5e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 TTGCTTGCCACT 15
DB 17 TTGCTTGCCACT 4

RESULT 39
US-08-203-198-31/c
Sequence 31, Application US/08203198
Patent No. 5512462
GENERAL INFORMATION:
APPLICANT: Cheng, Suzanne
TITLE OF INVENTION: Methods and Reagents for the Polymerase
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/203,198
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Percy Ph.D., Douglas A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 8894
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-203-198-31

Query Match 54.0%; Score 10.8; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 4.5e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 7 TTGCGCACTCAGAG 20
DB 21 TTGCGCACTCAGAG 8

RESULT 40
US-09-358-685-2
Sequence 2, Application US/09358685
Patent No. 6121047
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
TITLE OF INVENTION: ANTISENSE MODULATION OF SHP-1 EXPRESSION
FILE REFERENCE: RTS-0081
CURRENT APPLICATION NUMBER: US/09/358,685
CURRENT FILING DATE: 1999-07-21
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 2
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR Primer
US-09-358-685-2

Query Match 54.0%; Score 10.8; DB 3; Length 22;
Best Local Similarity 85.7%; Pred. No. 4.5e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 GTTGGCACTCAGA 19
DB 7 GTTGGCACTCAGA 20

Search completed: June 7, 2003, 09:45:29
Job time : 53.1818 secs

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OM nucleic - nucleic search, using sw model

Run on: June 7, 2003, 08:51:24 ; Search time 76.3636 Seconds
(without alignments)
366.546 Million cell updates/sec

Title: US-10-080-959A-2

Perfect score: 20

Sequence: 1 ttctgcttcgaccacagag 20

Scoring table:

IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 870385 seqs, 699768693 residues

Total number of hits satisfying chosen parameters: 359952

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	20	100.0	20	9	US-10-080-959A-2	Sequence 2, Appl
2	17	85.0	23	9	US-10-080-959A-4	Sequence 4, Appl
3	13.4	67.0	17	9	US-09-877-478-25	Sequence 25, Appl
4	13.2	66.0	23	10	US-09-972-467-10	Sequence 10, Appl
5	12.2	61.0	17	9	US-09-780-533A-2611	Sequence 2611, Ap
6	12.2	61.0	25	10	US-09-819-097-24	Sequence 24, Appl
7	12	60.0	23	10	US-09-821-821-22	Sequence 22, Appl
8	11.8	59.0	17	9	US-09-780-533A-2000	Sequence 2000, Ap
9	11.8	59.0	22	9	US-09-996-956-14	Sequence 14, Appl
10	11.6	58.0	21	10	US-09-368-834-3	Sequence 3, Appl
11	11.6	58.0	24	9	US-09-940-185-2248	Sequence 2248, Ap
12	11.4	57.0	24	8	US-08-844-215-30	Sequence 30, Appl
13	11.4	57.0	24	9	US-09-913-238-53	Sequence 53, Appl
14	11.4	57.0	25	9	US-10-215-112-10761	Sequence 10761, A
15	11.2	56.0	17	9	US-09-780-533A-505	Sequence 505, App
16	11.2	56.0	17	9	US-09-930-423-1153	Sequence 1153, Ap
17	11.2	56.0	19	9	US-10-206-839-96	Sequence 96, Appl
18	11.2	56.0	20	9	US-10-060-301-158	Sequence 158, App
19	11.2	56.0	20	9	US-10-060-301-160	Sequence 160, App

C	20	11.2	56.0	20	10	US-09-808-680-10	Sequence 10, Appl
C	21	11	55.0	12	9	US-10-117-108A-27	Sequence 27, Appl
C	22	11	55.0	19	9	US-10-175-225-65	Sequence 65, Appl
C	23	11	55.0	20	10	US-09-801-968-5	Sequence 5, Appl
C	24	10.8	54.0	17	9	US-09-780-533A-1366	Sequence 1366, Ap
C	25	10.8	54.0	20	9	US-10-087-082-2	Sequence 2, Appl
C	26	10.8	54.0	20	9	US-09-865-866-22	Sequence 22, Appl
C	27	10.8	54.0	20	9	US-09-865-866-23	Sequence 23, Appl
C	28	10.8	54.0	20	9	US-09-940-925A-68	Sequence 68, Appl
C	29	10.8	54.0	20	9	US-10-001-076-59	Sequence 59, Appl
C	30	10.8	54.0	20	12	US-10-011-119A-6	Sequence 6, Appl
C	31	10.8	54.0	21	9	US-10-135-629-15	Sequence 15, Appl
C	32	10.8	54.0	24	9	US-09-883-152-86	Sequence 86, Appl
C	33	10.8	54.0	24	9	US-09-940-185-2382	Sequence 2382, Ap
C	34	10.8	54.0	25	9	US-10-215-112-665	Sequence 665, App
C	35	10.8	54.0	25	9	US-10-215-112-791	Sequence 791, App
C	36	10.8	54.0	25	9	US-10-215-112-2803	Sequence 2803, App
C	37	10.8	54.0	25	9	US-10-215-112-2929	Sequence 2929, App
C	38	10.8	54.0	25	9	US-10-215-112-8357	Sequence 8357, App
C	39	10.8	54.0	25	9	US-10-215-112-11650	Sequence 11650, A
C	40	10.8	54.0	25	9	US-10-215-112-1458	Sequence 12458, A
C	41	10.6	53.0	20	9	US-09-784-674-1041	Sequence 1041, Ap
C	42	10.6	53.0	20	9	US-09-784-674-1042	Sequence 1042, Ap
C	43	10.6	53.0	20	9	US-09-784-674-1043	Sequence 1043, Ap
C	44	10.6	53.0	20	9	US-09-784-674-1044	Sequence 1044, Ap
C	45	10.6	53.0	20	9	US-09-953-611-82	Sequence 82, Appl
C	46	10.6	53.0	20	10	US-09-808-680-9	Sequence 9, Appl
C	47	10.6	53.0	21	9	US-10-116-949-91	Sequence 91, Appl
C	48	10.6	53.0	21	9	US-10-067-514-53	Sequence 53, Appl
C	49	10.6	53.0	22	10	US-09-804-987-5	Sequence 5, Appl
C	50	10.6	53.0	24	9	US-09-940-185-919	Sequence 919, App
C	51	10.6	53.0	24	9	US-09-940-185-1602	Sequence 1602, Ap
C	52	10.6	53.0	24	10	US-09-771-063-7	Sequence 7, Appl
C	53	10.6	53.0	25	9	US-10-045-631A-13	Sequence 13, Appl
C	54	10.6	53.0	25	9	US-10-215-112-3633	Sequence 3633, Ap
C	55	10.6	53.0	25	9	US-10-215-112-11760	Sequence 11760, A
C	56	10.4	52.0	12	9	US-10-117-108A-28	Sequence 28, Appl
C	57	10.4	52.0	17	9	US-09-848-754A-1238	Sequence 1238, Ap
C	58	10.4	52.0	17	9	US-09-848-754A-1239	Sequence 1239, Ap
C	59	10.4	52.0	17	9	US-09-848-754A-1240	Sequence 1240, Ap
C	60	10.4	52.0	17	9	US-09-848-754A-1241	Sequence 1241, Ap
C	61	10.4	52.0	17	9	US-09-848-754A-1242	Sequence 1242, Ap
C	62	10.4	52.0	19	10	US-09-726-774-107	Sequence 107, App
C	63	10.4	52.0	20	9	US-10-181-177-76	Sequence 76, Appl
C	64	10.4	52.0	20	9	US-10-238-443-24	Sequence 24, Appl
C	65	10.4	52.0	20	9	US-09-741-744A-25	Sequence 25, Appl
C	66	10.4	52.0	20	9	US-09-741-744A-53	Sequence 53, Appl
C	67	10.4	52.0	20	9	US-09-953-047-65	Sequence 65, Appl
C	68	10.4	52.0	20	10	US-09-320-337-18	Sequence 18, Appl
C	69	10.4	52.0	20	10	US-09-800-629A-40	Sequence 40, Appl
C	70	10.4	52.0	20	10	US-09-800-629A-65	Sequence 65, Appl
C	71	10.4	52.0	21	9	US-10-132-652-21	Sequence 21, Appl
C	72	10.4	52.0	21	10	US-09-809-333-75	Sequence 75, Appl
C	73	10.4	52.0	22	9	US-09-881-012-27	Sequence 27, Appl
C	74	10.4	52.0	22	9	US-10-156-610-2	Sequence 2, Appl
C	75	10.4	52.0	22	9	US-10-205-522-108	Sequence 108, Appl
C	76	10.4	52.0	22	9	US-10-057-833A-57	Sequence 67, Appl
C	77	10.4	52.0	24	9	US-09-940-185-103	Sequence 103, App
C	78	10.4	52.0	24	9	US-09-940-185-1485	Sequence 1485, Ap
C	79	10.4	52.0	24	10	US-09-809-333-74	Sequence 74, Appl
C	80	10.4	52.0	25	9	US-10-202-189-31	Sequence 31, Appl
C	81	10.4	52.0	25	9	US-09-258-113-28	Sequence 28, Appl
C	82	10.4	52.0	25	9	US-10-215-112-3137	Sequence 3137, Ap
C	83	10.4	52.0	25	9	US-10-215-112-8556	Sequence 8556, Ap
C	84	10.4	52.0	25	9	US-10-215-112-10887	Sequence 10887, A
C	85	10.4	52.0	25	9	US-09-940-185-4085	Sequence 4085, Ap
C	86	10.2	51.0	15	9	US-09-997-931-69	Sequence 69, Appl
C	87	10.2	51.0	17	9	US-09-780-533A-504	Sequence 504, App
C	88	10.2	51.0	17	9	US-09-877-478-1789	Sequence 1789, Ap
C	89	10.2	51.0	17	9	US-09-877-478-1854	Sequence 1854, App
C	90	10.2	51.0	17	9	US-09-930-423-286	Sequence 286, App
C	91	10.2	51.0	17	9	US-09-930-423-297	Sequence 297, App
C	92	10.2	51.0	18	9	US-10-191-029-13	Sequence 13, Appl

C 93	10.2	51.0	18	10	US-09-808-680-2	Sequence 2, Appl1	C 166	9.8	49.0	17	9	US-09-784-674-142	Sequence 142, App
C 94	10.2	51.0	19	10	US-09-735-995-13	Sequence 13, Appl1	C 167	9.8	49.0	17	9	US-09-784-674-143	Sequence 143, App
C 95	10.2	51.0	19	10	US-09-817-607-65	Sequence 65, Appl1	C 168	9.8	49.0	17	9	US-09-784-674-144	Sequence 144, App
C 96	10.2	51.0	20	8	US-08-988-605-427	Sequence 427, App	C 169	9.8	49.0	17	9	US-09-780-5334-1367	Sequence 1367, App
C 97	10.2	51.0	20	9	US-09-949-474-4	Sequence 4, Appl1	C 170	9.8	49.0	17	9	US-09-877-478-2109	Sequence 2109, App
C 98	10.2	51.0	20	9	US-09-965-551-1	Sequence 1, Appl1	C 171	9.8	49.0	17	10	US-09-866-108-7414	Sequence 7414, App
C 99	10.2	51.0	20	9	US-09-965-551-4	Sequence 4, Appl1	C 172	9.8	49.0	17	10	US-09-866-108-7415	Sequence 7415, App
C 100	10.2	51.0	20	9	US-09-965-551-5	Sequence 5, Appl1	C 173	9.8	49.0	17	10	US-09-866-108-7416	Sequence 7416, App
C 101	10.2	51.0	20	9	US-09-965-551-6	Sequence 6, Appl1	C 174	9.8	49.0	17	10	US-09-866-108-7417	Sequence 7417, App
C 102	10.2	51.0	20	9	US-09-965-551-7	Sequence 7, Appl1	C 175	9.8	49.0	17	10	US-09-866-108-7418	Sequence 7418, App
C 103	10.2	51.0	20	9	US-09-965-551-8	Sequence 8, Appl1	C 176	9.8	49.0	18	10	US-09-822-722-146	Sequence 146, App
C 104	10.2	51.0	20	9	US-09-965-551-9	Sequence 9, Appl1	C 177	9.8	49.0	18	10	US-09-822-722-147	Sequence 147, App
C 105	10.2	51.0	20	9	US-09-965-551-11	Sequence 11, Appl1	C 178	9.8	49.0	18	10	US-09-822-722-148	Sequence 148, App
C 106	10.2	51.0	20	9	US-09-965-551-13	Sequence 13, Appl1	C 179	9.8	49.0	19	9	US-09-935-338-164	Sequence 164, App
C 107	10.2	51.0	20	9	US-10-073-718-17	Sequence 17, Appl1	C 180	9.8	49.0	19	9	US-09-935-338-166	Sequence 166, App
C 108	10.2	51.0	20	9	US-09-824-322B-49	Sequence 49, Appl1	C 181	9.8	49.0	20	9	US-09-766-450-104	Sequence 104, App
C 109	10.2	51.0	20	9	US-10-117-267-8	Sequence 8, Appl1	C 182	9.8	49.0	20	9	US-09-935-166A-24	Sequence 24, Appl1
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C 111	10.2	51.0	20	9	US-09-370-541-18	Sequence 18, Appl1	C 184	9.8	49.0	20	9	US-09-972-115A-24	Sequence 24, Appl1
C 112	10.2	51.0	20	9	US-10-238-011-33	Sequence 33, Appl1	C 185	9.8	49.0	20	9	US-09-470-526-6	Sequence 6, Appl1
C 113	10.2	51.0	20	10	US-09-808-680-1	Sequence 1, Appl1	C 186	9.8	49.0	20	9	US-09-954-679-67	Sequence 47, Appl1
C 114	10.2	51.0	20	10	US-09-816-763-125	Sequence 125, App	C 187	9.8	49.0	20	9	US-09-752-639-113	Sequence 113, App
C 115	10.2	51.0	21	8	US-08-983-605-322	Sequence 322, App	C 188	9.8	49.0	20	10	US-09-984-198-113	Sequence 113, App
C 116	10.2	51.0	21	9	US-10-074-302-14	Sequence 14, Appl1	C 189	9.8	49.0	20	10	US-09-909-849-14	Sequence 14, Appl1
C 117	10.2	51.0	21	9	US-10-044-671-4	Sequence 4, Appl1	C 190	9.8	49.0	20	10	US-09-909-849-15	Sequence 15, Appl1
C 118	10.2	51.0	21	10	US-09-765-081-184	Sequence 184, App	C 191	9.8	49.0	20	10	US-09-736-084-91	Sequence 91, Appl1
C 119	10.2	51.0	21	10	US-09-013-135A-31	Sequence 31, Appl1	C 192	9.8	49.0	20	10	US-09-736-084-91	Sequence 91, Appl1
C 120	10.2	51.0	22	9	US-09-982-262B-27	Sequence 27, Appl1	C 193	9.8	49.0	21	9	US-09-734-672-45	Sequence 45, Appl1
C 121	10.2	51.0	23	9	US-09-949-427-282	Sequence 282, App	C 194	9.8	49.0	21	9	US-09-982-828-45	Sequence 45, Appl1
C 122	10.2	51.0	24	9	US-09-940-185-488	Sequence 488, App	C 195	9.8	49.0	21	9	US-10-022-819-40	Sequence 40, Appl1
C 123	10.2	51.0	24	9	US-09-940-185-3438	Sequence 3438, App	C 196	9.8	49.0	21	9	US-10-061-071-28	Sequence 28, Appl1
C 124	10.2	51.0	25	9	US-09-887-145-38	Sequence 38, Appl1	C 197	9.8	49.0	21	9	US-09-923-327-109	Sequence 109, App
C 125	10.2	51.0	25	9	US-10-215-112-2694	Sequence 2694, App	C 198	9.8	49.0	21	10	US-09-734-188-30	Sequence 30, Appl1
C 126	10.2	51.0	25	9	US-10-215-112-2820	Sequence 2820, App	C 199	9.8	49.0	21	10	US-09-769-207A-3	Sequence 3, Appl1
C 127	10.2	51.0	25	9	US-10-215-112-6849	Sequence 6849, App	C 200	9.8	49.0	22	9	US-09-769-207A-13	Sequence 13, Appl1
C 128	10.2	51.0	25	9	US-10-215-112-1303	Sequence 1303, A	C 201	9.8	49.0	22	10	US-09-798-584-11	Sequence 11, Appl1
C 129	10.2	51.0	25	9	US-10-215-112-14387	Sequence 4459, App	C 202	9.8	49.0	22	10	US-09-925-664-78	Sequence 78, Appl1
C 130	10.2	51.0	25	9	US-09-940-185-4459	Sequence 4459, App	C 203	9.8	49.0	23	9	US-09-886-156-22	Sequence 22, Appl1
C 131	10.2	51.0	25	9	US-09-940-185-4620	Sequence 4620, App	C 204	9.8	49.0	24	9	US-09-886-150-22	Sequence 22, Appl1
C 132	10.2	51.0	18	9	US-10-156-610-28	Sequence 28, Appl1	C 205	9.8	49.0	24	9	US-09-886-150-22	Sequence 22, Appl1
C 133	10.2	51.0	20	9	US-09-949-427-212	Sequence 212, App	C 206	9.8	49.0	24	9	US-10-062-051-25	Sequence 25, Appl1
C 134	10.2	51.0	20	9	US-09-956-712-62	Sequence 62, Appl1	C 207	9.8	49.0	24	9	US-09-926-666-246	Sequence 246, App
C 135	10.2	51.0	20	9	US-10-044-692-175	Sequence 175, App	C 208	9.8	49.0	24	9	US-09-992-666-246	Sequence 66, Appl1
C 136	10.2	51.0	20	9	US-10-044-692-176	Sequence 176, App	C 209	9.8	49.0	24	9	US-09-940-185-317	Sequence 317, App
C 137	10.2	51.0	20	9	US-10-044-692-175	Sequence 175, App	C 210	9.8	49.0	24	9	US-09-940-185-317	Sequence 317, App
C 138	10.2	51.0	20	9	US-10-044-539-175	Sequence 175, App	C 211	9.8	49.0	24	9	US-09-940-185-317	Sequence 317, App
C 139	10.2	51.0	20	9	US-10-044-539-176	Sequence 176, App	C 212	9.8	49.0	24	9	US-09-940-185-1087	Sequence 1087, App
C 140	10.2	51.0	20	10	US-09-734-846-31	Sequence 31, Appl1	C 213	9.8	49.0	24	9	US-10-062-920-25	Sequence 25, Appl1
C 141	10.2	51.0	20	10	US-09-725-178-3	Sequence 3, Appl1	C 214	9.8	49.0	24	12	US-10-062-664-45	Sequence 45, Appl1
C 142	10.2	51.0	20	10	US-09-734-847A-40	Sequence 40, Appl1	C 215	9.8	49.0	24	12	US-10-075-425-12	Sequence 12, Appl1
C 143	10.2	51.0	20	10	US-09-854-883-177	Sequence 177, App	C 216	9.8	49.0	24	12	US-10-215-112-1923	Sequence 1923, App
C 144	10.2	51.0	20	10	US-09-854-883-322	Sequence 322, App	C 217	9.8	49.0	25	9	US-10-215-112-3736	Sequence 3736, App
C 145	10.2	51.0	20	10	US-09-800-631-175	Sequence 175, App	C 218	9.8	49.0	25	9	US-10-215-112-6209	Sequence 6209, App
C 146	10.2	51.0	20	10	US-09-752-639-99	Sequence 99, Appl1	C 219	9.8	49.0	25	9	US-10-215-112-7804	Sequence 7804, App
C 147	10.2	51.0	20	10	US-09-984-198-99	Sequence 99, Appl1	C 220	9.8	49.0	25	9	US-10-215-112-7804	Sequence 7804, App
C 148	10.2	51.0	20	10	US-09-791-942-51	Sequence 51, Appl1	C 221	9.8	49.0	25	9	US-10-215-112-7804	Sequence 7804, App
C 149	10.2	51.0	21	9	US-09-232-785-46	Sequence 26, Appl1	C 222	9.8	49.0	25	9	US-10-215-112-8002	Sequence 8002, App
C 150	10.2	51.0	21	10	US-09-810-993-26	Sequence 27, Appl1	C 223	9.8	49.0	25	9	US-10-215-112-8002	Sequence 8002, App
C 151	10.2	51.0	22	9	US-09-947-063-37	Sequence 38, Appl1	C 224	9.8	49.0	25	9	US-09-940-185-4048	Sequence 4048, App
C 152	10.2	51.0	24	9	US-10-269-557-38	Sequence 898, App	C 225	9.8	49.0	25	9	US-09-940-185-4295	Sequence 4295, App
C 153	10.2	51.0	25	9	US-09-754-853A-898	Sequence 5389, App	C 226	9.8	49.0	25	9	US-09-940-185-4308	Sequence 4308, App
C 154	10.2	51.0	25	9	US-10-215-112-5389	Sequence 10985, App	C 227	9.8	49.0	25	10	US-09-866-108-12306	Sequence 12306, App
C 155	10.2	51.0	25	9	US-10-215-112-10985	Sequence 11111, App	C 228	9.8	49.0	25	10	US-09-866-108-12307	Sequence 12307, App
C 156	10.2	51.0	25	9	US-10-215-112-11111	Sequence 11111, App	C 229	9.8	49.0	25	10	US-09-866-108-12308	Sequence 12308, App
C 157	10.2	51.0	25	9	US-10-215-112-11811	Sequence 11811, App	C 230	9.8	49.0	25	10	US-09-866-108-12309	Sequence 12309, App
C 158	10.2	51.0	25	9	US-10-215-112-13132	Sequence 13132, App	C 231	9.8	49.0	25	10	US-09-866-108-12310	Sequence 12310, App
C 159	10.2	51.0	25	10	US-09-835-381-19	Sequence 19, Appl1	C 232	9.8	49.0	25	10	US-09-866-108-12311	Sequence 12311, App
C 160	9.8	49.0	13	9	US-10-043-875-567	Sequence 567, App	C 233	9.8	49.0	25	10	US-09-866-108-12312	Sequence 12312, App
C 161	9.8	49.0	13	9	US-10-043-875-570	Sequence 570, App	C 234	9.8	49.0	25	10	US-09-866-108-12313	Sequence 12313, App
C 162	9.8	49.0	17	9	US-09-916-510A-34	Sequence 34, Appl1	C 235	9.8	49.0	25	10	US-09-866-108-12314	Sequence 12314, App
C 163	9.8	49.0	17	9	US-09-818-875-631	Sequence 631, App	C 236	9.8	49.0	25	10	US-09-866-108-12315	Sequence 12315, App
C 164	9.8	49.0	17	9	US-09-818-875-632	Sequence 632, App	C 237	9.8	49.0	25	10	US-09-866-108-12316	Sequence 12316, App
C 165	9.8	49.0	17	9	US-09-784-674-141	Sequence 141, App	C 238	9.8	49.0	25	10	US-09-866-108-12317	Sequence 12317, App

C 239	9.8	49.0	25	10	US-09-866-108-12318	Sequence 12318, A	C 312	9.6	48.0	25	9	US-09-909-064-329	Sequence 329, App
C 240	9.6	48.0	17	9	US-09-825-805-473	Sequence 473, App	C 313	9.6	48.0	25	9	US-09-905-088-339	Sequence 329, App
C 241	9.6	48.0	17	9	US-09-877-478-257	Sequence 257, App	C 314	9.6	48.0	25	9	US-09-907-578-339	Sequence 329, App
C 242	9.6	48.0	17	9	US-09-877-478-258	Sequence 258, App	C 315	9.6	48.0	25	9	US-09-902-759-329	Sequence 329, App
C 243	9.6	48.0	18	9	US-09-853-526-387	Sequence 387, App	C 316	9.6	48.0	25	9	US-09-905-075-339	Sequence 329, App
C 244	9.6	48.0	18	9	US-09-824-3228-166	Sequence 166, App	C 317	9.6	48.0	25	9	US-09-902-634-329	Sequence 329, App
C 245	9.6	48.0	18	9	US-09-824-3228-167	Sequence 167, App	C 318	9.6	48.0	25	9	US-09-902-713-329	Sequence 329, App
C 246	9.6	48.0	18	9	US-09-824-3228-168	Sequence 168, App	C 319	9.6	48.0	25	9	US-09-907-979-329	Sequence 329, App
C 247	9.6	48.0	18	10	US-09-901-488A-387	Sequence 387, App	C 320	9.6	48.0	25	9	US-10-215-112-434	Sequence 424, App
C 248	9.6	48.0	19	9	US-10-116-949-114	Sequence 114, App	C 321	9.6	48.0	25	9	US-10-215-112-389	Sequence 389, App
C 249	9.6	48.0	20	8	US-08-983-605-420	Sequence 420, App	C 322	9.6	48.0	25	9	US-10-215-112-428	Sequence 428, App
C 250	9.6	48.0	20	9	US-09-834-721-6	Sequence 6, App1	C 323	9.6	48.0	25	9	US-10-215-112-4979	Sequence 4979, App
C 251	9.6	48.0	20	9	US-09-824-3228-147	Sequence 147, App	C 324	9.6	48.0	25	9	US-10-215-112-6159	Sequence 6159, App
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C 253	9.6	48.0	20	9	US-09-824-3228-149	Sequence 149, App	C 326	9.6	48.0	25	9	US-10-215-112-10484	Sequence 10484, A
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C 256	9.6	48.0	20	9	US-10-059-888-8	Sequence 3, App1	C 329	9.6	48.0	25	9	US-09-903-923-329	Sequence 329, App
C 257	9.6	48.0	20	9	US-10-059-888-30	Sequence 30, App1	C 330	9.6	48.0	25	9	US-09-906-760A-329	Sequence 329, App
C 258	9.6	48.0	20	9	US-10-099-570-6	Sequence 5, App1	C 331	9.6	48.0	25	10	US-09-909-320-329	Sequence 329, App
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C 260	9.6	48.0	20	9	US-09-784-674-1040	Sequence 1040, App	C 333	9.6	48.0	25	12	US-10-139-262-16	Sequence 16, App1
C 261	9.6	48.0	20	9	US-09-784-674-1045	Sequence 1045, App	C 334	9.4	47.0	12	9	US-10-117-267-12	Sequence 12, App1
C 262	9.6	48.0	20	9	US-09-040-736-46	Sequence 46, App	C 335	9.4	47.0	13	9	US-10-043-875-568	Sequence 568, App
C 263	9.6	48.0	20	9	US-09-906-158-86	Sequence 86, App1	C 336	9.4	47.0	14	9	US-10-043-875-569	Sequence 569, App
C 264	9.6	48.0	20	9	US-10-144-577-10	Sequence 10, App1	C 337	9.4	47.0	15	9	US-10-010-802-161	Sequence 161, App
C 265	9.6	48.0	20	9	US-10-144-577-17	Sequence 17, App1	C 338	9.4	47.0	15	9	US-10-010-802-163	Sequence 163, App
C 266	9.6	48.0	20	9	US-10-094-458A-15	Sequence 15, App1	C 339	9.4	47.0	17	9	US-10-125-792-17	Sequence 17, App1
C 267	9.6	48.0	20	9	US-10-145-4938-20	Sequence 20, App1	C 340	9.4	47.0	17	9	US-10-125-792-19	Sequence 19, App1
C 268	9.6	48.0	20	9	US-10-145-4938-21	Sequence 21, App1	C 341	9.4	47.0	17	9	US-09-780-533A-1368	Sequence 1368, App
C 269	9.6	48.0	20	9	US-10-145-4938-22	Sequence 22, App1	C 342	9.4	47.0	17	9	US-09-848-754A-365	Sequence 365, App
C 270	9.6	48.0	20	10	US-09-733-299A-56	Sequence 56, App1	C 343	9.4	47.0	17	9	US-09-848-754A-366	Sequence 366, App
C 271	9.6	48.0	20	10	US-09-951-536-6	Sequence 6, App1	C 344	9.4	47.0	17	9	US-09-848-754A-2509	Sequence 2509, App
C 272	9.6	48.0	20	10	US-09-963-521-6	Sequence 23, App1	C 345	9.4	47.0	17	9	US-09-848-754A-3339	Sequence 3339, App
C 273	9.6	48.0	20	10	US-09-950-046A-23	Sequence 86, App1	C 346	9.4	47.0	17	9	US-10-125-778-17	Sequence 17, App1
C 274	9.6	48.0	21	9	US-09-904-968A-86	Sequence 46, App1	C 347	9.4	47.0	17	9	US-10-125-778-19	Sequence 19, App1
C 275	9.6	48.0	21	10	US-09-371-307-46	Sequence 11, App1	C 348	9.4	47.0	17	9	US-09-930-423-1017	Sequence 1207, App
C 276	9.6	48.0	21	10	US-09-853-033-11	Sequence 2, App1	C 349	9.4	47.0	17	9	US-09-930-423-1207	Sequence 1207, App
C 277	9.6	48.0	24	9	US-09-864-321-2	Sequence 2414, App	C 350	9.4	47.0	17	9	US-09-930-423-1554	Sequence 1554, App
C 278	9.6	48.0	24	9	US-09-940-185-2414	Sequence 329, App	C 351	9.4	47.0	17	9	US-09-930-423-1555	Sequence 1555, App
C 279	9.6	48.0	25	9	US-09-905-291A-329	Sequence 1251, App	C 352	9.4	47.0	17	9	US-09-930-423-1556	Sequence 1556, App
C 280	9.6	48.0	25	9	US-09-764-868-1251	Sequence 329, App	C 353	9.4	47.0	17	9	US-09-969-373-2605	Sequence 2605, App
C 281	9.6	48.0	25	9	US-09-902-853-329	Sequence 329, App	C 354	9.4	47.0	18	10	US-09-969-373-2607	Sequence 2607, App
C 282	9.6	48.0	25	9	US-09-907-824-329	Sequence 329, App	C 355	9.4	47.0	18	10	US-09-969-373-2608	Sequence 2608, App
C 283	9.6	48.0	25	9	US-09-907-841-329	Sequence 329, App	C 356	9.4	47.0	18	10	US-09-969-373-2609	Sequence 2609, App
C 284	9.6	48.0	25	9	US-09-904-011-329	Sequence 329, App	C 357	9.4	47.0	19	10	US-09-969-373-2610	Sequence 2610, App
C 285	9.6	48.0	25	9	US-09-906-742-329	Sequence 329, App	C 358	9.4	47.0	19	10	US-09-969-373-2620	Sequence 2620, App
C 286	9.6	48.0	25	9	US-09-906-838-329	Sequence 329, App	C 359	9.4	47.0	20	9	US-09-950-840-6	Sequence 8, App1
C 287	9.6	48.0	25	9	US-09-907-613-329	Sequence 329, App	C 360	9.4	47.0	20	9	US-09-828-344-145	Sequence 145, App
C 288	9.6	48.0	25	9	US-09-907-942-329	Sequence 71, App1	C 361	9.4	47.0	20	9	US-09-832-785-172	Sequence 172, App
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C 290	9.6	48.0	25	9	US-09-904-820-329	Sequence 329, App	C 363	9.4	47.0	20	9	US-09-784-674-1047	Sequence 1047, App
C 291	9.6	48.0	25	9	US-09-904-859-329	Sequence 329, App	C 364	9.4	47.0	20	9	US-09-784-674-1048	Sequence 1048, App
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C 294	9.6	48.0	25	9	US-09-904-786-329	Sequence 329, App	C 367	9.4	47.0	20	9	US-10-067-514-32	Sequence 32, App1
C 295	9.6	48.0	25	9	US-09-906-646-329	Sequence 329, App	C 368	9.4	47.0	20	9	US-10-116-437A-37	Sequence 37, App1
C 296	9.6	48.0	25	9	US-09-906-700-329	Sequence 329, App	C 369	9.4	47.0	20	9	US-10-1229-735-45	Sequence 45, App1
C 297	9.6	48.0	25	9	US-09-902-903-329	Sequence 329, App	C 370	9.4	47.0	20	9	US-09-953-047-80	Sequence 80, App1
C 298	9.6	48.0	25	9	US-09-903-749A-329	Sequence 329, App	C 371	9.4	47.0	20	9	US-09-953-047-81	Sequence 81, App1
C 299	9.6	48.0	25	9	US-09-903-786-329	Sequence 329, App	C 372	9.4	47.0	20	10	US-09-853-053-9	Sequence 9, App1
C 300	9.6	48.0	25	9	US-09-902-736-329	Sequence 329, App	C 373	9.4	47.0	20	10	US-09-731-188-23	Sequence 23, App1
C 301	9.6	48.0	25	9	US-09-904-119-329	Sequence 329, App	C 374	9.4	47.0	20	10	US-09-969-373-3098	Sequence 3098, App
C 302	9.6	48.0	25	9	US-09-904-956-329	Sequence 329, App	C 375	9.4	47.0	20	10	US-09-969-373-3098	Sequence 329, App
C 303	9.6	48.0	25	9	US-09-907-794-329	Sequence 329, App	C 376	9.4	47.0	20	10	US-09-985-675-14	Sequence 14, App1
C 304	9.6	48.0	25	9	US-09-902-692-329	Sequence 329, App	C 377	9.4	47.0	20	10	US-09-791-243-29	Sequence 29, App1
C 305	9.6	48.0	25	9	US-09-903-520-329	Sequence 329, App	C 378	9.4	47.0	21	9	US-09-759-508B-3	Sequence 3, App1
C 306	9.6	48.0	25	9	US-09-903-943-329	Sequence 329, App	C 379	9.4	47.0	21	9	US-09-759-508B-10	Sequence 10, App1
C 307	9.6	48.0	25	9	US-09-904-462-329	Sequence 329, App	C 380	9.4	47.0	21	9	US-10-002-974-50	Sequence 50, App1
C 308	9.6	48.0	25	9	US-09-905-056-329	Sequence 329, App	C 381	9.4	47.0	21	9	US-09-906-408A-26	Sequence 26, App1
C 309	9.6	48.0	25	9	US-09-907-925-329	Sequence 329, App	C 382	9.4	47.0	21	9	US-09-950-935-16	Sequence 16, App1
C 310	9.6	48.0	25	9	US-09-904-553-329	Sequence 329, App	C 383	9.4	47.0	21	9	US-09-906-419-62	Sequence 62, App1
C 311	9.6	48.0	25	9	US-09-905-381-329	Sequence 329, App	C 384	9.4	47.0	21	9	US-09-906-419-62	Sequence 62, App1

385	9.4	47.0	21	9	US-09-360-244A-7	Sequence 7, Appl1	C 458	9.2	46.0	18	9	US-09-907-942-52	Sequence 52, Appl1
386	9.4	47.0	21	9	US-09-365-940-14	Sequence 14, Appl1	C 459	9.2	46.0	18	9	US-09-952-267-72	Sequence 72, Appl1
387	9.4	47.0	21	9	US-10-119-136-62	Sequence 62, Appl1	C 460	9.2	46.0	18	9	US-09-904-820-52	Sequence 52, Appl1
388	9.4	47.0	21	10	US-09-765-081-88	Sequence 88, Appl1	C 461	9.2	46.0	18	9	US-09-904-853-52	Sequence 52, Appl1
389	9.4	47.0	21	10	US-09-921-992-66	Sequence 66, Appl1	C 462	9.2	46.0	18	9	US-09-909-204-52	Sequence 52, Appl1
390	9.4	47.0	21	12	US-10-014-269-50	Sequence 50, Appl1	C 463	9.2	46.0	18	9	US-09-904-786-52	Sequence 52, Appl1
391	9.4	47.0	22	9	US-09-992-665-87	Sequence 87, Appl1	C 464	9.2	46.0	18	9	US-09-906-646-52	Sequence 52, Appl1
392	9.4	47.0	22	10	US-09-986-676A-8	Sequence 8, Appl1	C 465	9.2	46.0	18	9	US-09-906-700-52	Sequence 52, Appl1
393	9.4	47.0	23	9	US-10-005-530-13	Sequence 13, Appl1	C 466	9.2	46.0	18	9	US-09-902-900-52	Sequence 52, Appl1
394	9.4	47.0	23	9	US-10-084-826-37	Sequence 37, Appl1	C 467	9.2	46.0	18	9	US-09-903-742A-52	Sequence 52, Appl1
395	9.4	47.0	23	10	US-09-844-508-37	Sequence 37, Appl1	C 468	9.2	46.0	18	9	US-09-903-786-52	Sequence 52, Appl1
396	9.4	47.0	23	10	US-09-975-579-9	Sequence 9, Appl1	C 469	9.2	46.0	18	9	US-09-902-736-52	Sequence 52, Appl1
397	9.4	47.0	23	12	US-10-075-579-9	Sequence 9, Appl1	C 470	9.2	46.0	18	9	US-09-904-119-52	Sequence 52, Appl1
398	9.4	47.0	24	7	US-08-979-847-18	Sequence 18, Appl1	C 471	9.2	46.0	18	9	US-09-904-956-52	Sequence 52, Appl1
399	9.4	47.0	24	7	US-08-979-847-18	Sequence 34, Appl1	C 472	9.2	46.0	18	9	US-09-907-794-52	Sequence 52, Appl1
400	9.4	47.0	24	9	US-09-818-991-34	Sequence 160, Appl1	C 473	9.2	46.0	18	9	US-09-902-692-52	Sequence 52, Appl1
401	9.4	47.0	24	9	US-10-201-386-25	Sequence 25, Appl1	C 474	9.2	46.0	18	9	US-09-903-520-52	Sequence 52, Appl1
402	9.4	47.0	24	9	US-09-911-904-10	Sequence 10, Appl1	C 475	9.2	46.0	18	9	US-09-903-944-52	Sequence 52, Appl1
403	9.4	47.0	24	9	US-09-940-185-242	Sequence 242, Appl1	C 476	9.2	46.0	18	9	US-09-904-462-52	Sequence 52, Appl1
404	9.4	47.0	24	9	US-09-940-185-1002	Sequence 1002, Ap	C 477	9.2	46.0	18	9	US-09-905-056-52	Sequence 52, Appl1
405	9.4	47.0	24	9	US-09-940-185-2529	Sequence 2529, Ap	C 478	9.2	46.0	18	9	US-09-907-925-52	Sequence 52, Appl1
406	9.4	47.0	24	10	US-09-832-250-37	Sequence 37, Appl1	C 479	9.2	46.0	18	9	US-09-904-553-52	Sequence 52, Appl1
407	9.4	47.0	24	10	US-09-778-546-7	Sequence 7, Appl1	C 480	9.2	46.0	18	9	US-09-905-381-52	Sequence 52, Appl1
408	9.4	47.0	25	9	US-10-037-558-12	Sequence 12, Appl1	C 481	9.2	46.0	18	9	US-09-905-064-52	Sequence 52, Appl1
409	9.4	47.0	25	9	US-09-745-317-46	Sequence 46, Appl1	C 482	9.2	46.0	18	9	US-09-905-088-52	Sequence 52, Appl1
410	9.4	47.0	25	9	US-10-108-211-4	Sequence 4, Appl1	C 483	9.2	46.0	18	9	US-09-907-575-52	Sequence 52, Appl1
411	9.4	47.0	25	9	US-09-754-853A-1037	Sequence 1037, Ap	C 484	9.2	46.0	18	9	US-09-902-759-52	Sequence 52, Appl1
412	9.4	47.0	25	9	US-10-215-112-300	Sequence 300, App	C 485	9.2	46.0	18	9	US-09-905-075-52	Sequence 52, Appl1
413	9.4	47.0	25	9	US-10-215-112-1011	Sequence 301, Ap	C 486	9.2	46.0	18	9	US-09-902-634-52	Sequence 52, Appl1
414	9.4	47.0	25	9	US-10-215-112-6097	Sequence 6097, Ap	C 487	9.2	46.0	18	9	US-09-902-713-52	Sequence 52, Appl1
415	9.4	47.0	25	9	US-10-215-112-6959	Sequence 6959, Ap	C 488	9.2	46.0	18	9	US-09-907-979-52	Sequence 52, Appl1
416	9.4	47.0	25	9	US-10-215-112-8682	Sequence 8682, Ap	C 489	9.2	46.0	18	9	US-09-902-615-52	Sequence 52, Appl1
417	9.4	47.0	25	9	US-10-215-112-9627	Sequence 9627, Ap	C 490	9.2	46.0	18	9	US-09-902-625-52	Sequence 52, Appl1
418	9.4	47.0	25	9	US-10-215-112-10409	Sequence 10409, A	C 491	9.2	46.0	18	9	US-09-906-760A-52	Sequence 52, Appl1
419	9.4	47.0	25	9	US-10-215-112-12376	Sequence 12376, A	C 492	9.2	46.0	18	10	US-09-828-366-9	Sequence 9, Appl1
420	9.4	47.0	25	9	US-09-992-665-357	Sequence 357, App	C 493	9.2	46.0	18	10	US-09-865-018-21	Sequence 21, Appl1
421	9.4	47.0	25	9	US-09-940-185-4223	Sequence 4223, Ap	C 494	9.2	46.0	18	10	US-09-909-320-52	Sequence 52, Appl1
422	9.4	47.0	25	9	US-09-940-185-4300	Sequence 4300, Ap	C 495	9.2	46.0	18	10	US-09-969-373-4389	Sequence 4389, Ap
423	9.4	47.0	25	9	US-09-940-185-4700	Sequence 4700, Ap	C 496	9.2	46.0	18	10	US-08-424-550B-107	Sequence 107, App
424	9.4	47.0	25	10	US-09-804-690-16	Sequence 16, Appl1	C 497	9.2	46.0	19	10	US-09-844-493-18	Sequence 18, Appl1
425	9.4	47.0	25	10	US-09-827-998-1014	Sequence 1014, Ap	C 498	9.2	46.0	19	10	US-09-844-501-18	Sequence 18, Appl1
426	9.4	47.0	25	10	US-09-827-998-1015	Sequence 1015, Ap	C 499	9.2	46.0	19	10	US-09-844-501-18	Sequence 18, Appl1
427	9.4	47.0	25	10	US-09-827-998-1016	Sequence 1016, Ap	C 500	9.2	46.0	20	8	US-08-424-550B-107	Sequence 107, App
428	9.4	47.0	25	10	US-09-827-998-1017	Sequence 1017, Ap	C 501	9.2	46.0	20	8	US-10-125-751-4	Sequence 4, Appl1
429	9.4	47.0	25	10	US-09-827-998-1018	Sequence 1018, Ap	C 502	9.2	46.0	20	9	US-10-125-751-4	Sequence 4, Appl1
430	9.4	47.0	25	10	US-09-827-998-1019	Sequence 1019, Ap	C 503	9.2	46.0	20	9	US-10-125-751-4	Sequence 4, Appl1
431	9.4	47.0	25	10	US-09-827-998-1020	Sequence 1020, Ap	C 504	9.2	46.0	20	9	US-09-881-012-29	Sequence 29, Appl1
432	9.2	46.0	14	9	US-10-146-058-135	Sequence 135, App	C 505	9.2	46.0	20	9	US-09-881-012-29	Sequence 29, Appl1
433	9.2	46.0	16	10	US-09-774-021-9	Sequence 9, Appl1	C 506	9.2	46.0	20	9	US-09-863-806-175	Sequence 175, App
434	9.2	46.0	17	9	US-09-825-805-840	Sequence 840, App	C 507	9.2	46.0	20	9	US-09-863-806-183	Sequence 183, App
435	9.2	46.0	17	9	US-09-780-533A-1365	Sequence 1365, Ap	C 508	9.2	46.0	20	9	US-09-824-322B-145	Sequence 145, App
436	9.2	46.0	17	9	US-09-877-478-1279	Sequence 1279, Ap	C 509	9.2	46.0	20	9	US-09-824-322B-146	Sequence 146, App
437	9.2	46.0	17	9	US-09-877-478-1705	Sequence 1705, Ap	C 510	9.2	46.0	20	9	US-09-935-916A-11	Sequence 11, Appl1
438	9.2	46.0	17	9	US-10-213-878-2	Sequence 2, Appl1	C 511	9.2	46.0	20	9	US-09-935-916A-24	Sequence 24, Appl1
439	9.2	46.0	17	9	US-10-214-059-2	Sequence 2, Appl1	C 512	9.2	46.0	20	9	US-10-036-949-43	Sequence 43, Appl1
440	9.2	46.0	17	9	US-09-310-423-298	Sequence 298, App	C 513	9.2	46.0	20	9	US-09-223-785-182	Sequence 182, App
441	9.2	46.0	17	10	US-09-866-108-9894	Sequence 9894, Ap	C 514	9.2	46.0	20	9	US-09-846-430A-3	Sequence 3, Appl1
442	9.2	46.0	17	10	US-09-866-108-9895	Sequence 9895, Ap	C 515	9.2	46.0	20	9	US-10-143-122A-7	Sequence 7, Appl1
443	9.2	46.0	17	10	US-09-866-108-9896	Sequence 9896, Ap	C 516	9.2	46.0	20	9	US-09-784-674-1038	Sequence 1038, Ap
444	9.2	46.0	17	10	US-09-866-108-9897	Sequence 9897, Ap	C 517	9.2	46.0	20	9	US-09-784-674-1039	Sequence 1039, Ap
445	9.2	46.0	17	10	US-09-866-108-9898	Sequence 9898, Ap	C 518	9.2	46.0	20	9	US-09-972-469-113	Sequence 113, App
446	9.2	46.0	18	9	US-09-905-291A-52	Sequence 52, Appl1	C 519	9.2	46.0	20	9	US-10-238-443-45	Sequence 45, Appl1
447	9.2	46.0	18	9	US-09-529-759-7	Sequence 7, Appl1	C 520	9.2	46.0	20	9	US-10-238-443-45	Sequence 45, Appl1
448	9.2	46.0	18	9	US-09-529-759-11	Sequence 11, Appl1	C 521	9.2	46.0	20	9	US-10-271-887-74	Sequence 74, Appl1
449	9.2	46.0	18	9	US-09-502-853-52	Sequence 52, Appl1	C 522	9.2	46.0	20	9	US-10-271-887-74	Sequence 74, Appl1
450	9.2	46.0	18	9	US-09-507-824-52	Sequence 52, Appl1	C 523	9.2	46.0	20	9	US-10-145-493B-8	Sequence 8, Appl1
451	9.2	46.0	18	9	US-09-507-824-52	Sequence 52, Appl1	C 524	9.2	46.0	20	9	US-10-219-834-38	Sequence 38, Appl1
452	9.2	46.0	18	9	US-09-904-011-52	Sequence 52, Appl1	C 525	9.2	46.0	20	10	US-09-752-983-167	Sequence 167, App
453	9.2	46.0	18	9	US-09-904-011-52	Sequence 52, Appl1	C 526	9.2	46.0	20	10	US-09-736-863-34	Sequence 34, Appl1
454	9.2	46.0	18	9	US-09-824-322B-164	Sequence 164, App	C 527	9.2	46.0	20	10	US-09-179-536B-66	Sequence 66, Appl1
455	9.2	46.0	18	9	US-09-824-322B-165	Sequence 165, App	C 528	9.2	46.0	20	10	US-09-954-695-19	Sequence 19, Appl1
456	9.2	46.0	18	9	US-09-906-742-52	Sequence 52, Appl1	C 529	9.2	46.0	20	10	US-09-954-695-55	Sequence 55, Appl1
457	9.2	46.0	18	9	US-09-906-838-52	Sequence 52, Appl1	C 530	9.2	46.0	20	10	US-09-954-695-61	Sequence 61, Appl1

C 531	9.2	46.0	20	10	US-09-954-695-67	Sequence 67, Appl	604	9.2	46.0	22	10	US-09-777-732-22	Sequence 26, Appl
C 532	9.2	46.0	20	10	US-09-817-913-23	Sequence 23, Appl	C 605	9.2	46.0	22	10	US-09-909-320-62	Sequence 62, Appl
C 533	9.2	46.0	20	10	US-09-918-029-8	Sequence 4, Appl	C 606	9.2	46.0	22	10	US-09-909-088B-62	Sequence 62, Appl
C 534	9.2	46.0	20	10	US-09-927-668-18	Sequence 16, Appl	C 607	9.2	46.0	23	9	US-09-853-526-172	Sequence 172, Appl
C 535	9.2	46.0	20	10	US-09-900-062-30	Sequence 30, Appl	C 608	9.2	46.0	23	9	US-09-770-107-111	Sequence 111, Appl
C 536	9.2	46.0	20	10	US-09-817-538-23	Sequence 23, Appl	C 609	9.2	46.0	23	9	US-09-964-895-25	Sequence 25, Appl
C 537	9.2	46.0	20	10	US-09-954-586-49	Sequence 49, Appl	C 610	9.2	46.0	23	10	US-09-851-859A-29	Sequence 29, Appl
C 538	9.2	46.0	20	10	US-09-954-586-55	Sequence 55, Appl	C 611	9.2	46.0	23	10	US-09-908-500A-35	Sequence 35, Appl
C 539	9.2	46.0	20	10	US-09-954-586-61	Sequence 61, Appl	C 612	9.2	46.0	23	10	US-09-901-484A-172	Sequence 172, Appl
C 540	9.2	46.0	20	10	US-09-954-586-67	Sequence 67, Appl	C 613	9.2	46.0	23	10	US-09-728-574-3	Sequence 3, Appl
C 541	9.2	46.0	20	10	US-09-263-959-1053	Sequence 1053, Ap	C 614	9.2	46.0	23	12	US-10-068-067-1	Sequence 1, Appl
C 542	9.2	46.0	20	12	US-10-038-271-4	Sequence 4, Appl	C 615	9.2	46.0	24	9	US-09-784-674-1	Sequence 1, Appl
C 543	9.2	46.0	21	10	US-10-600-639-14	Sequence 14, Appl	C 616	9.2	46.0	24	9	US-09-940-185-514	Sequence 514, Appl
C 544	9.2	46.0	21	10	US-09-759-584-53	Sequence 53, Appl	C 617	9.2	46.0	24	9	US-09-940-185-654	Sequence 654, Appl
C 545	9.2	46.0	21	10	US-09-179-538B-32	Sequence 32, Appl	C 618	9.2	46.0	24	9	US-09-940-185-807	Sequence 807, Appl
C 546	9.2	46.0	21	10	US-09-726-774-32	Sequence 32, Appl	C 619	9.2	46.0	24	9	US-09-940-185-877	Sequence 877, Appl
C 547	9.2	46.0	21	10	US-09-848-585-42	Sequence 42, Appl	C 620	9.2	46.0	24	9	US-09-940-185-878	Sequence 1078, Appl
C 548	9.2	46.0	21	10	US-09-263-959-1165	Sequence 1165, Ap	C 621	9.2	46.0	24	9	US-09-940-185-2109	Sequence 2109, Appl
C 549	9.2	46.0	22	9	US-09-624-647-4	Sequence 4, Appl	C 622	9.2	46.0	24	9	US-09-940-185-2910	Sequence 2910, Appl
C 550	9.2	46.0	22	9	US-09-905-291A-62	Sequence 62, Appl	C 623	9.2	46.0	24	9	US-09-940-185-3016	Sequence 3016, Appl
C 551	9.2	46.0	22	9	US-10-136-517-15	Sequence 15, Appl	C 624	9.2	46.0	24	9	US-09-940-185-3066	Sequence 3066, Appl
C 552	9.2	46.0	22	9	US-10-066-500-89	Sequence 89, Appl	C 625	9.2	46.0	24	9	US-09-940-185-3409	Sequence 3409, Appl
C 553	9.2	46.0	22	9	US-09-881-012-22	Sequence 22, Appl	C 626	9.2	46.0	24	9	US-09-940-185-3500	Sequence 3500, Appl
C 554	9.2	46.0	22	9	US-09-902-853-62	Sequence 62, Appl	C 627	9.2	46.0	24	9	US-10-167-127-25	Sequence 25, Appl
C 555	9.2	46.0	22	9	US-09-907-824-62	Sequence 62, Appl	C 628	9.2	46.0	24	9	US-09-733-151-6	Sequence 6, Appl
C 556	9.2	46.0	22	9	US-09-907-841-62	Sequence 62, Appl	C 629	9.2	46.0	24	10	US-09-758-575-4	Sequence 4, Appl
C 557	9.2	46.0	22	9	US-09-904-011-62	Sequence 62, Appl	C 630	9.2	46.0	24	10	US-09-758-585A-588	Sequence 588, Appl
C 558	9.2	46.0	22	9	US-09-906-742-62	Sequence 62, Appl	C 631	9.2	46.0	25	9	US-09-938-689-1	Sequence 1, Appl
C 559	9.2	46.0	22	9	US-09-906-838-62	Sequence 62, Appl	C 632	9.2	46.0	25	9	US-10-071-370A-12	Sequence 12, Appl
C 560	9.2	46.0	22	9	US-09-907-613-62	Sequence 62, Appl	C 633	9.2	46.0	25	9	US-10-215-112-3046	Sequence 3046, Appl
C 561	9.2	46.0	22	9	US-09-907-942-62	Sequence 62, Appl	C 634	9.2	46.0	25	9	US-10-215-112-4300	Sequence 4300, Appl
C 562	9.2	46.0	22	9	US-10-002-796-89	Sequence 89, Appl	C 635	9.2	46.0	25	9	US-10-215-112-4594	Sequence 4594, Appl
C 563	9.2	46.0	22	9	US-10-066-773-89	Sequence 89, Appl	C 636	9.2	46.0	25	9	US-10-215-112-6705	Sequence 6705, Appl
C 564	9.2	46.0	22	9	US-10-066-944-89	Sequence 89, Appl	C 637	9.2	46.0	25	9	US-10-215-112-6831	Sequence 6831, Appl
C 565	9.2	46.0	22	9	US-09-904-859-62	Sequence 62, Appl	C 638	9.2	46.0	25	9	US-10-215-112-6835	Sequence 6835, Appl
C 566	9.2	46.0	22	9	US-09-904-859-62	Sequence 62, Appl	C 639	9.2	46.0	25	9	US-10-215-112-6973	Sequence 6973, Appl
C 567	9.2	46.0	22	9	US-09-909-204-62	Sequence 62, Appl	C 640	9.2	46.0	25	9	US-10-215-112-7502	Sequence 7502, Appl
C 568	9.2	46.0	22	9	US-09-904-786-62	Sequence 62, Appl	C 641	9.2	46.0	25	9	US-10-215-112-8231	Sequence 8231, Appl
C 569	9.2	46.0	22	9	US-09-906-646-62	Sequence 62, Appl	C 642	9.2	46.0	25	9	US-10-215-112-9112	Sequence 9112, Appl
C 570	9.2	46.0	22	9	US-09-906-700-62	Sequence 62, Appl	C 643	9.2	46.0	25	9	US-10-215-112-101383	Sequence 101383, Appl
C 571	9.2	46.0	22	9	US-10-066-269-89	Sequence 89, Appl	C 644	9.2	46.0	25	9	US-10-215-112-10383	Sequence 10383, Appl
C 572	9.2	46.0	22	9	US-09-836-439-6	Sequence 6, Appl	C 645	9.2	46.0	25	9	US-10-215-112-10888	Sequence 10888, Appl
C 573	9.2	46.0	22	9	US-09-902-903-62	Sequence 62, Appl	C 646	9.2	46.0	25	9	US-10-215-112-10963	Sequence 10963, Appl
C 574	9.2	46.0	22	9	US-09-903-749A-62	Sequence 62, Appl	C 647	9.2	46.0	25	9	US-10-215-112-11524	Sequence 11524, Appl
C 575	9.2	46.0	22	9	US-09-903-786-62	Sequence 62, Appl	C 648	9.2	46.0	25	9	US-10-215-112-12332	Sequence 12332, Appl
C 576	9.2	46.0	22	9	US-10-066-193-89	Sequence 89, Appl	C 649	9.2	46.0	25	9	US-10-215-112-13265	Sequence 13265, Appl
C 577	9.2	46.0	22	9	US-10-066-211-89	Sequence 89, Appl	C 650	9.2	46.0	25	9	US-10-215-112-13409	Sequence 14049, Appl
C 578	9.2	46.0	22	9	US-09-902-736-62	Sequence 62, Appl	C 651	9.2	46.0	25	9	US-10-215-112-14567	Sequence 14567, Appl
C 579	9.2	46.0	22	9	US-09-904-119-62	Sequence 62, Appl	C 652	9.2	46.0	25	9	US-09-940-185-4484	Sequence 4484, Appl
C 580	9.2	46.0	22	9	US-09-904-956-62	Sequence 62, Appl	C 653	9.2	46.0	25	10	US-09-866-108-14786	Sequence 14786, Appl
C 581	9.2	46.0	22	9	US-09-907-794-62	Sequence 62, Appl	C 654	9.2	46.0	25	10	US-09-866-108-14787	Sequence 14787, Appl
C 582	9.2	46.0	22	9	US-09-902-692-62	Sequence 62, Appl	C 655	9.2	46.0	25	10	US-09-866-108-14788	Sequence 14788, Appl
C 583	9.2	46.0	22	9	US-09-903-520-62	Sequence 62, Appl	C 656	9.2	46.0	25	10	US-09-866-108-14789	Sequence 14789, Appl
C 584	9.2	46.0	22	9	US-09-903-943-62	Sequence 62, Appl	C 657	9.2	46.0	25	10	US-09-866-108-14790	Sequence 14790, Appl
C 585	9.2	46.0	22	9	US-09-904-462-62	Sequence 62, Appl	C 658	9.2	46.0	25	10	US-09-866-108-14791	Sequence 14791, Appl
C 586	9.2	46.0	22	9	US-09-905-056-62	Sequence 62, Appl	C 659	9.2	46.0	25	10	US-09-866-108-14792	Sequence 14792, Appl
C 587	9.2	46.0	22	9	US-09-907-925-62	Sequence 62, Appl	C 660	9.2	46.0	25	10	US-09-866-108-14793	Sequence 14793, Appl
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C 590	9.2	46.0	22	9	US-09-909-064-62	Sequence 62, Appl	C 663	9.2	46.0	25	10	US-09-866-108-14796	Sequence 14796, Appl
C 591	9.2	46.0	22	9	US-09-905-088-62	Sequence 62, Appl	C 664	9.2	46.0	25	10	US-09-866-108-14797	Sequence 14797, Appl
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C 593	9.2	46.0	22	9	US-09-902-759-62	Sequence 62, Appl	C 666	9.2	46.0	25	10	US-09-866-108-14799	Sequence 14799, Appl
C 594	9.2	46.0	22	9	US-09-905-075-62	Sequence 62, Appl	C 667	9.2	46.0	25	12	US-10-076-900-5	Sequence 5, Appl
C 595	9.2	46.0	22	9	US-09-902-634-62	Sequence 62, Appl	C 668	9.2	46.0	10	12	US-10-033-145-141	Sequence 141, Appl
C 596	9.2	46.0	22	9	US-09-902-713-62	Sequence 62, Appl	C 669	9.2	46.0	12	9	US-10-117-108A-23	Sequence 23, Appl
C 597	9.2	46.0	22	9	US-09-907-979-62	Sequence 62, Appl	C 670	9.2	46.0	15	9	US-09-848-754A-9294	Sequence 9294, Appl
C 598	9.2	46.0	22	9	US-09-902-615-62	Sequence 62, Appl	C 671	9.2	46.0	15	10	US-09-504-231A-873	Sequence 873, Appl
C 599	9.2	46.0	22	9	US-09-903-925-62	Sequence 62, Appl	C 672	9.2	46.0	15	10	US-09-274-755D-873	Sequence 873, Appl
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C 602	9.2	46.0	22	10	US-09-284-663A-18	Sequence 18, Appl	C 675	9.2	46.0	17	9	US-09-825-805-517	Sequence 517, Appl
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C 862	9	45.0	24	10	US-09-896-096A-14	Sequence 14, App1	C 935	9	45.0	25	10	US-09-866-108-11697	Sequence 11697, App
C 863	9	45.0	24	10	US-09-894-924-14	Sequence 14, App1	C 936	9	45.0	25	10	US-09-866-108-11698	Sequence 11698, App
C 864	9	45.0	24	10	US-09-886-241-8	Sequence 8, App1	C 937	9	45.0	25	10	US-09-866-108-11699	Sequence 11699, App
C 865	9	45.0	25	9	US-09-992-598-237	Sequence 237, App1	C 938	9	45.0	25	10	US-09-866-108-11699	Sequence 11699, App
C 866	9	45.0	25	9	US-10-005-057A-25	Sequence 25, App1	C 939	9	45.0	25	10	US-09-866-108-11700	Sequence 11700, App
C 867	9	45.0	25	9	US-09-989-293A-237	Sequence 237, App	C 940	9	45.0	25	10	US-09-866-108-11701	Sequence 11701, App
C 868	9	45.0	25	9	US-09-989-733-237	Sequence 237, App	C 941	9	45.0	25	10	US-09-866-108-11702	Sequence 11702, App
C 869	9	45.0	25	9	US-09-990-444-237	Sequence 237, App	C 942	9	45.0	25	10	US-09-866-108-11703	Sequence 11703, App
C 870	9	45.0	25	9	US-09-989-730-237	Sequence 237, App	C 943	9	45.0	25	10	US-09-866-108-11704	Sequence 11704, App
C 871	9	45.0	25	9	US-09-990-436-237	Sequence 237, App	C 944	9	45.0	25	10	US-09-866-108-11399	Sequence 11399, App
C 872	9	45.0	25	9	US-09-991-181-237	Sequence 237, App	C 945	9	45.0	25	10	US-09-866-108-11399	Sequence 11399, App
C 873	9	45.0	25	9	US-09-993-687-237	Sequence 237, App	C 946	9	45.0	25	10	US-09-866-108-11392	Sequence 11392, App
C 874	9	45.0	25	9	US-09-754-853A-687	Sequence 687, App	C 947	9	45.0	25	10	US-09-866-108-11393	Sequence 11393, App
C 875	9	45.0	25	9	US-09-754-853A-720	Sequence 720, App	C 948	9	45.0	25	10	US-09-866-108-11394	Sequence 11394, App
C 876	9	45.0	25	9	US-09-754-853A-824	Sequence 824, App	C 949	9	45.0	25	10	US-09-866-108-11395	Sequence 11395, App
C 877	9	45.0	25	9	US-09-989-734-237	Sequence 237, App	C 950	9	45.0	25	10	US-09-866-108-11396	Sequence 11396, App
C 878	9	45.0	25	9	US-09-997-653-237	Sequence 237, App	C 951	9	45.0	25	10	US-09-866-108-11397	Sequence 11397, App
C 879	9	45.0	25	9	US-09-993-667-237	Sequence 237, App	C 952	9	45.0	25	10	US-09-866-108-11398	Sequence 11398, App
C 880	9	45.0	25	9	US-09-990-436-237	Sequence 237, App	C 953	9	45.0	25	10	US-09-866-108-11399	Sequence 11399, App
C 881	9	45.0	25	9	US-09-990-562-237	Sequence 237, App	C 954	9	45.0	25	10	US-09-866-108-11812	Sequence 11812, App
C 882	9	45.0	25	9	US-09-997-428-237	Sequence 237, App	C 955	9	45.0	25	10	US-09-866-108-11813	Sequence 11813, App
C 883	9	45.0	25	9	US-09-997-666-237	Sequence 237, App	C 956	9	45.0	25	10	US-09-866-108-11814	Sequence 11814, App
C 884	9	45.0	25	9	US-09-990-711-237	Sequence 237, App	C 957	9	45.0	25	10	US-09-866-108-11815	Sequence 11815, App
C 885	9	45.0	25	9	US-09-989-726-237	Sequence 237, App	C 958	9	45.0	25	10	US-09-866-108-11817	Sequence 11817, App
C 886	9	45.0	25	9	US-09-990-437-237	Sequence 237, App	C 959	9	45.0	25	10	US-09-866-108-11818	Sequence 11818, App
C 887	9	45.0	25	9	US-09-998-156-237	Sequence 237, App	C 960	9	45.0	25	10	US-09-866-108-11819	Sequence 11819, App
C 888	9	45.0	25	9	US-10-071-370A-112	Sequence 12, App1	C 961	9	45.0	25	10	US-09-866-108-11820	Sequence 11820, App
C 889	9	45.0	25	9	US-09-991-157-237	Sequence 237, App	C 962	9	45.0	25	10	US-09-989-723-237	Sequence 237, App
C 890	9	45.0	25	9	US-09-991-172-237	Sequence 237, App	C 963	9	45.0	25	10	US-09-989-723-237	Sequence 237, App
C 891	9	45.0	25	9	US-09-997-514-237	Sequence 237, App	C 964	9	45.0	25	10	US-09-989-727-237	Sequence 237, App
C 892	9	45.0	25	9	US-09-997-573-237	Sequence 237, App	C 965	9	45.0	25	10	US-09-915-593-15	Sequence 15, App1
C 893	9	45.0	25	9	US-09-990-443-237	Sequence 237, App	C 966	9	45.0	25	10	US-09-827-996-1573	Sequence 1573, App
C 894	9	45.0	25	9	US-09-990-726-237	Sequence 237, App	C 967	9	45.0	25	10	US-09-827-996-1574	Sequence 1574, App
C 895	9	45.0	25	9	US-09-997-559-237	Sequence 237, App	C 968	9	45.0	25	10	US-09-997-601-237	Sequence 237, App

969 9 45.0 25 10 US-09-827-998-1575 Sequence 1575, Ap
970 9 45.0 25 10 US-09-827-998-1576 Sequence 1576, Ap
971 9 45.0 25 10 US-09-827-998-1577 Sequence 1577, Ap
972 9 45.0 25 10 US-09-827-998-1578 Sequence 1578, Ap
973 9 45.0 25 10 US-09-827-998-1579 Sequence 1579, Ap
974 9 45.0 25 10 US-09-827-998-1580 Sequence 1580, Ap
975 9 45.0 25 10 US-09-827-998-1581 Sequence 1581, Ap
976 9 45.0 25 10 US-09-827-998-1582 Sequence 1582, Ap
977 9 45.0 25 10 US-09-827-998-1583 Sequence 1583, Ap
978 9 45.0 25 10 US-09-827-998-1584 Sequence 1584, Ap
979 9 45.0 25 10 US-09-827-998-1585 Sequence 1585, Ap
980 9 45.0 25 10 US-09-827-998-1586 Sequence 1586, Ap
981 9 45.0 25 10 US-09-827-998-1587 Sequence 1587, Ap
982 9 45.0 25 10 US-09-827-998-1588 Sequence 1588, Ap
983 9 45.0 25 10 US-09-827-998-1589 Sequence 1589, Ap
984 9 45.0 25 10 US-09-827-998-1590 Sequence 1590, Ap
985 9 45.0 25 10 US-09-827-998-1591 Sequence 1591, Ap
986 9 45.0 25 10 US-09-827-998-1592 Sequence 1592, Ap
987 9 45.0 25 10 US-09-827-998-1593 Sequence 1593, Ap
988 9 45.0 25 10 US-09-827-998-1594 Sequence 1594, Ap
989 9 45.0 25 10 US-09-827-998-1595 Sequence 1595, Ap
990 9 45.0 25 10 US-09-827-998-1596 Sequence 1596, Ap
991 9 45.0 25 10 US-09-827-998-1597 Sequence 1597, Ap
992 9 45.0 25 10 US-09-827-998-1598 Sequence 1598, Ap
993 9 45.0 25 10 US-09-827-998-1599 Sequence 1599, Ap
994 9 45.0 25 10 US-09-827-998-1600 Sequence 1600, Ap
995 9 45.0 25 10 US-09-827-998-1601 Sequence 1601, Ap
996 9 45.0 25 10 US-09-827-998-1602 Sequence 1602, Ap
997 9 45.0 25 10 US-09-827-998-1603 Sequence 1603, Ap
998 9 45.0 25 10 US-09-827-998-1604 Sequence 1604, Ap
999 9 45.0 25 10 US-09-827-998-1605 Sequence 1605, Ap
1000 9 45.0 25 10 US-09-827-998-1606 Sequence 1606, Ap

ALIGNMENTS

RESULT 1
US-10-080-959A-2
Sequence 2, Application US/10080959A
Publication No. US20030054369A1
GENERAL INFORMATION:
APPLICANT: Cruz-Perez, Patricia
APPLICANT: Buttner, Mark P.
TITLE OF INVENTION: Method for Detection of Stachybotrys chartarum in Pure Culture an
FILE REFERENCE: 0001-00001
CURRENT APPLICATION NUMBER: US/10/080,959A
CURRENT FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: US 60/280,712
PRIOR FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 5
SEQ ID NO 2
LENGTH: 20
TYPE: DNA
ORGANISM: Stachybotrys chartarum
FEATURE:
NAME/KEY:
LOCATION:
OTHER INFORMATION:
US-10-080-959A-2

Query Match 100.0%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.29; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCGTTGGCACTCAGAG 20
DB 1 TTTCGTTGGCACTCAGAG 20

RESULT 2
US-10-080-959A-4

Sequence 4, Application US/10080959A
Publication No. US20030054369A1
GENERAL INFORMATION:
APPLICANT: Cruz-Perez, Patricia
APPLICANT: Buttner, Mark P.
TITLE OF INVENTION: Method for Detection of Stachybotrys chartarum in Pure Culture an
FILE REFERENCE: 0001-00001
CURRENT APPLICATION NUMBER: US/10/080,959A
CURRENT FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: US 60/280,712
PRIOR FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 5
SEQ ID NO 4
LENGTH: 23
TYPE: DNA
ORGANISM: Stachybotrys chartarum
FEATURE:
NAME/KEY:
LOCATION:
OTHER INFORMATION:
US-10-080-959A-4

Query Match 85.0%; Score 17; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCGTTGGCACTCAGAG 20
DB 1 GCGTTGGCACTCAGAG 17

RESULT 3
US-09-877-478-25/c
Sequence 25, Application US/09877478
Publication No. US20030068301A1
GENERAL INFORMATION:
APPLICANT: Draper, Kenneth
APPLICANT: Blact, Larry
APPLICANT: McSwigen, Jim
APPLICANT: Morrissey, Dave
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REFERENCE: MBH00-845-H (400/029)
CURRENT APPLICATION NUMBER: US/09/877,478
CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: US 07/882,712
PRIOR FILING DATE: 1992-05-14
PRIOR APPLICATION NUMBER: US 09/531,025
PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: US 09/636,385
PRIOR FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: US 09/696,347
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 08/193,627
PRIOR FILING DATE: 1994-02-07
PRIOR APPLICATION NUMBER: US 08/433,993
PRIOR FILING DATE: 1995-05-04
PRIOR APPLICATION NUMBER: US 08/434,504
PRIOR FILING DATE: 1995-05-04
PRIOR APPLICATION NUMBER: US 09/436,430
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 6586
SOFTWARE: PatentIn version 3.0
SEQ ID NO 25
LENGTH: 17
TYPE: RNA
ORGANISM: Hepatitis B virus
US-09-877-478-25

Query Match 67.0%; Score 13.4; DB 9; Length 17;
Best Local Similarity 93.3%; Pred. No. 9.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCCTTGGCCACTCAG 18
 DB 15 GAGTTTGCCACTCAG 1

RESULT 4
 US-09-972-467-10/c
 ; Sequence 10, Application US/09972467
 ; Patent No. US20020090373A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pfizer, Inc.
 ; TITLE OF INVENTION: ADAMTS POLYPEPTIDES, NUCLEIC ACIDS ENCODING THEM, AND
 ; FILE REFERENCE: PC10850A
 ; CURRENT APPLICATION NUMBER: US/09/972,467
 ; CURRENT FILING DATE: 2001-10-05
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 10
 ; LENGTH: 23
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-972-467-10

Query Match 66.0%; Score 13.2; DB 10; Length 23;
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TGGCTTGGCCACTCAG 20
 DB 19 TGGCTTGGCCACTCAG 2

RESULT 5
 US-09-780-533A-2611
 ; Sequence 2611, Application US/09780533A
 ; Publication No. US20030060611A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Blatt, Larry
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Chowdhry, Bharat
 ; APPLICANT: Heberli, Pete
 ; TITLE OF INVENTION: Method and Reagent for the Inhibition of NCO Gene
 ; FILE REFERENCE: MHB00.878-A (400/011)
 ; CURRENT APPLICATION NUMBER: US/09/780,533A
 ; CURRENT FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: US 60/181,797
 ; PRIOR FILING DATE: 2000-02-11
 ; NUMBER OF SEQ ID NOS: 6679
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 2611
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 ; US-09-780-533A-2611

Query Match 61.0%; Score 12.2; DB 9; Length 17;
 Best Local Similarity 52.9%; Pred. No. 4.1e+03;
 Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTGGCTTGGCCACTCA 17
 DB 1 UCUCUCUUGGCCACUCA 17

RESULT 6
 US-09-819-097-24/c
 ; Sequence 24, Application US/09819097
 ; Patent No. US20020106347A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Douglae, Andrea M.

APPLICANT: Begley, Colin G.
 ; TITLE OF INVENTION: CYTOKINES AND THEIR USE IN TREATMENT AND/OR PROPHYLAXIS
 ; FILE REFERENCE: 113752
 ; CURRENT APPLICATION NUMBER: US/09/819,097
 ; CURRENT FILING DATE: 2001-03-05
 ; PRIOR APPLICATION NUMBER: 09/051,939
 ; PRIOR FILING DATE: 1998-10-16
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 24
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: IL-3R (

Query Match 61.0%; Score 12.2; DB 10; Length 25;
 Best Local Similarity 83.4%; Pred. No. 4.2e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TGGCTTGGCCACTCAGA 19
 DB 20 TGGCTTGGCCACTCGGA 4

RESULT 7
 US-09-821-821-22/c
 ; Sequence 22, Application US/09821821
 ; Patent No. US20020064823A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Welcher, Andrew A.
 ; APPLICANT: Calzone, Frank J.
 ; TITLE OF INVENTION: CD20/19E-Receptor Like Molecules and Uses Thereof
 ; FILE REFERENCE: 01017/36938A
 ; CURRENT APPLICATION NUMBER: US/09/821,821
 ; CURRENT FILING DATE: 2001-03-29
 ; PRIOR APPLICATION NUMBER: US 09/723,258
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: US 60/193,728
 ; PRIOR FILING DATE: 2000-03-30
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 22
 ; LENGTH: 23
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Primer 2323-70.

Query Match 60.0%; Score 12; DB 10; Length 23;
 Best Local Similarity 100.0%; Pred. No. 5.3e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGGCCACTCAG 20
 DB 23 TGGCCACTCAG 12

RESULT 8
 US-09-780-533A-2000
 ; Sequence 2000, Application US/09780533A
 ; Publication No. US20030060611A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Blatt, Larry
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Chowdhry, Bharat
 ; APPLICANT: Heberli, Pete
 ; TITLE OF INVENTION: Method and Reagent for the Inhibition of NCO Gene

```
FILE REFERENCE: MEHBO0,878-A (400/011)
CURRENT APPLICATION NUMBER: US/09/780,533A
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,797
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 6679
SOFTWARE: Patentin version 3.0
SEQ ID NO 2000
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-780-533A-2000

Query Match
Best Local Similarity 59.0%; Score 11.8; DB 9; Length 17;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGCCTTGGCCACTCA 17
Db 2 UGCCTTGGCCACTCA 16

RESULT 9
US-09-996-956-14
Sequence 14, Application US/09996956
Patent No. US2002015463A1
GENERAL INFORMATION:
APPLICANT: Origene Technologies, Inc
TITLE OF INVENTION: Prostate Polynucleotides and Uses
FILE REFERENCE: 9U 301 R1
CURRENT APPLICATION NUMBER: US/09/996,956
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/250,354
PRIOR FILING DATE: 2001-12-01
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
SEQ ID NO 14
LENGTH: 22
TYPE: DNA
ORGANISM: Homo sapiens
US-09-996-956-14

Query Match
Best Local Similarity 59.0%; Score 11.8; DB 9; Length 22;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGCCTTGGCCACTCA 17
Db 5 TGCCTTGGCCACTCA 19

RESULT 10
US-09-368-834-3
Sequence 3, Application US/09368834
Patent No. US20020068317A1
GENERAL INFORMATION:
APPLICANT: Mundechaek, David
Smith, Leonard
TITLE OF INVENTION: Polypeptide Compositions and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: Fredrikson & Byron, P.A.
STREET: 900 Second Avenue South
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
ZIP: 55402-3397
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows-95
SOFTWARE: ASCII files
CURRENT APPLICATION DATA:
```

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APPLICATION NUMBER: US/09/368,834
FILING DATE: 05-Aug-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/908,212
FILING DATE: 07 August 1997
APPLICATION NUMBER: 08/644,399
FILING DATE: 10 May 1996
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Philip M.
REGISTRATION NUMBER: 31,162
REFERENCE/DOCKET NUMBER: 15050.1.2.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 347-7088
TELEFAX: (612) 347-7077
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-368-834-3

Query Match
Best Local Similarity 58.0%; Score 11.6; DB 10; Length 21;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTTCCTTGGCCACTCAG 18
Db 2 TTTCCTTGGCCACTCAG 19

RESULT 11
US-09-940-185-2248/c
Sequence 2248, Application US/09940185
Publication No. US20030096239A1
GENERAL INFORMATION:
APPLICANT: Gunderson, Kevin
Chee, Mark
TITLE OF INVENTION: Probes and Decoder Oligonucleotides
FILE REFERENCE: A-69605-1
CURRENT APPLICATION NUMBER: US/09/940,185
CURRENT FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: US 60/227,948
PRIOR FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: US 60/228,854
PRIOR FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 4768
SOFTWARE: Patentin version 3.1
SEQ ID NO 2248
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-2248

Query Match
Best Local Similarity 58.0%; Score 11.6; DB 9; Length 24;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTTCCTTGGCCACTCAG 18
Db 18 TTTCCTTGGCCACTCAG 1

RESULT 12
US-08-844-215-30
Sequence 30, Application US/08844215
Patent No. US20020016445A1
GENERAL INFORMATION:
APPLICANT: PERSSON, MATS AXEL
```

APPLICANT: ALLANDER, TOBIAS ERIK
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR
TITLE OF INVENTION: HEPATITIS C VIRUS (HCV) E2 ANTIGEN
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,215
FILING DATE: 17-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/635,109
FILING DATE: 19-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 80146.002
TELEPHONE: (650) 325-7812
TELEFAX: (650) 325-7823
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-844-215-30

Query Match 57.0%; Score 11.4; DB 8; Length 24;
Best Local Similarity 92.3%; Pred. No. 1.1e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGGCGTTGCCA 13
DB 10 TTAGCGTTGCCA 22

RESULT 13
US-09-913-238-53
Sequence 53, Application US/09913238
Publication No. US20030049251A1
GENERAL INFORMATION:
APPLICANT: Barbas, Carlos F.
APPLICANT: Steinberger, Peter
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR
TITLE OF INVENTION: INHIBITING CCR5-DEPENDENT INFECTION OF CELLS BY HIV-1
FILE REFERENCE: TSRI 728.1
CURRENT APPLICATION NUMBER: US/09/913,238
CURRENT FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: PCT/EPO 0/12419
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: US 60/169,653
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 85
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 53
LENGTH: 24
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Synthesized
US-09-913-238-53

Query Match 57.0%; Score 11.4; DB 9; Length 24;
Best Local Similarity 92.3%; Pred. No. 1.1e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGGCGTTGCCA 13
DB 10 TTAGCGTTGCCA 22

RESULT 14
US-10-215-112-10761
Sequence 10761, Application US/10215112
Publication No. US20030082596A1
GENERAL INFORMATION:
APPLICANT: Michael Miltman
TITLE OF INVENTION: Method of Genetic Analysis of Probes:
FILE REFERENCE: 3119
CURRENT APPLICATION NUMBER: US/10/215,112
CURRENT FILING DATE: 2002-08-08
NUMBER OF SEQ ID NOS: 14936
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10761
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-10761

Query Match 57.0%; Score 11.4; DB 9; Length 25;
Best Local Similarity 92.3%; Pred. No. 1.1e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TTGCCACTCAGAG 20
DB 13 TTGCCGCTCAGAG 25

RESULT 15
US-09-780-533A-505
Sequence 505, Application US/09780533A
Publication No. US20030060611A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: McSwigen, Jim
APPLICANT: Chowdhry, Bharat
APPLICANT: Haebertl, Pete
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
FILE REFERENCE: MBH00, 878-A (400/011)
CURRENT APPLICATION NUMBER: US/09/780,533A
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,797
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 6679
SOFTWARE: Patentin version 3.0
SEQ ID NO 505
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-780-533A-505

Query Match 56.0%; Score 11.2; DB 9; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.4e+04;
Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTGGCTTGGCACTC 16
DB 2 UUGGCUUGGCCACUC 17

```
RESULT 16
US-09-930-423-1153/c
; Sequence 1153, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blact, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MHH00, 918-A, 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1153
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-1153

Query Match          56.0%; Score 11.2; DB 9; Length 17;
Best Local Similarity 81.2%; Pred. No. 1.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TGGCTTGGCCACTCAG 18
    |||||
DB 17 TGGCTTGGCTGCTCAG 2

RESULT 17
US-10-206-839-96
; Sequence 96, Application US/10206839
; Publication No. US20030099977A1
; GENERAL INFORMATION:
; APPLICANT: Guida, Marco
; APPLICANT: Kurth, Janice
; TITLE OF INVENTION: Genotyping Human Phenol Sulfotransferase
; FILE REFERENCE: 4389-6 (formerly SEQ-16P)
; CURRENT APPLICATION NUMBER: US/10/206,839
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 09/328,174
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 96
; LENGTH: 19
; TYPE: DNA
; ORGANISM: H. sapiens
US-10-206-839-96

Query Match          56.0%; Score 11.2; DB 9; Length 19;
Best Local Similarity 81.2%; Pred. No. 1.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CGTTGGCACTCAG 20
    |||||
DB 1 CTTTGGCCCAAG 16

RESULT 18
US-10-060-301-158
; Sequence 158, Application US/10060301
; Publication No. US20020182622A1
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, Yusuke et al.
; TITLE OF INVENTION: A METHOD FOR SNP (SINGLE NUCLEOTIDE POLYMORPHISM) TYPING
; FILE REFERENCE: 1254-0195D
; CURRENT APPLICATION NUMBER: US/10/060,301
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: JP 2001-25700
; PRIOR FILING DATE: 2001-02-01
; NUMBER OF SEQ ID NOS: 200
```

```
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 158
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Reverse Primer for SNP ID 79
US-10-060-301-158

Query Match          56.0%; Score 11.2; DB 9; Length 20;
Best Local Similarity 81.2%; Pred. No. 1.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TGGCTTGGCCACTCAG 18
    |||||
DB 5 TGGCTTGGCCACTCAG 20

RESULT 19
US-10-060-301-160
; Sequence 160, Application US/10060301
; Publication No. US20020182622A1
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, Yusuke et al.
; TITLE OF INVENTION: A METHOD FOR SNP (SINGLE NUCLEOTIDE POLYMORPHISM) TYPING
; FILE REFERENCE: 1254-0195D
; CURRENT APPLICATION NUMBER: US/10/060,301
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: JP 2001-25700
; PRIOR FILING DATE: 2001-02-01
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 160
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Reverse Primer for SNP ID 80
US-10-060-301-160

Query Match          56.0%; Score 11.2; DB 9; Length 20;
Best Local Similarity 81.2%; Pred. No. 1.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TGGCTTGGCCACTCAG 18
    |||||
DB 5 TGGCTTGGCCACTCAG 20

RESULT 20
US-09-808-680-10/c
; Sequence 10, Application US/09808680
; Patent No. US20020052331A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda F
; APPLICANT: Bennett, C. Frank
; APPLICANT: Anderson, Kevin P
; APPLICANT: Condon, Thomas P
; TITLE OF INVENTION: Compositions and Methods for Antisense Inhibition of
; TITLE OF INVENTION: Protein Translation
; FILE REFERENCE: ISPH-0557
; CURRENT APPLICATION NUMBER: US/09/808,680
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/194,230
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: PCT/US97/07132
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: 08/653,653
; PRIOR FILING DATE: 1996-05-24
; PRIOR APPLICATION NUMBER: 08/440,740
; PRIOR FILING DATE: 1995-05-12
```

PRIOR APPLICATION NUMBER: 08/063,167
PRIOR FILING DATE: 1993-05-17
PRIOR APPLICATION NUMBER: 08/007,997
PRIOR FILING DATE: 1993-01-21
PRIOR APPLICATION NUMBER: 07/939,855
PRIOR FILING DATE: 1992-09-02
PRIOR APPLICATION NUMBER: 07/567,286
PRIOR FILING DATE: 1990-08-14
PRIOR APPLICATION NUMBER: 07/927,506
PRIOR FILING DATE: 1992-11-19
PRIOR APPLICATION NUMBER: 07/568,366
PRIOR FILING DATE: 1990-08-16
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-808-680-10

Query Match 56.0%; Score 11.2; DB 10; Length 20;
Best Local Similarity 81.2%; Pred. No. 1.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CGTTGCCACTCAGAG 20
DB 20 CCTCTGCTACTCAGAG 5

RESULT 21
US-10-117-108A-27
Sequence 27, Application US/10117108A
Publication No. US20030082571A1
GENERAL INFORMATION:
APPLICANT: KACHAB, Edward H.
TITLE OF INVENTION: LINEAR NUCLEIC ACID AND SEQUENCE THEREFOR
FILE REFERENCE: 37955-0004
CURRENT APPLICATION NUMBER: US/10/117,108A
CURRENT FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US 60/282,491
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn version 3.1
SEQ ID NO 27
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
NAME/KEY: misc feature
LOCATION: (1)-(6)
OTHER INFORMATION: The monomer ttgcgcg may be repeated from 2-20 times
US-10-117-108A-27

Query Match 55.0%; Score 11; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCGCTTTCG 11
DB 1 TTTCGCTTTCG 11

RESULT 22
US-10-175-225-65
Sequence 65, Application US/10175225
Publication No. US2003008582A1
GENERAL INFORMATION:
APPLICANT: Richard A. Gatti

TITLE OF INVENTION: METHODS FOR DETECTION OF ATAXIA
TITLE OF INVENTION: TELANGIECTASIA MUTATIONS
FILE REFERENCE: US078,001DVI
CURRENT APPLICATION NUMBER: US/10/175,225
CURRENT FILING DATE: 2002-08-23
PRIOR APPLICATION NUMBER: US 09/360,416
PRIOR FILING DATE: 1999-07-23
NUMBER OF SEQ ID NOS: 143
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 65
LENGTH: 19
TYPE: DNA
ORGANISM: Human
US-10-175-225-65

Query Match 55.0%; Score 11; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGGCACTCAGA 19
DB 2 TGGCACTCAGA 12

RESULT 23
US-09-801-968-5
Sequence 5, Application US/09801968
Patent No. US20020082205A1
GENERAL INFORMATION:
APPLICANT: Itoh, No. US20020082205A1uyuk1
TITLE OF INVENTION: HUMAN RGF-23 GENE AND GENE EXPRESSION
FILE REFERENCE: PP-17150,001/201130,40901
CURRENT APPLICATION NUMBER: US/09/801,968
CURRENT FILING DATE: 2001-03-07
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Sense PCR primer
US-09-801-968-5

Query Match 55.0%; Score 11; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GCCACTCAGAG 20
DB 8 GCCACTCAGAG 18

RESULT 24
US-09-780-533A-1366
Sequence 1366, Application US/09780533A
Publication No. US20030060611A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blate, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: Chowitra, Bharat
APPLICANT: Haebertl, Pete
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
FILE REFERENCE: MBH00,878-A (400/011)
CURRENT APPLICATION NUMBER: US/09/780,533A
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,797
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 6679
SOFTWARE: PatentIn version 3.0

SEQ ID NO 1366
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-780-533A-1366

Query Match 54.0%; Score 10.8; DB 9; Length 17;
Best Local Similarity 64.3%; Pred. No. 2.3e+04;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 4 GCGTTGGCCTCA 17
1 GCUUGGCCACUCA 14

RESULT 25
US-10-087-082-2/c
Sequence 2, Application US/10087082
Patent No. US2002016040A1
GENERAL INFORMATION:
APPLICANT: Diemaler, Wolfgang
APPLICANT: Ruschoff, Josef
TITLE OF INVENTION: IMPROVED METHOD OF PRIMER-EXTENSION PREAMPLIFICATION PCR
FILE REFERENCE: 4802
CURRENT APPLICATION NUMBER: US/10/087,082
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: DE 198 13 317.0
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patent in version 3.1
SEQ ID NO 2
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Description of artificial sequence: Primer for Human genomic sequ
US-10-087-082-2

Query Match 54.0%; Score 10.8; DB 9; Length 20;
Best Local Similarity 85.7%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 TTGGCCTCAGAG 20
DB 19 TTGGCCTCAGAG 6

RESULT 26
US-09-865-866-22
Sequence 22, Application US/09865866
Publication No. US20030045487A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
FILE REFERENCE: RTS-0221
CURRENT APPLICATION NUMBER: US/09/865,866
CURRENT FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 173
SEQ ID NO 22
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-865-866-22

Query Match 54.0%; Score 10.8; DB 9; Length 20;
Best Local Similarity 85.7%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 TTGGCCTCAGAG 20
DB 19 TTGGCCTCAGAG 6

Db 4 TTACTCTCAGAG 17

RESULT 27
US-09-865-866-23
Sequence 23, Application US/09865866
Publication No. US20030045487A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) E
FILE REFERENCE: RTS-0221
CURRENT APPLICATION NUMBER: US/09/865,866
CURRENT FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 173
SEQ ID NO 23
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-865-866-23

Query Match 54.0%; Score 10.8; DB 9; Length 20;
Best Local Similarity 85.7%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 TTGGCCTCAGAG 20
DB 7 TTACTCTCAGAG 20

RESULT 28
US-09-940-925A-68/c
Sequence 68, Application US/09940925A
Publication No. US20030054338A1
GENERAL INFORMATION:
APPLICANT: BROW, MARY ANN D.
APPLICANT: LYAMICHEV, VICTOR I.
OLIVE, DAVID M.
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
PATHOGENS
NUMBER OF SEQUENCES: 165
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/940,925A
FILING DATE: 10-Jun-2002
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-01756
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 68:
US-09-940-925A-68

Query Match 54.0%; Score 10.8; DB 9; Length 20;
Best Local Similarity 85.7%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 TTGGCCACTGAG 20
Db 19 TTGGCCACTGAG 6

RESULT 29
US-10-001-076-59
Sequence 59, Application US/10001076
Publication No. US20030096775A1

GENERAL INFORMATION:
APPLICANT: Mark J. Graham
TITLE OF INVENTION: ANTISENSE MODULATION OF COMPLEMENT COMPONENT C3 EXPRESSION
FILE REFERENCE: RTS-0329
CURRENT APPLICATION NUMBER: US/10/001,076
PRIORITY FILING DATE: 2001-10-23
NUMBER OF SEQ ID NOS: 179
SEQ ID NO 59
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-076-59

Query Match 54.0%; Score 10.8; DB 9; Length 20;
Best Local Similarity 85.7%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GTTGCACACTGAGA 19
Db 2 GTTGCACACTGAGA 15

RESULT 30
US-10-011-119A-6/c
Sequence 6, Application US/10011119A
Patent No. US20020150928A1

GENERAL INFORMATION:
APPLICANT: Manson, Per
TITLE OF INVENTION: DNA-EMBEDDING MEDIUM AND METHOD OF USE
FILE REFERENCE: P/2432-45
CURRENT APPLICATION NUMBER: US/10/011,119A
PRIORITY FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: 09/605,611
PRIORITY FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 6
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-011-119A-6

Query Match 54.0%; Score 10.8; DB 12; Length 20;
Best Local Similarity 85.7%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 TTGGCCACTGAG 20
Db 19 TTGGCCACTGAG 6

RESULT 31
US-10-135-629-15

Sequence 15, Application US/10135629
Publication No. US20030073657A1
GENERAL INFORMATION:
APPLICANT: Halle, Jorn-Peter
TITLE OF INVENTION: Use of Alpha 1-Antichymotrypsin
TITLE OF INVENTION: Polypeptides, or Nucleic Acids Encoding Them, or of a Cell
TITLE OF INVENTION: Which is Expressing an ACT Polypeptide, or a Nucleic Acid
TITLE OF INVENTION: Encoding It, For Treatment and/or Prevention of
TITLE OF INVENTION: Diabetes-Associated and/or Arterial Poorly Healing Wounds
TITLE OF INVENTION: and For Identifying Pharmacologically Active Substances
FILE REFERENCE: 50125/033002
CURRENT APPLICATION NUMBER: US/10/135,629
PRIORITY FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: DE 10121225.0
PRIORITY FILING DATE: 2001-04-30
PRIOR APPLICATION NUMBER: US 60/323,348
PRIORITY FILING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 21
TYPE: DNA
ORGANISM: Homo sapiens
US-10-135-629-15

Query Match 54.0%; Score 10.8; DB 9; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GCGTTGCCACTCA 17
Db 3 GCGTTGCCACTCA 16

RESULT 32
US-09-883-152-86

Sequence 86, Application US/09883152
Publication No. US2003008284A1
GENERAL INFORMATION:
APPLICANT: Kennedy, Giulia
TITLE OF INVENTION: POLYNUCLEOTIDES RELATED TO COLON CANCER
FILE REFERENCE: 2300-1663
CURRENT APPLICATION NUMBER: US/09/883,152
PRIORITY FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/211,835
PRIORITY FILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 127
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 86
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
US-09-883-152-86

Query Match 54.0%; Score 10.8; DB 9; Length 24;
Best Local Similarity 85.7%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TGCCTTGCCTC 16
Db 3 TGCCTTGCCTC 16

```
RESULT 33
US-09-940-185-2382
; Sequence 2382, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09/940.185
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/227,948
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 4768
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2382
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-2382

Query Match      54.0%; Score 10.8; DB 9; Length 24;
Best Local Similarity 85.7%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 3 TGGCTTGGCACTC 16
Db 2 TGTGTTGCCACGC 15

RESULT 34
US-10-215-112-665
; Sequence 665, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: Test3
; CURRENT APPLICATION NUMBER: US/10/215.112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 665
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-665

Query Match      54.0%; Score 10.8; DB 9; Length 25;
Best Local Similarity 85.7%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 4 GCGTTGGCACTCA 17
Db 5 GCATTGGCTACTCA 18

RESULT 35
US-10-215-112-791
; Sequence 791, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: Test3
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-791
```

```
; CURRENT APPLICATION NUMBER: US/10/215.112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 791
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-791

Query Match      54.0%; Score 10.8; DB 9; Length 25;
Best Local Similarity 85.7%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 4 GCGTTGGCACTCA 17
Db 5 GCATTGGCTACTCA 18

RESULT 36
US-10-215-112-2803/c
; Sequence 2803, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: Test3
; CURRENT APPLICATION NUMBER: US/10/215.112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2803
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-2803

Query Match      54.0%; Score 10.8; DB 9; Length 25;
Best Local Similarity 85.7%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 4 GCGTTGGCACTCA 17
Db 21 GCATTGGCTACTCA 8

RESULT 37
US-10-215-112-2929/c
; Sequence 2929, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: Test3
; CURRENT APPLICATION NUMBER: US/10/215.112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2929
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-2929

Query Match      54.0%; Score 10.8; DB 9; Length 25;
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```
Best Local Similarity 85.7%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCGTTGCCACTCA 17
   |||||
Db 21 GCATTGCCACTCA 8

RESULT 38
US-10-215-112-8357
; Sequence 8357, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8357
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-8357

Query Match 54.0%; Score 10.8; DB 9; Length 25;
Best Local Similarity 85.7%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGTGGCCACTCAG 18
   |||||
Db 2 CTTTGTCTCTCAG 15

RESULT 39
US-10-215-112-11650/c
; Sequence 11650, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11650
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-11650

Query Match 54.0%; Score 10.8; DB 9; Length 25;
Best Local Similarity 85.7%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGTGGCCACTCAG 18
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Db 24 CTTTGTCTCTCAG 11

RESULT 40
US-10-215-112-12458
; Sequence 12458, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
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; APPLICANT: Michael Miltmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12458
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-12458

Query Match 54.0%; Score 10.8; DB 9; Length 25;
Best Local Similarity 85.7%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGGCGTTGCCAC 14
   |||||
Db 2 TTTGTGTTGTCTAC 15
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Search completed: June 7, 2003, 11:39:08
Job time : 89.3636 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 7, 2003, 08:05:49 / Search time 1145.09 Seconds
(without alignments)
282.868 Million cell updates/sec

Title: US-10-080-959A-2
Perfect score: 20
Sequence: 1 ttgcgttcgcacacagag 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 18144

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :
1: em_ests:
2: em_estnum:
3: em_estin:
4: em_estnu:
5: em_estov:
6: em_estpl:
7: em_estro:
8: em_hic:
9: gb_est1:
10: gb_est2:
11: gb_hic:
12: gb_est3:
13: gb_est4:
14: gb_est5:
15: em_estfun:
16: em_estcom:
17: gb_ges:
18: em_ges_hum:
19: em_ges_inv:
20: em_ges_pin:
21: em_ges_vrt:
22: em_ges_fun:
23: em_ges_mam:
24: em_ges_mus:
25: em_ges_other:
26: em_ges_pro:
27: em_ges_tod:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match length	ID	Description
C 1	11.6	58.0	20	9	AU256704	AU256704 AU256704
C 2	11.2	56.0	25	9	AU189662	AU189662 qd18n06.x
C 3	11	55.0	24	9	AU257541	AU257541 AU257541
C 4	10.8	54.0	20	14	D18747	D18747 MUSGS01809
C 5	10.6	53.0	22	17	AZ79532	AZ79532 2M0016K03
C 6	10	50.0	19	17	AZ65339	AZ65339 1M0464F13

C 7	10	50.0	21	9	AU254819	AU254819 AU254819
C 8	10	50.0	21	17	AZ785704	AZ785704 2M0029C21
C 9	10	50.0	24	17	BH813511	BH813511 SALK_0643
C 10	9.8	49.0	24	17	AZ762000	AZ762000 1M0556F08
C 11	9.8	49.0	24	17	TA259C080	TA259C080 T. brucei
C 12	9.6	48.0	22	9	AA916047	AA916047 og3id01.B
C 13	9.6	48.0	22	17	AZ592068	AZ592068 1M0402H08
C 14	9.6	48.0	22	17	AZ771198	AZ771198 1M0573M08
C 15	9.6	48.0	22	17	TA223E07P	TA223E07P T. brucei
C 16	9.6	48.0	23	17	TA202H11Q	TA202H11Q T. brucei
C 17	9.6	48.0	25	17	BH864166	BH864166 SALK_0954
C 18	9.6	48.0	25	17	BH864216	BH864216 SALK_0955
C 19	9.4	47.0	20	17	AZ589990	AZ589990 1M0399016
C 20	9.4	47.0	21	17	AZ812038	AZ812038 2M0078022
C 21	9.4	47.0	22	17	AZ662093	AZ662093 1M0541C05
C 22	9.4	47.0	22	17	AZ612609	AZ612609 1M0439P23
C 23	9.4	47.0	24	17	TA186D08P	TA186D08P T. brucei
C 24	9.2	46.0	21	17	AZ405188	AZ405188 1M0173G15
C 25	9.2	46.0	21	17	AZ427688	AZ427688 1M0209J15
C 26	9.2	46.0	21	17	AZ948720	AZ948720 2M0211D23
C 27	9.2	46.0	22	17	AZ583690	AZ583690 1M0378E16
C 28	9.2	46.0	23	17	AZ634674	AZ634674 1M0490A11
C 29	9.2	46.0	23	17	AZ646716	AZ646716 1M0512D23
C 30	9.2	46.0	24	17	AZ418103	AZ418103 1M0194L03
C 31	9.2	46.0	24	17	AZ829689	AZ829689 2M0107C22
C 32	9.2	46.0	25	17	AZ379234	AZ379234 1M0134P16
C 33	9.2	46.0	25	17	BH759341	BH759341 KG02510-3
C 34	9.2	46.0	25	17	AZ954781	AZ954781 2M0220C07
C 35	9.2	46.0	19	17	AZ435809	AZ435809 1M0223L03
C 36	9.2	46.0	20	17	AZ991405	AZ991405 2M0275004
C 37	9.2	46.0	20	17	TA361F06P	TA361F06P T. brucei
C 38	9.2	46.0	21	17	TA62B07P	TA62B07P T. brucei
C 39	9.2	46.0	22	17	AT186405	AT186405 qd20e05.x
C 40	9.2	46.0	22	17	AZ367707	AZ367707 1M0117N08
C 41	9.2	46.0	23	17	TA101C01Q	TA101C01Q T. brucei
C 42	9.2	46.0	24	17	AZ612609	AZ612609 1M0439P23
C 43	9.2	46.0	25	17	AQ073480	AQ073480 EP(2)2310
C 44	9.2	46.0	25	17	AZ514617	AZ514617 1M0361N23
C 45	9.2	46.0	19	17	AZ773052	AZ773052 1M0584C20
C 46	8.8	44.0	21	17	AZ307601	AZ307601 1M0009C16
C 47	8.8	44.0	21	17	AZ375290	AZ375290 1M0128N01
C 48	8.8	44.0	22	9	A1047128	A1047128 uh58d11.x
C 49	8.8	44.0	22	9	A1804482	A1804482 cg71909.x
C 50	8.8	44.0	23	17	AZ572556	AZ572556 AU2527256
C 51	8.8	44.0	23	17	AZ335754	AZ335754 1M0065P22
C 52	8.8	44.0	24	17	AZ957958	AZ957958 2M0225G04
C 53	8.8	44.0	25	17	AZ588895	AZ588895 1M0397R04
C 54	8.8	44.0	25	17	TA263F03Q	TA263F03Q T. brucei
C 55	8.6	43.0	20	9	AU254453	AU254453 AU254453
C 56	8.6	43.0	20	9	AU267884	AU267884 AU267884
C 57	8.6	43.0	20	17	AZ395013	AZ395013 1M0158M18
C 58	8.6	43.0	20	17	AZ793050	AZ793050 2M0045M15
C 59	8.6	43.0	20	17	AZ992248	AZ992248 2M0276M17
C 60	8.6	43.0	21	14	D20000	D20000 HUMGS00970
C 61	8.6	43.0	21	17	AZ472579	AZ472579 1M0287R21
C 62	8.6	43.0	21	17	AZ949072	AZ949072 2M0212D19
C 63	8.6	43.0	21	17	AZ991096	AZ991096 2M0275C09
C 64	8.6	43.0	22	9	A1120642	A1120642 ub71a05.x
C 65	8.6	43.0	22	17	TA33D08P	TA33D08P T. brucei
C 66	8.6	43.0	24	17	AZ502375	AZ502375 1M0341R08
C 67	8.6	43.0	24	17	AZ662752	AZ662752 1M0542G05
C 68	8.6	43.0	24	17	AZ805590	AZ805590 2M0067L05
C 69	8.6	43.0	24	17	TA100C01Q	TA100C01Q T. brucei
C 70	8.6	43.0	25	14	L76129	L76129 SCRAPO223
C 71	8.4	42.0	15	14	BH840574	BH840574 KG05441-5
C 72	8.4	42.0	19	17	AZ370656	AZ370656 1M0121R18
C 73	8.4	42.0	19	17	AZ807609	AZ807609 2M0070M03
C 74	8.4	42.0	20	17	AZ782243	AZ782243 2M0022B21
C 75	8.4	42.0	20	17	TA359F10Q	TA359F10Q T. brucei
C 76	8.4	42.0	21	17	AZ610564	AZ610564 1M0435D23
C 77	8.4	42.0	21	17	TA23D03P	TA23D03P T. brucei
C 78	8.4	42.0	22	17	AZ309687	AZ309687 1M0016B17
C 79	8.4	42.0	22	17	AZ442914	AZ442914 1M0237A24

C 80	8.4	42.0	22	17	A2476175	A2476175	1M0294E14	C 153	8	40.0	25	9	A1143800	A1143800	qc01c03.x
C 81	8.4	42.0	22	17	A2844290	A2844290	2M0143A10	C 154	8	40.0	25	9	A1539240	A1539240	cp64b08.x
C 82	8.4	42.0	23	17	A2474907	A2474907	1M0245118	C 155	8	40.0	25	9	AU254451	AU254451	AU254451
C 83	8.4	42.0	23	17	A2789956	A2789956	2M0038L05	C 156	8	40.0	25	13	BC924523	BC924523	HNC27-1-G
C 84	8.4	42.0	23	17	TA111H02Q	TA111H02Q	AL460694 T. brucei	C 157	8	40.0	25	17	A2368070	A2368070	1M0118A01
C 85	8.4	42.0	23	17	TA144D040	TA144D040	AL466870 T. brucei	C 158	8	40.0	25	17	A2621173	A2621173	2M0016P21
C 86	8.4	42.0	23	17	TA380G080	TA380G080	AL497844 T. brucei	C 159	8	40.0	25	17	A2780039	A2780039	2M0068P24
C 87	8.4	42.0	23	17	TA78E03P	TA78E03P	AL461956 T. brucei	C 160	8	40.0	25	17	A2806433	A2806433	2M0059P13
C 88	8.4	42.0	24	17	AW248929	AW248929	AW248929 2819212.3	C 161	8	40.0	25	17	A2806897	A2806897	2M0107M02
C 89	8.4	42.0	24	17	AZ307682	AZ307682	AZ307682 1M0009P21	C 162	8	40.0	25	17	A2829742	A2829742	2M0107M02
C 90	8.4	42.0	24	17	AZ309981	AZ309981	AZ309981 1M0018H06	C 163	8	40.0	25	17	TA20D01P	TA20D01P	1M0435P20
C 91	8.4	42.0	24	17	AZ476569	AZ476569	AZ476569 1M0295C03	C 164	8	39.0	19	17	A2610584	A2610584	1M0371P12
C 92	8.4	42.0	24	17	AZ585729	AZ585729	AZ585729 1M0391A08	C 165	8	39.0	19	17	A2679992	A2679992	2M0135C23
C 93	8.4	42.0	24	17	AZ819874	AZ819874	AZ819874 2M0091F13	C 166	8	39.0	19	17	AZ839642	AZ839642	1M0036L10
C 94	8.4	42.0	25	9	AL181643	AL181643	AL181643 ub79h08.x	C 167	8	39.0	20	17	A2317789	A2317789	1M0036L10
C 95	8.4	42.0	25	9	AZ312923	AZ312923	AZ312923 1M0029L01	C 168	8	39.0	20	17	A2485309	A2485309	1M0319H15
C 96	8.4	42.0	25	17	AZ818404	AZ818404	AZ818404 2M0088122	C 169	8	39.0	20	17	A2489135	A2489135	2M0044B24
C 97	8.4	42.0	25	17	TA208E01Q	TA208E01Q	AL479320 T. brucei	C 170	8	39.0	20	17	A2615164	A2615164	2M0099P103
C 98	8.4	42.0	25	17	TA266100	TA266100	AL452958 T. brucei	C 171	8	39.0	20	17	A2780925	A2780925	2M0099P103
C 99	8.2	41.0	19	17	AZ441752	AZ441752	AZ441752 1M0234K06	C 172	8	39.0	20	17	A2824749	A2824749	1M0041C24
C 100	8.2	41.0	19	17	AZ509071	AZ509071	AZ509071 1M0351A21	C 173	8	39.0	20	17	TA196G02Q	TA196G02Q	1M0074F05
C 101	8.2	41.0	20	17	AZ390214	AZ390214	AZ390214 1M0151O21	C 174	8	39.0	21	17	A2341842	A2341842	2M0034F05
C 102	8.2	41.0	22	14	D18746	D18746	AZ455534 1M0259L13	C 175	8	39.0	21	17	A2443639	A2443639	2M0027118
C 103	8.2	41.0	22	14	AZ430117	AZ430117	D18746 M0SGS01808	C 176	8	39.0	21	17	A2486694	A2486694	2M0027118
C 104	8.2	41.0	22	17	AZ444633	AZ444633	AZ444633 1M0239122	C 177	8	39.0	21	17	A2784525	A2784525	2M0051O13
C 105	8.2	41.0	22	17	AZ620271	AZ620271	AZ620271 1M0452L22	C 178	8	39.0	21	17	A2786205	A2786205	2M0051O13
C 106	8.2	41.0	22	17	AZ623308	AZ623308	AZ623308 1M0460P21	C 179	8	39.0	21	17	A2786205	A2786205	2M0051O13
C 107	8.2	41.0	22	17	TA184A12P	TA184A12P	AL47431 T. brucei	C 180	8	39.0	22	9	AU254611	AU254611	ny10g07.8
C 108	8.2	41.0	22	9	AU255370	AU255370	AU255370 AU255370	C 181	8	39.0	22	9	AU254611	AU254611	ny10g07.8
C 109	8.2	41.0	23	17	AZ665877	AZ665877	AZ665877 1M0547L01	C 182	8	39.0	22	17	AZ360276	AZ360276	1M0103P23
C 110	8.2	41.0	23	17	AZ781989	AZ781989	AZ781989 2M0021P18	C 183	8	39.0	22	17	AZ476175	AZ476175	1M0294E14
C 111	8.2	41.0	23	17	TA201F03Q	TA201F03Q	AL477466 T. brucei	C 184	8	39.0	22	17	AZ588797	AZ588797	1M0397D21
C 112	8.2	41.0	23	17	TA314B11Q	TA314B11Q	AL489852 T. brucei	C 185	8	39.0	22	17	AZ623402	AZ623402	1M0461001
C 113	8.2	41.0	23	17	TA3164F07P	TA3164F07P	AL494487 T. brucei	C 186	8	39.0	22	17	AZ794867	AZ794867	2M0048015
C 114	8.2	41.0	23	17	AZ812679	AZ812679	AZ812679 2M0079H03	C 187	8	39.0	22	17	TA8C02P	TA8C02P	2M0079H03
C 115	8.2	41.0	24	17	BH848943	BH848943	BH848943 SALK 0690	C 188	8	39.0	22	17	AZ863707	AZ863707	2M0171N19
C 116	8.2	41.0	25	9	AL049424	AL049424	AL049424 ub33f08.x	C 189	8	39.0	23	17	AZ309657	AZ309657	1M0167324
C 117	8.2	41.0	25	17	AQ025409	AQ025409	AQ025409 EP(X)1348	C 190	8	39.0	23	17	AZ345606	AZ345606	1M0080C19
C 118	8.2	41.0	25	17	AQ210966	AQ210966	AQ210966 1M0026K08	C 191	8	39.0	23	17	AZ387861	AZ387861	1M0318N21
C 119	8.2	41.0	25	17	AZ3128535	AZ3128535	AZ3128535 1M0052B21	C 192	8	39.0	23	17	AZ488263	AZ488263	1M0147M21
C 120	8.2	41.0	25	17	AZ818404	AZ818404	AZ818404 2M0088122	C 193	8	39.0	23	17	AZ785466	AZ785466	2M0029C23
C 121	8.2	41.0	25	17	AZ818404	AZ818404	AZ818404 2M0088122	C 194	8	39.0	23	17	AZ806458	AZ806458	2M0068F02
C 122	8.2	41.0	25	17	BH866379	BH866379	BH866379 SALK 1012	C 195	8	39.0	23	17	AZ859707	AZ859707	2M0051D09
C 123	8.2	41.0	25	17	AZ608537	AZ608537	AZ608537 1M0432N14	C 196	8	39.0	23	17	TA129F12P	TA129F12P	2M0068D02
C 124	8.2	41.0	25	17	AZ627654	AZ627654	AZ627654 2M0104O12	C 197	8	39.0	23	17	TA242D06P	TA242D06P	2M0278L04
C 125	8.2	41.0	25	17	AZ588000	AZ588000	AZ588000 1M0356J03	C 198	8	39.0	23	17	TA30F09P	TA30F09P	2M0278L04
C 126	8.2	41.0	25	17	AZ761543	AZ761543	AZ761543 1M0555J03	C 199	8	39.0	23	17	TA30F09P	TA30F09P	2M0278L04
C 127	8.2	41.0	25	17	AZ809111	AZ809111	AZ809111 2M0072P23	C 200	8	39.0	24	14	L32034	L32034	1M0004I20
C 128	8.2	41.0	25	17	AZ951314	AZ951314	AZ951314 2M0215O12	C 201	8	39.0	24	14	L32034	L32034	1M0004I20
C 129	8.2	41.0	25	17	TA30G04Q	TA30G04Q	AL452902 T. brucei	C 202	8	39.0	24	17	AZ304717	AZ304717	1M0073F24
C 130	8.2	41.0	25	17	AU256158	AU256158	AU256158 AU256158	C 203	8	39.0	24	17	AZ341147	AZ341147	1M0466109
C 131	8.2	41.0	25	17	AW248836	AW248836	AW248836 2821108.3	C 204	8	39.0	24	17	AZ626098	AZ626098	1M0466109
C 132	8.2	41.0	25	17	AA907590	AA907590	AA907590 cm29e05.s	C 205	8	39.0	24	17	AZ795736	AZ795736	2M0051D09
C 133	8.2	41.0	25	17	AZ486932	AZ486932	AZ486932 1M0316F14	C 206	8	39.0	24	17	AZ809979	AZ809979	2M0074B13
C 134	8.2	41.0	25	17	AT7233256	AT7233256	AT7233256 fc34g02.x	C 207	8	39.0	24	17	AZ813287	AZ813287	2M0080D02
C 135	8.2	41.0	25	17	TA129B01P	TA129B01P	AZ313245 1M0063K01	C 208	8	39.0	24	17	TA129B01P	TA129B01P	2M0278L04
C 136	8.2	41.0	25	17	TA129B01P	TA129B01P	AL464939 T. brucei	C 209	8	39.0	24	17	TA129B01P	TA129B01P	2M0278L04
C 137	8.2	41.0	25	17	AZ621487	AZ621487	AZ621487 1M0037N21	C 210	8	39.0	24	17	TA129B01P	TA129B01P	2M0278L04
C 138	8.2	41.0	25	17	AZ658085	AZ658085	AZ658085 1M0534U07	C 211	8	39.0	24	17	TA129B01P	TA129B01P	2M0278L04
C 139	8.2	41.0	25	17	AZ800080	AZ800080	AZ800080 2M0057122	C 212	8	39.0	24	17	TA129B01P	TA129B01P	2M0278L04
C 140	8.2	41.0	25	17	AZ826455	AZ826455	AZ826455 2M0102P09	C 213	8	39.0	24	17	TA129B01P	TA129B01P	2M0278L04
C 141	8.2	41.0	25	17	TA114F03Q	TA114F03Q	AL464296 T. brucei	C 214	8	39.0	24	17	TA129B01P	TA129B01P	2M0278L04
C 142	8.2	41.0	25	17	D18741	D18741	D18741 M0SGS01803	C 215	8	39.0	24	17	TA129B01P	TA129B01P	2M0278L04
C 143	8.2	41.0	25	17	AZ617463	AZ617463	AZ617463 1M0448F15	C 216	8	39.0	24	17	TA129B01P	TA129B01P	2M0278L04
C 144	8.2	41.0	25	17	AZ655394	AZ655394	AZ655394 1M0530C05	C 217	8	39.0	24	17	TA129B01P	TA129B01P	2M0278L04
C 145	8.2	41.0	25	17	AZ762011	AZ762011	AZ762011 1M0556P09	C 218	8	39.0	24	17	TA129B01P	TA129B01P	2M0278L04
C 146	8.2	41.0	25	17	AZ805440	AZ805440	AZ805440 2M0065P15	C 219	8	39.0	24	17	TA129B01P	TA129B01P	2M0278L04
C 147	8.2	41.0	25	17	AZ817941	AZ817941	AZ817941 2M0087M05	C 220	8	39.0	24	17	TA129B01P	TA129B01P	2M0278L04
C 148	8.2	41.0	25	17	AZ833716	AZ833716	AZ833716 2M0116D02	C 221	8	39.0	24	17	TA129B01P	TA129B01P	2M0278L04
C 149	8.2	41.0	25	17	TA200H11P	TA200H11P	AL475521 T. brucei	C 222	8	39.0	24	17	TA129B01P	TA129B01P	2M0278L04
C 150	8.2	41.0	25	17	TA200H11P	TA200H11P	AL475521 T. brucei	C 223	8	39.0	24	17	TA129B01P	TA129B01P	2M0278L04
C 151	8.2	41.0	25	17	TA200H11P	TA200H11P	AL475521 T. brucei	C 224	8	39.0	24	17	TA129B01P	TA129B01P	2M0278L04
C 152	8.2	41.0	25	17	TA200H11P	TA200H11P	AL475521 T. brucei	C 225	8	39.0	24	17	TA129B01P	TA129B01P	2M0278L04

226	7.6	38.0	19	17	AZ345359	AZ345159	1M0079D23	299	7.4	37.0	20	17	AZ787173	AZ781173	2M0033006
227	7.6	38.0	19	17	AZ411255	AZ411355	1M0184C18	300	7.4	37.0	21	17	AZ818067	AZ818067	2M0083E20
228	7.6	38.0	19	17	AZ413276	AZ413776	1M0197L07	301	7.4	37.0	20	17	AU060547	AU060547	AU060547
229	7.6	38.0	19	17	AZ785324	AZ785324	2M0029G11	302	7.4	37.0	21	17	AZ344683	AZ344683	1M0046P13
230	7.6	38.0	20	17	AZ316884	AZ316884	1M0035106	303	7.4	37.0	21	17	AZ330777	AZ330777	1M0056P08
231	7.6	38.0	20	17	AZ435809	AZ435809	1M0223L03	304	7.4	37.0	21	17	AZ453588	AZ453588	1M0255M02
232	7.6	38.0	20	17	AZ438858	AZ438858	1M0229T10	305	7.4	37.0	21	17	AZ453806	AZ453806	1M0272G19
233	7.6	38.0	20	17	AZ478502	AZ478502	1M0298B09	306	7.4	37.0	21	17	AZ613931	AZ613931	1M0442P01
234	7.6	38.0	20	17	AZ651194	AZ651194	1M0521E18	307	7.4	37.0	21	17	AZ628010	AZ628010	1M0476K09
235	7.6	38.0	20	17	AZ658035	AZ658035	1M0534P03	308	7.4	37.0	21	17	AZ663326	AZ663326	1M0506C18
236	7.6	38.0	21	9	AU258664	AU258664	AU258664	309	7.4	37.0	21	17	AZ800303	AZ800303	2M0058E14
237	7.6	38.0	21	9	AZ377507	AZ377507	1M0131G21	310	7.4	37.0	21	17	AZ829064	AZ829064	2M0106G01
238	7.6	38.0	21	17	AZ595078	AZ595078	1M0407R03	311	7.4	37.0	21	17	AZ834643	AZ834643	2M0130B15
239	7.6	38.0	21	17	AZ813392	AZ813392	2M0080T08	312	7.4	37.0	21	17	AZ836111	AZ836111	2M0130B15
240	7.6	38.0	21	17	AZ833301	AZ833301	2M0112T10	313	7.4	37.0	22	9	AU938474	AU938474	AU938474
241	7.6	38.0	21	17	TA365F030	TA365F030	T. brucei	314	7.4	37.0	22	9	AU101575	AU101575	AU101575
242	7.6	38.0	22	17	AZ419130	AZ419130	1M0195D03	315	7.4	37.0	22	9	AU1016967	AU1016967	ou27d12.8
243	7.6	38.0	22	17	AZ603366	AZ603366	1M0422L17	316	7.4	37.0	22	9	AU1685766	AU1685766	ou27d12.8
244	7.6	38.0	22	17	AZ822991	AZ822991	2M0096C13	317	7.4	37.0	22	9	AU1708831	AU1708831	ou27d12.8
245	7.6	38.0	22	17	AZ991196	AZ991196	2M0275F13	318	7.4	37.0	22	9	AU1915487	AU1915487	ou27d12.8
246	7.6	38.0	22	17	TA330G090	TA330G090	T. brucei	319	7.4	37.0	22	17	AZ342148	AZ342148	1M0075L01
247	7.6	38.0	23	9	HSW004394	HSW004394	HSW004394	320	7.4	37.0	22	17	AZ376795	AZ376795	1M0130N14
248	7.6	38.0	23	9	AU256581	AU256581	AU256581	321	7.4	37.0	22	17	AZ442121	AZ442121	1M0234M07
249	7.6	38.0	23	9	AU271099	AU271099	AU271099	322	7.4	37.0	22	17	AZ442529	AZ442529	1M0236H10
250	7.6	38.0	23	14	D45826	D45826	HMG503046	323	7.4	37.0	22	17	AZ482536	AZ482536	1M0307D12
251	7.6	38.0	23	17	AZ307616	AZ307616	1M0009H17	324	7.4	37.0	22	17	AZ633539	AZ633539	1M0543A15
252	7.6	38.0	23	17	AZ309458	AZ309458	1M0013F14	325	7.4	37.0	22	17	AZ761211	AZ761211	1M0555I22
253	7.6	38.0	23	17	AZ372664	AZ372664	1M0124E09	326	7.4	37.0	22	17	AZ794203	AZ794203	2M0049I07
254	7.6	38.0	23	17	AZ483352	AZ483352	1M0246M06	327	7.4	37.0	22	17	AZ801266	AZ801266	2M0059I07
255	7.6	38.0	23	17	AZ514463	AZ514463	1M0361A19	328	7.4	37.0	22	17	AZ809838	AZ809838	2M0074G04
256	7.6	38.0	23	17	AZ808551	AZ808551	2M0072G08	329	7.4	37.0	22	17	AZ810608	AZ810608	2M0076D15
257	7.6	38.0	23	17	AZ822271	AZ822271	2M0095C18	330	7.4	37.0	22	17	AZ819824	AZ819824	2M0091K07
258	7.6	38.0	23	17	AZ824868	AZ824868	2M0099C15	331	7.4	37.0	22	17	AZ829430	AZ829430	2M0107A09
259	7.6	38.0	23	17	AZ858813	AZ858813	2M0164H10	332	7.4	37.0	22	17	AZ936470	AZ936470	2M0193J08
260	7.6	38.0	23	17	AZ973344	AZ973344	2M0247H06	333	7.4	37.0	22	17	TA200B03P	TA200B03P	TA200B03P
261	7.6	38.0	23	17	BH811375	BH811375	SALK_0585	334	7.4	37.0	22	17	TA361H12P	TA361H12P	TA361H12P
262	7.6	38.0	23	17	TA270E010	TA270E010	T. brucei	335	7.4	37.0	22	17	TA71G05P	TA71G05P	TA71G05P
263	7.6	38.0	23	17	TA369A110	TA369A110	T. brucei	336	7.4	37.0	22	17	TA80B09P	TA80B09P	TA80B09P
264	7.6	38.0	24	17	AZ441888	AZ441888	1M0234K14	337	7.4	37.0	22	13	BG927951	BG927951	1M0013F14
265	7.6	38.0	24	17	AZ476937	AZ476937	1M0296G12	338	7.4	37.0	23	17	AZ309458	AZ309458	1M0013F14
266	7.6	38.0	24	17	AZ786547	AZ786547	2M0032B10	339	7.4	37.0	23	17	AZ376108	AZ376108	1M0129N14
267	7.6	38.0	24	17	AZ822664	AZ822664	2M0096M07	340	7.4	37.0	23	17	AZ434508	AZ434508	1M0220K22
268	7.6	38.0	25	9	AA881443	AA881443	vx19a01.r	341	7.4	37.0	23	17	AZ458587	AZ458587	1M0331P21
269	7.6	38.0	25	9	A1361952	A1361952	qy37E02.x	342	7.4	37.0	23	17	AZ617124	AZ617124	1M0448B15
270	7.6	38.0	25	9	A1635253	A1635253	tz79G05.x	343	7.4	37.0	23	17	AZ784247	AZ784247	2M0026D20
271	7.6	38.0	25	10	AV740046	AV740046	AV740046	344	7.4	37.0	23	17	AZ785027	AZ785027	2M0026D20
272	7.6	38.0	25	17	AZ802490	AZ802490	2M0061I12	345	7.4	37.0	23	17	AZ788088	AZ788088	2M0034P19
273	7.6	38.0	25	17	AZ809292	AZ809292	2M0073A17	346	7.4	37.0	23	17	AZ796147	AZ796147	2M0053F06
274	7.6	38.0	25	17	AZ827658	AZ827658	2M0104P12	347	7.4	37.0	23	17	AZ797023	AZ797023	2M0053F06
275	7.6	38.0	25	17	AZ979867	AZ979867	2M0256B11	348	7.4	37.0	23	17	AZ800080	AZ800080	2M0057I22
276	7.6	38.0	25	17	BH851330	BH851330	SALK_0728	349	7.4	37.0	23	17	AZ808416	AZ808416	2M0071M22
277	7.6	38.0	25	17	TA48G070	TA48G070	T. brucei	350	7.4	37.0	23	17	AZ863841	AZ863841	2M0173P09
278	7.4	37.0	15	13	BM658732	BM658732	LZV602768	351	7.4	37.0	23	17	TA25D04P	TA25D04P	TA25D04P
279	7.4	37.0	15	14	R41075	R41075	HK082-f Adu	352	7.4	37.0	23	17	TA66H11P	TA66H11P	TA66H11P
280	7.4	37.0	19	9	AT241100	AT241100	qK05d10.x	353	7.4	37.0	24	10	AM064435	AM064435	SP1032 KR
281	7.4	37.0	19	9	A1524591	A1524591	tz43f09.x	354	7.4	37.0	24	17	AZ345465	AZ345465	1M0080N09
282	7.4	37.0	19	14	C00646	C00646	HMG5000819	355	7.4	37.0	24	17	AZ445509	AZ445509	1M0080N09
283	7.4	37.0	19	14	AZ342555	AZ342555	1M0075K11	356	7.4	37.0	24	17	AZ445509	AZ445509	1M0080N09
284	7.4	37.0	19	17	AZ386064	AZ386064	1M0145C04	357	7.4	37.0	24	17	AZ480697	AZ480697	1M0241L17
285	7.4	37.0	19	17	AZ423190	AZ423190	1M0202L11	358	7.4	37.0	24	17	AZ491111	AZ491111	1M0324D03
286	7.4	37.0	19	17	AZ465132	AZ465132	1M0274D24	359	7.4	37.0	24	17	AZ493317	AZ493317	1M0327L24
287	7.4	37.0	19	17	AZ489350	AZ489350	1M0321K14	360	7.4	37.0	24	17	AZ579593	AZ579593	1M0367O09
288	7.4	37.0	19	17	BH000474	BH000474	2M0288B20	361	7.4	37.0	24	17	AZ582169	AZ582169	1M0374F20
289	7.4	37.0	20	17	AZ309121	AZ309121	1M0012G24	362	7.4	37.0	24	17	AZ586687	AZ586687	1M0392K16
290	7.4	37.0	20	17	AZ331630	AZ331630	1M0059N08	363	7.4	37.0	24	17	AZ621109	AZ621109	1M0454D12
291	7.4	37.0	20	17	AZ451921	AZ451921	1M0251C05	364	7.4	37.0	24	17	AZ776570	AZ776570	2M0010L14
292	7.4	37.0	20	17	AZ479222	AZ479222	1M0299A13	365	7.4	37.0	24	17	AZ799324	AZ799324	2M0056B11
293	7.4	37.0	20	17	AZ510137	AZ510137	1M0354O19	366	7.4	37.0	24	17	AZ819888	AZ819888	2M0091H18
294	7.4	37.0	20	17	AZ588658	AZ588658	1M0397F08	367	7.4	37.0	24	17	AZ996858	AZ996858	2M0283L08
295	7.4	37.0	20	17	AZ601843	AZ601843	1M0420M13	368	7.4	37.0	24	17	TA114801P	TA114801P	TA114801P
296	7.4	37.0	20	17	AZ632650	AZ632650	1M0487H23	369	7.4	37.0	24	17	TA144805P	TA144805P	TA144805P
297	7.4	37.0	20	17	AZ759840	AZ759840	1M0553B05	370	7.4	37.0	24	17	TA306812P	TA306812P	TA306812P
298	7.4	37.0	20	17	AZ766476	AZ766476	1M0568D08	371	7.4	37.0	24	17	TA80A11P	TA80A11P	TA80A11P

C 372	7.4	37.0	25	9	A1327424	mq45d06.x	445	7.2	36.0	23	17	A2476931	A2476931	1M0296F09
C 373	7.4	37.0	25	9	A1589311	cf58h04.x	446	7.2	36.0	23	17	A2784247	A2784247	2M0026D20
C 374	7.4	37.0	25	9	A1633471	fh62d09.x	447	7.2	36.0	23	17	A2785027	A2785027	2M0028H03
375	7.4	37.0	25	9	A1971185	wr26b10.x	448	7.2	36.0	23	17	A2785578	A2785578	2M0029M01
376	7.4	37.0	25	10	AW245275	AW245275	449	7.2	36.0	23	17	A2863968	A2863968	2M0173M17
377	7.4	37.0	25	10	AW247153	AW247153	450	7.2	36.0	23	17	A2954682	A2954682	2M0220P23
378	7.4	37.0	25	14	H26073	H26073 y156a12.r1	451	7.2	36.0	23	17	BH7992497	BH7992497	SALK_0646
C 379	7.4	37.0	25	14	A2393511	1M0156B07	452	7.2	36.0	23	17	TA13300P	TA13300P	1M0237G08
C 380	7.4	37.0	25	17	A2427752	1M0209N21	453	7.2	36.0	23	17	TA175H02P	TA175H02P	1M0237G08
C 381	7.4	37.0	25	17	A2442576	1M0236K13	454	7.2	36.0	23	17	TA233E11P	TA233E11P	1M0237G08
382	7.4	37.0	25	17	A2513056	1M0359E05	455	7.2	36.0	23	17	TA268C02P	TA268C02P	1M0237G08
C 383	7.4	37.0	25	17	A2580365	1M0368E02	456	7.2	36.0	23	17	TA354H05O	TA354H05O	1M0237G08
C 384	7.4	37.0	25	17	A2586010	1M0391D12	457	7.2	36.0	23	17	TA353D03Q	TA353D03Q	1M0237G08
C 385	7.4	37.0	25	17	A2606311	1M0428G09	458	7.2	36.0	24	9	AU270898	AU270898	1M0237G08
C 386	7.4	37.0	25	17	A2611849	1M0438M21	459	7.2	36.0	24	14	D45825	D45825	1M0237G08
C 387	7.4	37.0	25	17	A2781720	2M0021G16	460	7.2	36.0	24	17	A2354131	A2354131	1M0093F15
C 388	7.4	37.0	25	17	A2792292	2M0043H11	461	7.2	36.0	24	17	A2443047	A2443047	1M0237G08
C 389	7.4	37.0	25	17	A2798748	2M0055P12	462	7.2	36.0	24	17	A2443113	A2443113	1M0237G08
C 390	7.4	37.0	25	17	A2808849	2M0273B24	463	7.2	36.0	24	17	A2444127	A2444127	1M0237G08
C 391	7.4	37.0	25	17	A2890228	BH812755 SALK_0630	464	7.2	36.0	24	17	A2460288	A2460288	1M0237G08
C 392	7.4	37.0	25	17	BH812755	BH812755 SALK_0685	465	7.2	36.0	24	17	A2467278	A2467278	1M0237G08
C 393	7.4	37.0	25	17	BH848553	BH848553 SALK_1001	466	7.2	36.0	24	17	A2478673	A2478673	1M0237G08
C 394	7.4	37.0	25	17	BH865973	BH865973 T. brucei	467	7.2	36.0	24	17	A2486450	A2486450	1M0237G08
C 395	7.4	37.0	25	17	TA234H10Q	TA234H10Q	468	7.2	36.0	24	17	A2492799	A2492799	1M0237G08
C 396	7.2	36.0	19	12	A1174345	A1174345 an17f09.s	469	7.2	36.0	24	17	A2505251	A2505251	1M0446B03
C 397	7.2	36.0	19	12	BG869649	BG869649 HOA59-1.C	470	7.2	36.0	24	17	A2623508	A2623508	1M0446B03
C 398	7.2	36.0	19	17	A2309531	A2309531 1M0013X06	471	7.2	36.0	24	17	A2755639	A2755639	1M0552D02
C 399	7.2	36.0	19	17	A2775273	A2775273 2M0007F04	472	7.2	36.0	24	17	A2761320	A2761320	1M0555A03
C 400	7.2	36.0	19	17	A2779085	A2779085 2M0015B01	473	7.2	36.0	24	17	A2771365	A2771365	1M0573A02
C 401	7.2	36.0	19	17	A2799057	A2799057 2M0056B20	474	7.2	36.0	24	17	A2807619	A2807619	2M0070001
C 402	7.2	36.0	19	17	A2822385	A2822385 2M0095F09	475	7.2	36.0	24	17	A2817310	A2817310	2M0093C13
C 403	7.2	36.0	19	17	A2822713	A2822713 2M0096M08	476	7.2	36.0	24	17	A2820794	A2820794	2M0093C13
C 404	7.2	36.0	19	17	A2842166	A2842166 2M0103M22	477	7.2	36.0	24	17	TA20811P	TA20811P	1M0237G08
C 405	7.2	36.0	19	17	A2842166	A2842166 2M0103M22	478	7.2	36.0	24	17	TA20811P	TA20811P	1M0237G08
C 406	7.2	36.0	20	17	A2329547	A2329547 1M0053P17	479	7.2	36.0	24	17	TA20811P	TA20811P	1M0237G08
C 407	7.2	36.0	20	17	A2346702	A2346702 1M0082L01	480	7.2	36.0	25	9	AA877944	AA877944	0101B01.s
C 408	7.2	36.0	20	17	A2407675	A2407675 1M0178B04	481	7.2	36.0	25	9	AA877944	AA877944	0101B01.s
C 409	7.2	36.0	20	17	A2433830	A2433830 1M0219T22	482	7.2	36.0	25	9	AA877944	AA877944	0101B01.s
C 410	7.2	36.0	20	17	A2445436	A2445436 1M0241B15	483	7.2	36.0	25	9	AA877944	AA877944	0101B01.s
C 411	7.2	36.0	20	17	A2486007	A2486007 1M0313E17	484	7.2	36.0	25	9	AA877944	AA877944	0101B01.s
C 412	7.2	36.0	20	17	A2581146	A2581146 1M0359G14	485	7.2	36.0	25	9	AA877944	AA877944	0101B01.s
C 413	7.2	36.0	20	17	A2587020	A2587020 1M0394E19	486	7.2	36.0	25	13	BM397641	BM397641	5009-0-35
C 414	7.2	36.0	20	17	A2662848	A2662848 1M0542K07	487	7.2	36.0	25	14	H93534	H93534	yv08912.t1
C 415	7.2	36.0	20	17	A275705	A275705 2M0008P11	488	7.2	36.0	25	17	A2312923	A2312923	1M0029L01
C 416	7.2	36.0	20	17	A2859065	A2859065 2M0164F06	489	7.2	36.0	25	17	A2404619	A2404619	1M0173L20
C 417	7.2	36.0	20	17	TA18A08P	TA18A08P	490	7.2	36.0	25	17	A2606849	A2606849	1M0429A06
C 418	7.2	36.0	20	17	TA207803O	TA207803O	491	7.2	36.0	25	17	A2641910	A2641910	1M0504N09
C 419	7.2	36.0	20	17	TA345E06Q	TA345E06Q	492	7.2	36.0	25	17	A2781719	A2781719	2M0076114
C 420	7.2	36.0	21	17	A2341757	A2341757 1M0074P18	493	7.2	36.0	25	17	A2810630	A2810630	2M0213B07
C 421	7.2	36.0	21	17	A2342282	A2342282 1M0075H14	494	7.2	36.0	25	17	A2893079	A2893079	2M0213B07
C 422	7.2	36.0	21	17	A2345496	A2345496 1M0080F03	495	7.2	36.0	25	17	A2898054	A2898054	2M0213B07
C 423	7.2	36.0	21	17	A2462647	A2462647 1M0269N08	496	7.2	36.0	25	17	A2950699	A2950699	2M0213B07
C 424	7.2	36.0	21	17	A2626965	A2626965 1M0467E15	497	7.2	36.0	25	17	A2993079	A2993079	2M0213B07
C 425	7.2	36.0	21	17	A2663083	A2663083 1M05042H02	498	7.2	36.0	25	17	TA237D08Q	TA237D08Q	1M0429A06
C 426	7.2	36.0	21	17	A2787674	A2787674 2M0034H14	499	7.2	36.0	25	17	TA237D08Q	TA237D08Q	1M0429A06
C 427	7.2	36.0	22	9	A1032023	A1032023 ow68a04.x	500	7.2	36.0	11	13	BM397641	BM397641	5009-0-35
C 428	7.2	36.0	22	13	BG928486	BG928486 HNC48-1-H	501	7.2	36.0	11	13	BM397641	BM397641	5009-0-35
C 429	7.2	36.0	22	14	C21207	C21207 HUMGS000223	502	7.2	36.0	16	13	BM401358	BM401358	2822262.5
C 430	7.2	36.0	22	17	A2314756	A2314756 1M0030C08	503	7.2	36.0	17	10	BM401358	BM401358	2822262.5
C 431	7.2	36.0	22	17	A2341756	A2341756 1M0074P17	504	7.2	36.0	18	10	BM401358	BM401358	2822262.5
C 432	7.2	36.0	22	17	A2396435	A2396435 1M0161C03	505	7.2	36.0	18	12	BM401358	BM401358	2822262.5
C 433	7.2	36.0	22	17	A2446753	A2446753 1M0238C08	506	7.2	36.0	19	9	BM401358	BM401358	2822262.5
C 434	7.2	36.0	22	17	A2488753	A2488753 1M0319M12	507	7.2	36.0	19	9	BM401358	BM401358	2822262.5
C 435	7.2	36.0	22	17	A2598225	A2598225 1M0412K22	508	7.2	36.0	19	10	BM401358	BM401358	2822262.5
C 436	7.2	36.0	22	17	A2727718	A2727718 1M0583O13	509	7.2	36.0	19	10	BM401358	BM401358	2822262.5
C 437	7.2	36.0	22	17	A2864907	A2864907 2M0174E13	510	7.2	36.0	19	10	BM401358	BM401358	2822262.5
C 438	7.2	36.0	22	17	TA119B07P	TA119B07P	511	7.2	36.0	19	10	BM401358	BM401358	2822262.5
C 439	7.2	36.0	22	17	TA197A04Q	TA197A04Q	512	7.2	36.0	19	10	BM401358	BM401358	2822262.5
C 440	7.2	36.0	23	14	D18240	D18240 HUMGS000520	513	7.2	36.0	19	10	BM401358	BM401358	2822262.5
C 441	7.2	36.0	23	14	D19998	D19998 HUMGS000968	514	7.2	36.0	19	10	BM401358	BM401358	2822262.5
C 442	7.2	36.0	23	17	A2307555	A2307555 1M0009M19	515	7.2	36.0	19	10	BM401358	BM401358	2822262.5
C 443	7.2	36.0	23	17	A2387178	A2387178 1M0146K19	516	7.2	36.0	19	10	BM401358	BM401358	2822262.5
C 444	7.2	36.0	23	17	A2393604	A2393604 1M0156C14	517	7.2	36.0	19	10	BM401358	BM401358	2822262.5

518	7	35.0	19	17	A2991531	A2991531	2M0275X15	591	7	35.0	24	17	A2864947	A2864947	2M0174N14
519	7	35.0	20	10	AM246466	AM246466	2821777.3	592	7	35.0	24	17	A2866692	A2866692	2M0177P18
520	7	35.0	20	17	A2307088	A2307088	1M0008M23	593	7	35.0	24	17	BH790798	BH790798	1M0008M23
521	7	35.0	20	17	A2339957	A2339957	1M0071K07	594	7	35.0	24	17	TA161D07P	TA161D07P	1M0071K07
522	7	35.0	20	17	A2445437	A2445437	1M0241B16	595	7	35.0	24	17	TA245F07P	TA245F07P	1M0241B16
523	7	35.0	20	17	A2456534	A2456534	1M0259L03	596	7	35.0	25	9	AA918137	AA918137	QC46502.8
524	7	35.0	20	17	A2478502	A2478502	1M0298B09	597	7	35.0	25	9	AA1127762	AA1127762	QC31D01.X
525	7	35.0	20	17	A2479732	A2479732	1M0300A09	598	7	35.0	25	9	AA181406	AA181406	UC59A04.X
526	7	35.0	20	17	A2479985	A2479985	1M0301C08	599	7	35.0	25	9	AA181643	AA181643	UB79A08.X
527	7	35.0	20	17	A2588882	A2588882	1M0339702	600	7	35.0	25	9	AA199484	AA199484	UC02809.X
528	7	35.0	20	17	A2637794	A2637794	1M0497D02	601	7	35.0	25	13	BM400178	BM400178	5009--0.68
529	7	35.0	20	17	A2654725	A2654725	1M0529003	602	7	35.0	25	14	CO1243	CO1243	HUMG500796
530	7	35.0	20	17	A2660921	A2660921	1M0539E18	603	7	35.0	25	17	A2307549	A2307549	1M0009J24
531	7	35.0	20	17	A2776807	A2776807	2M0010H14	604	7	35.0	25	17	A2324338	A2324338	1M0046D14
532	7	35.0	20	17	A2809111	A2809111	2M0072P23	605	7	35.0	25	17	A2336975	A2336975	1M0067A03
533	7	35.0	20	17	A2827842	A2827842	2M0104F03	606	7	35.0	25	17	A2391004	A2391004	1M05152017
534	7	35.0	20	17	A2991405	A2991405	2M0275004	607	7	35.0	25	17	A2654166	A2654166	1M0528M12
535	7	35.0	21	9	AU112051	AU112051	AA112051	608	7	35.0	25	17	A2785568	A2785568	2M0029K02
536	7	35.0	21	9	AU112155	AU112155	AA112155	609	7	35.0	25	17	A2809149	A2809149	2M0073G05
537	7	35.0	21	17	A2312710	A2312710	1M0028P04	610	7	35.0	25	17	A2816517	A2816517	2M0085N20
538	7	35.0	21	17	A2823340	A2823340	1M0460021	611	7	35.0	25	17	A2989054	A2989054	2M0272H13
539	7	35.0	21	17	A2860221	A2860221	1M0538M09	612	7	35.0	25	17	A2993079	A2993079	2M0277P20
540	7	35.0	21	17	A2795028	A2795028	2M0049L03	613	7	35.0	25	17	A2998093	A2998093	2M0284D21
541	7	35.0	21	17	A2806440	A2806440	2M0068B05	614	7	35.0	25	17	BH759548	BH759548	KG04960--5
542	7	35.0	21	17	TA185E09P	TA185E09P	AL474070 T. Brucei	615	7	35.0	25	17	BH789667	BH789667	SALK_0423
543	7	35.0	22	9	AA928512	AA928512	OM17G11.8	616	7	35.0	25	17	BH855488	BH855488	SALK_0850
544	7	35.0	22	9	AA978189	AA978189	OP33C10.8	617	7	35.0	25	17	TA185D02P	TA185D02P	T. Brucei
545	7	35.0	22	9	AI016967	AI016967	OU27H03.X	618	7	35.0	25	17	AM059513	AM059513	HUTR.Baet
546	7	35.0	22	9	AI080445	AI080445	OX82D10.8	619	7	35.0	25	17	BH754332	BH754332	SAIK_0393
547	7	35.0	22	9	AI1226666	AI1226666	UJ13C01.Y	620	7	35.0	25	17	AI154875	AI154875	UC80E04.X
548	7	35.0	22	13	BG927952	BG927952	HNC45--1-F	621	7	35.0	25	17	AI169566	AI169566	UC60E06.X
549	7	35.0	22	13	BG928008	BG928008	HNC46--1-H	622	7	35.0	25	17	BG900981	BG900981	HOA52--1-D
550	7	35.0	22	13	BG928097	BG928097	HNC46--1-C	623	7	35.0	25	17	BG928060	BG928060	HNC11--1-G
551	7	35.0	22	17	A2346298	A2346298	1M0081B18	624	7	35.0	25	17	AM249856	AM249856	2821566.3
552	7	35.0	22	17	A2407386	A2407386	1M02178K06	625	7	35.0	25	17	AM250449	AM250449	2822458.3
553	7	35.0	22	17	A2482444	A2482444	1M0245M15	626	7	35.0	25	17	AA916934	AA916934	OM14A09..8
554	7	35.0	22	17	A2483833	A2483833	1M0310H03	627	7	35.0	25	17	AA934303	AA934303	SMOVC13CAN
555	7	35.0	22	17	A2582417	A2582417	1M0374H13	628	7	35.0	25	17	AA977115	AA977115	OG24C08..8
556	7	35.0	22	17	A2590903	A2590903	1M0400B15	629	7	35.0	25	17	AI004427	AI004427	OG24C01.8
557	7	35.0	22	17	A2623338	A2623338	1M0460019	630	7	35.0	25	17	AI1120725	AI1120725	UB72D11..X
558	7	35.0	22	17	A2761113	A2761113	1M0555G13	631	7	35.0	25	17	AM063940	AM063940	DP0975 KR
559	7	35.0	22	17	A2812224	A2812224	2M0078G13	632	7	35.0	25	17	A2309987	A2309987	1M0018K04
560	7	35.0	22	17	A2854429	A2854429	2M0157C14	633	7	35.0	25	17	A2339986	A2339986	1M0045P09
561	7	35.0	22	17	TA118E05P	TA118E05P	AL463374 T. Brucei	634	7	35.0	25	17	A2338061	A2338061	1M0069B05
562	7	35.0	22	17	TA118E06P	TA118E06P	AL479258 T. Brucei	635	7	35.0	25	17	A2375581	A2375581	1M0129E05
563	7	35.0	22	17	TA245C11P	TA245C11P	AL483574 T. Brucei	636	7	35.0	25	17	A2439162	A2439162	1M0229I08
564	7	35.0	23	9	AU254983	AU254983	AU254983	637	7	35.0	25	17	A2445942	A2445942	1M0248M23
565	7	35.0	23	9	AU264172	AU264172	AU264172	638	7	35.0	25	17	A2450047	A2450047	1M02448M08
566	7	35.0	23	17	A2341368	A2341368	1M0073L05	639	7	35.0	25	17	A2617087	A2617087	1M0448M12
567	7	35.0	23	17	A2357282	A2357282	1M0098A16	640	7	35.0	25	17	A2635086	A2635086	1M0491P17
568	7	35.0	23	17	A2417030	A2417030	1M0192H05	641	7	35.0	25	17	A2653488	A2653488	1M0529C20
569	7	35.0	23	17	A2418429	A2418429	1M0194F02	642	7	35.0	25	17	A2657651	A2657651	1M0534C03
570	7	35.0	23	17	A2479801	A2479801	1M0300G16	643	7	35.0	25	17	A2663881	A2663881	1M0543D15
571	7	35.0	23	17	A2613963	A2613963	1M0442K06	644	7	35.0	25	17	A2769244	A2769244	1M0569N12
572	7	35.0	23	17	A2634998	A2634998	1M0491B10	645	7	35.0	25	17	A2777644	A2777644	2M0012M24
573	7	35.0	23	17	A2655243	A2655243	1M0530D07	646	7	35.0	25	17	A2784639	A2784639	2M0027B10
574	7	35.0	23	17	A2762970	A2762970	1M0558C14	647	7	35.0	25	17	A2805949	A2805949	2M0067F07
575	7	35.0	23	17	A2768060	A2768060	1M0567P13	648	7	35.0	25	17	A2805995	A2805995	2M0067F13
576	7	35.0	23	17	A2772591	A2772591	1M0583P03	649	7	35.0	25	17	A2818421	A2818421	2M0088M19
577	7	35.0	23	17	A2779607	A2779607	2M0016E18	650	7	35.0	25	17	A2830578	A2830578	2M0109H23
578	7	35.0	23	17	A2807926	A2807926	2M0071C09	651	7	35.0	25	17	A2865832	A2865832	2M0176D09
579	7	35.0	23	17	A2824304	A2824304	2M0098N17	652	7	35.0	25	17	A2865832	A2865832	2M0176D09
580	7	35.0	23	17	BH792865	BH792865	SALK_0651	653	7	35.0	25	9	AL695159	AL695159	AL695159
581	7	35.0	23	17	TA122H08P	TA122H08P	AL462672 T. Brucei	654	7	35.0	25	9	AU254453	AU254453	AU254453
582	7	35.0	24	17	A2316663	A2316663	1M0034G22	655	7	35.0	25	9	AU257355	AU257355	AU257355
583	7	35.0	24	17	A2324350	A2324350	1M0046F14	656	7	35.0	25	14	BQ789787	BQ789787	hag6002AB
584	7	35.0	24	17	A2331594	A2331594	1M0059D12	657	7	35.0	25	17	A2307506	A2307506	1M0009T16
585	7	35.0	24	17	A2351302	A2351302	1M0089T17	658	7	35.0	25	17	A2345926	A2345926	1M0080T23
586	7	35.0	24	17	A2411813	A2411813	1M0185H03	659	7	35.0	25	17	A2366205	A2366205	1M0118L07
587	7	35.0	24	17	A2440877	A2440877	1M0232K11	660	7	35.0	25	17	A2404619	A2404619	1M0172A15
588	7	35.0	24	17	A2505865	A2505865	1M0346C18	661	7	35.0	25	17	A2436106	A2436106	1M0233H07
589	7	35.0	24	17	A2586934	A2586934	1M0394B13	662	7	35.0	25	17	A2448577	A2448577	1M0246A22
590	7	35.0	24	17	A2760063	A2760063	1M0553A04	663	7	35.0	25	17	A2449127	A2449127	1M0247A17

C 664	6.8	34.0	20	17	AZ467382	AZ467332	1M0278C14	737	6.8	34.0	22	17	AZ806598	AZ806598	2M0068G16
C 665	6.8	34.0	20	17	AZ468701	AZ468712	1M0281A18	738	6.8	34.0	22	17	AZ824702	AZ824702	2M0099P20
C 666	6.8	34.0	20	17	AZ469472	AZ469472	1M0283A06	739	6.8	34.0	22	17	AZ829109	AZ829109	2M0106L03
C 667	6.8	34.0	20	17	AZ490187	AZ490187	1M0333E06	740	6.8	34.0	22	17	AZ831937	AZ831937	2M0111P22
C 668	6.8	34.0	20	17	AZ514794	AZ514794	1M0361C13	741	6.8	34.0	22	17	BH852180	BH852180	SALK_0742
C 669	6.8	34.0	20	17	AZ611386	AZ611386	1M0437N08	742	6.8	34.0	22	17	TA175C05P	TA175C05P	AL475137 T. brucei
C 670	6.8	34.0	20	17	AZ622553	AZ622553	1M0459C04	743	6.8	34.0	22	17	TA259C06P	TA259C06P	AL484347 T. brucei
C 671	6.8	34.0	20	17	AZ654458	AZ654458	1M0528G10	744	6.8	34.0	22	17	TA28D010	TA28D010	AL453252 T. brucei
C 672	6.8	34.0	20	17	AZ660043	AZ660043	1M0537E20	745	6.8	34.0	22	17	TA3276010	TA3276010	AL493268 T. brucei
C 673	6.8	34.0	20	17	AZ660124	AZ660124	1M0538F03	746	6.8	34.0	22	17	TA348C120	TA348C120	AL496112 T. brucei
C 674	6.8	34.0	20	17	AZ759844	AZ759844	1M0553C04	747	6.8	34.0	23	17	AZ333226	AZ333226	1M0062P12
C 675	6.8	34.0	20	17	AZ769811	AZ769811	1M0570B23	748	6.8	34.0	23	17	AZ335717	AZ335717	1M0065J20
C 676	6.8	34.0	20	17	AZ785549	AZ785549	2M0029F01	749	6.8	34.0	23	17	AZ398730	AZ398730	1M0164F15
C 677	6.8	34.0	20	17	AZ788116	AZ788116	2M0035E06	750	6.8	34.0	23	17	AZ442542	AZ442542	1M0266P11
C 678	6.8	34.0	20	17	AZ795472	AZ795472	2M0049A14	751	6.8	34.0	23	17	AZ460491	AZ460491	1M0265A21
C 679	6.8	34.0	20	17	AZ795800	AZ795800	2M0051P08	752	6.8	34.0	23	17	AZ468097	AZ468097	1M0279K22
C 680	6.8	34.0	20	17	AZ799305	AZ799305	2M0056N05	753	6.8	34.0	23	17	AZ480535	AZ480535	1M0302E10
C 681	6.8	34.0	20	17	AZ816496	AZ816496	2M0085G16	754	6.8	34.0	23	17	AZ493087	AZ493087	1M0327L24
C 682	6.8	34.0	20	17	AZ828544	AZ828544	2M0105O04	755	6.8	34.0	23	17	AZ495857	AZ495857	1M0331P21
C 683	6.8	34.0	20	17	AZ845673	AZ845673	2M0145N04	756	6.8	34.0	23	17	AZ588253	AZ588253	1M0374B24
C 684	6.8	34.0	20	17	AZ946089	AZ946089	2M0207A13	757	6.8	34.0	23	17	AZ584523	AZ584523	1M0389C10
C 685	6.8	34.0	20	17	TA339D11Q	TA339D11Q	AL492597 T. brucei	758	6.8	34.0	23	17	AZ609822	AZ609822	1M0434J13
C 686	6.8	34.0	21	17	AZ424095	AZ424095	1M0203E03	759	6.8	34.0	23	17	AZ622923	AZ622923	1M0460J05
C 687	6.8	34.0	21	17	AZ4375798	AZ4375798	1M0219C32	760	6.8	34.0	23	17	AZ622923	AZ622923	1M0460J05
C 688	6.8	34.0	21	17	AZ433959	AZ433959	1M0220B12	761	6.8	34.0	23	17	AZ659339	AZ659339	1M0536I07
C 689	6.8	34.0	21	17	AZ452622	AZ452622	1M0259C08	762	6.8	34.0	23	17	AZ666452	AZ666452	1M0548A07
C 690	6.8	34.0	21	17	AZ4712579	AZ4712579	1M0287F21	763	6.8	34.0	23	17	AZ771926	AZ771926	1M0574P20
C 691	6.8	34.0	21	17	AZ482019	AZ482019	1M0306I17	764	6.8	34.0	23	17	AZ775677	AZ775677	2M0008F10
C 692	6.8	34.0	21	17	AZ483617	AZ483617	1M0309A05	765	6.8	34.0	23	17	AZ783377	AZ783377	2M0025I04
C 693	6.8	34.0	21	17	AZ490638	AZ490638	1M0323B13	766	6.8	34.0	23	17	AZ785098	AZ785098	2M0028N07
C 694	6.8	34.0	21	17	AZ521072	AZ521072	1M0454M05	767	6.8	34.0	23	17	AZ785926	AZ785926	2M0030X08
C 695	6.8	34.0	21	17	AZ623540	AZ623540	1M0461G23	768	6.8	34.0	23	17	AZ789371	AZ789371	2M0037L01
C 696	6.8	34.0	21	17	AZ657958	AZ657958	1M0534B02	769	6.8	34.0	23	17	AZ800969	AZ800969	2M0059D17
C 697	6.8	34.0	21	17	AZ665302	AZ665302	1M0546J09	770	6.8	34.0	23	17	AZ807263	AZ807263	2M0070C02
C 698	6.8	34.0	21	17	AZ781467	AZ781467	2M0019F23	771	6.8	34.0	23	17	AZ807926	AZ807926	2M0071C09
C 699	6.8	34.0	21	17	AZ782494	AZ782494	2M0022I23	772	6.8	34.0	23	17	AZ808894	AZ808894	2M0072G09
C 700	6.8	34.0	21	17	AZ796355	AZ796355	2M0052I06	773	6.8	34.0	23	17	AZ834916	AZ834916	2M0117C22
C 701	6.8	34.0	21	17	AZ799765	AZ799765	2M0057I20	774	6.8	34.0	23	17	AZ840208	AZ840208	2M0136H12
C 702	6.8	34.0	21	17	AZ800744	AZ800744	2M0058K24	775	6.8	34.0	23	17	AZ844206	AZ844206	2M0143I11
C 703	6.8	34.0	21	17	AZ806440	AZ806440	2M0068B05	776	6.8	34.0	23	17	AZ844951	AZ844951	2M0144H22
C 704	6.8	34.0	21	17	AZ812038	AZ812038	2M0078C22	777	6.8	34.0	23	17	AZ853913	AZ853913	2M0219D19
C 705	6.8	34.0	21	17	AZ821784	AZ821784	2M0094N09	778	6.8	34.0	23	17	AZ891550	AZ891550	2M0275O18
C 706	6.8	34.0	21	17	AZ933804	AZ933804	2M0279D05	779	6.8	34.0	23	17	BH469744	BH469744	AL473175 T. brucei
C 707	6.8	34.0	22	9	AA885905	AA885905	oj19h02.8	780	6.8	34.0	23	17	TA251E06Q	TA251E06Q	AL482245 T. brucei
C 708	6.8	34.0	22	9	AA931331	AA931331	oo6fc03.8	781	6.8	34.0	23	17	TA26H0H1P	TA26H0H1P	AL485135 T. brucei
C 709	6.8	34.0	22	9	AA99803	AA99803	oo84d04.8	782	6.8	34.0	23	17	TA338E01P	TA338E01P	AL493153 T. brucei
C 710	6.8	34.0	22	9	AI021002	AI021002	ua98e09.x	783	6.8	34.0	23	17	TA88A08P	TA88A08P	AL495996 T. brucei
C 711	6.8	34.0	22	9	AI057600	AI057600	ov31d12.x	784	6.8	34.0	23	17	AL047412	AL047412	DKFZPS86E
C 712	6.8	34.0	22	9	AI174110	AI174110	v287d11.x	785	6.8	34.0	24	9	AL585768	AL585768	AL585768
C 713	6.8	34.0	22	9	AI569444	AI569444	cn86n06.x	786	6.8	34.0	24	9	AU257684	AU257684	AU257684
C 714	6.8	34.0	22	9	AI687266	AI687266	cp94d10.x	787	6.8	34.0	24	13	BM399103	BM399103	5009-0-53
C 715	6.8	34.0	22	9	AU259732	AU259732	AU259732	788	6.8	34.0	24	14	D18741	D18741	MUSGS01803
C 716	6.8	34.0	22	17	AZ310074	AZ310074	1M0018I15	789	6.8	34.0	24	17	AZ308225	AZ308225	1M0011E06
C 717	6.8	34.0	22	17	AZ345644	AZ345644	1M0080J22	790	6.8	34.0	24	17	AZ314798	AZ314798	1M0031G16
C 718	6.8	34.0	22	17	AZ464298	AZ464298	1M0080B18	791	6.8	34.0	24	17	AZ338159	AZ338159	1M0069C11
C 719	6.8	34.0	22	17	AZ407386	AZ407386	1M0178K06	792	6.8	34.0	24	17	AZ374821	AZ374821	1M0127G19
C 720	6.8	34.0	22	17	AZ459715	AZ459715	1M0264E13	793	6.8	34.0	24	17	AZ510127	AZ510127	1M0354L21
C 721	6.8	34.0	22	17	AZ468023	AZ468023	1M0279L15	794	6.8	34.0	24	17	AZ514486	AZ514486	1M0351F23
C 722	6.8	34.0	22	17	AZ468023	AZ468023	1M0279L15	795	6.8	34.0	24	17	AZ514503	AZ514503	1M0361J08
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C 724	6.8	34.0	22	17	AZ482536	AZ482536	1M0307D12	797	6.8	34.0	24	17	AZ579480	AZ579480	1M0367B02
C 725	6.8	34.0	22	17	AZ484950	AZ484950	1M0311K16	798	6.8	34.0	24	17	AZ617422	AZ617422	1M0448M12
C 726	6.8	34.0	22	17	AZ505790	AZ505790	1M0346F07	799	6.8	34.0	24	17	AZ623955	AZ623955	1M0462M12
C 727	6.8	34.0	22	17	AZ579602	AZ579602	1M0367P10	800	6.8	34.0	24	17	AZ655652	AZ655652	1M0530D13
C 728	6.8	34.0	22	17	AZ592068	AZ592068	1M0402H08	801	6.8	34.0	24	17	AZ658406	AZ658406	1M0535N17
C 729	6.8	34.0	22	17	AZ621531	AZ621531	1M0454K17	802	6.8	34.0	24	17	AZ666923	AZ666923	1M0549P24
C 730	6.8	34.0	22	17	AZ652627	AZ652627	1M0525K12	803	6.8	34.0	24	17	AZ791436	AZ791436	2M0041B21
C 731	6.8	34.0	22	17	AZ655943	AZ655943	1M0531M12	804	6.8	34.0	24	17	AZ807619	AZ807619	2M0070001
C 732	6.8	34.0	22	17	AZ658507	AZ658507	1M0535N12	805	6.8	34.0	24	17	AZ811237	AZ811237	2M0077K19
C 733	6.8	34.0	22	17	AZ767724	AZ767724	1M0567H12	806	6.8	34.0	24	17	AZ822069	AZ822069	2M0095D03
C 734	6.8	34.0	22	17	AZ784203	AZ784203	2M0026G16	807	6.8	34.0	24	17	AZ859121	AZ859121	2M0164A07
C 735	6.8	34.0	22	17	AZ785474	AZ785474	2M0029E19	808	6.8	34.0	24	17	BH810305	BH810305	SALK_0488
C 736	6.8	34.0	22	17	AZ803634	AZ803634	2M0064F11	809	6.8	34.0	24	17	BH846871	BH846871	SALK_0108

956	6.6	33.0	24	17	A2467728	A2467778	1M0278K02
C 957	6.6	33.0	24	17	A2488765	A2488765	1M0319P08
C 958	6.6	33.0	24	17	A2507096	A2507096	1M0348M03
C 959	6.6	33.0	24	17	A2587901	A2587901	1M0395F24
C 960	6.6	33.0	24	17	A2593115	A2593115	1M0404A02
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962	6.6	33.0	24	17	A2779026	A2779026	2M0014M18
963	6.6	33.0	24	17	A2781144	A2781144	2M0019R08
964	6.6	33.0	24	17	A2787523	A2787523	2M0034E04
965	6.6	33.0	24	17	A2813332	A2813332	2M0080M04
966	6.6	33.0	24	17	A2852748	A2852748	2M0155G09
967	6.6	33.0	24	17	Ta255C04B	AL842493 T. brucei	
C 968	6.6	33.0	24	17	Ta6A05P	AL84285 T. brucei	
C 969	6.6	33.0	25	9	AA887932	AA887932	n13607.s
C 970	6.6	33.0	25	9	AA908637	AA908637	CG86507.s
C 971	6.6	33.0	25	9	A1307726	A1307726	LB36111.x
C 972	6.6	33.0	25	9	A1469251	A1469251	tm07d09.x
C 973	6.6	33.0	25	9	A1565893	A1565893	tf93g08.x
974	6.6	33.0	25	9	AU254704	AU254704	AU254704
975	6.6	33.0	25	13	BM3995574	BM3995574	5009-0-59
976	6.6	33.0	25	14	H30582	H30582	y124e12. r1
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C 978	6.6	33.0	25	17	A2307438	A2307438	1M0009B03
C 979	6.6	33.0	25	17	A2333359	A2333359	1M0062U19
C 980	6.6	33.0	25	17	A2364143	A2364143	1M0110B16
C 981	6.6	33.0	25	17	A2465944	A2465944	1M0276C14
C 982	6.6	33.0	25	17	A2591143	A2591143	1M0401C16
C 983	6.6	33.0	25	17	A2598351	A2598351	1M0413D12
C 984	6.6	33.0	25	17	A2658622	A2658622	1M0535F04
C 985	6.6	33.0	25	17	A2818624	A2818624	2M0088E16
C 986	6.6	33.0	25	17	A2841072	A2841072	2M0138F23
C 987	6.6	33.0	25	17	Ta126H06P	AL46356 T. brucei	
C 988	6.6	33.0	25	17	Ta131D07P	AL464180 T. brucei	
C 989	6.6	33.0	25	17	Ta350F08O	AL496767 T. brucei	
C 990	6.6	33.0	25	17	Ta98B020	AL496767 T. brucei	
991	6.4	32.0	15	12	BP317507	BP317507	24C6-43
992	6.4	32.0	16	9	A1000182	A1000182	0845E11. b
C 993	6.4	32.0	16	9	A1588511	A1588511	qW40C04. x
C 994	6.4	32.0	16	10	A1685758	A1685758	tu37G09. x
995	6.4	32.0	16	10	AW245338	AW245338	28322905.3
C 996	6.4	32.0	16	10	AW246490	AW246490	2831591.3
C 997	6.4	32.0	16	10	AW2560981	AW2560981	2832267.3
998	6.4	32.0	16	17	AZ044922	AZ044922	GSS7G1076
999	6.4	32.0	17	10	AW246446	AW246446	2821601.3
1000	6.4	32.0	18	13	BG925569	BG925569	HNC5-1-E2

ALIGNMENTS

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Location/Qualifiers
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/organism="Mus musculus"
/db_xref="xaxon:10090"
/clone="BED0008872"
/clone_lib="3'-directed mouse cDNA library"
/tissue_type="brain"
/note="Vector: pGem-T-easy"
BASE COUNT      8 a          3 c          3 t
ORIGIN
Query Match      58.0%; Score 11.6; DB 9; Length 20;
Best Local Similarity .77.8%; Pred. No. 9.1e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0
Oy      2 TTGGCTTGGCCACTCAGA 19
      ||| ||| ||| ||| ||| |||
Db      20 TTCTCTTCGCGAGTCAGA 3
RESULT 2
LOCUS      A1189662      25 bp      mRNA      linear      EST 28-OCT-1996
DEFINITION      gd418h06.x1 Soares placenta Bco9weeks 2NBHP8ct09W Homo sapiens cDNA
clone IMAGE:1724123 3' similar to TR:Q14211 Q14211 E4BP4 GENE. [1]
; mRNA sequence.
ACCESSION      A1189662
VERSION      A1189662.1 GI:3740871
KEYWORDS
SOURCE      EST.
ORGANISM      human.
Homosapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 25)
AUTHORS      NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP) ,
Tumor Gene Index
Unpublished (1997)
JOURNAL
COMMENT      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LNLN; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 812 Std Error: 0.00

```

[illegible]

Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5581
Fax: 81-743-72-5589
E-mail: kkatco@bs.nist-nara.ac.jp

BASE COUNT	2	a	4	c	5	g	14	t
ORIGIN								
Query Match			56.0%;	Score 11.2;	DB 9;		Length 25;	
Best Local Similarity			81.2%;	Pred. No. 1.5e+05;				
Matches 13;			Conservative	0;	Mismatches	3;	Indels	0;
Gaps								0;
3			TGC		GTTC		CCATC	
AG			18					

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Db      1  |||||
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RESULT 3
LOCUS   AU257541
DEFINITION AU257541 3'-directed mouse cDNA library Mus musculus cDNA clone
ACCESSION BED0010829 3', mRNA sequence.
VERSION   AU257541
KEYWORDS  AU257541.1 GI:20322263
SOURCE    EST.
          house mouse.
ORGANISM  Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS   Kato K. and Matoba R.
TITLE     Generation of expressed sequence tags from mouse brain.
JOURNAL   Unpublished (2002)
COMMENT   Contact: Kikuya Kato
          Graduate School of Biological Sciences
          Nara Institute of Science and Technology
          8916-5 Takayama, Ikoma, Nara 630-0101, Japan
          Tel: 81-743-72-5581
          Fax: 81-743-72-5589
          Email: kkatob@is.tnara.ac.jp,
          URL: http://love2.aist-nara.ac.jp/BED/index.html.

FEATURES
SOURCE    1..24
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          /note="Vector: pGEM-T-easy"

BASE COUNT      6 a      3 c      6 g      9 t

ORIGIN
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Best Local Similarity 73.7%; Pred. No. 1.9e+05;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy      1  |||||
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          |||||
          6 TGTGTGTTGACAGTCAAA 24

RESULT 4
LOCUS   D18747
DEFINITION MUGS01809 Mouse 3'-directed Mus musculus domesticus cDNA clone
ACCESSION m0270 3', mRNA sequence.
VERSION   D18747
KEYWORDS  D18747.1 GI:1100716
SOURCE    EST.
          western European house mouse.
ORGANISM  Mus musculus domesticus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS   Kawamoto S., Okubo K., Yoshii J., Katsuki M. and Matsubara K.
TITLE     Analysis of gene expression in mouse embryogenesis by 3'-directed
          cDNA sequencing
JOURNAL   Unpublished (1995)
COMMENT   Contact: Kawamoto S., Okubo K., Yoshii J., Katsuki M. and Matsubara
          K.
          Institute for Cellular and Molecular Biology
          Osaka University
          3-1 Yamada-oka, Suita, Osaka 565, Japan.
          Location/Qualifiers
          1..20
          /organism="Mus musculus domesticus"

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BASE COUNT      9 a      3 c      4 g      4 t

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Query Match      54.0%; Score 10.8; DB 14; Length 20;
Best Local Similarity 85.7%; Pred. No. 2.3e+05;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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          |||||
          20 TTTGCTTTGACAC 7

RESULT 5
LOCUS   A2779522/c
DEFINITION 2M0016K03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION 2M0016K03F
VERSION   A2779522
KEYWORDS  A2779522.1 GI:12910259
SOURCE    GSS.
          house mouse.
ORGANISM  Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS   Dunn D., Aoyagi A., Barber M., Beacorn T., Duval B., Hamli C.,
          Islam H., Longacre S., Mahmoud M., Meenen E., Pedersen T., Rellly
          M., Rose M., Rose R., Stokes R., Tinsley A., von Niederhausern A.
          and Wright D., Weiss R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts
JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
          University of Utah
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177
          Email: ddu@genetics.utah.edu
          Insert Length: 10000 Std Error: 0.00
          Plate: 0016 row: K column: 03
          Seq primer: CGTGTAAACGACGCCACGT
          Class: plasmid ends
          High quality sequence stop: 22.
          Location/Qualifiers
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          /clone_1lb="Mouse 10kb plasmid UUGC1M library"
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          /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
          /note="Vector: pMD42nv; Purified genomic DNA from M.
          musculus C57BL/6J (male) was obtained from the Jackson
          Laboratory Mouse DNA Resource
          (http://www.jax.org/resources/documents/dnares/). The DNA
          was hydrodynamically sheared by repeated passage through a
          0.005 inch orifice at constant velocity. The sheared DNA
          was blunt end-repaired with T4 DNA polymerase and T4
          polynucleotide kinase. Adaptor oligonucleotides were
          ligated to the blunt ends in high molar excess. The
          10.5 kb range using preparative agarose gel
          electrophoresis. Vector DNA was prepared from a derivative
          of pMD42 (GI14732114|gb|AF129072.1), a copy-number
          inducible derivative of plasmid R1. The vector was ligated

```

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 10 a 6 c 3 g 3 t

BASE COUNT 4 a 2 c 6 g 7 t

Query Match 53.0%; Score 10.6; DB 17; Length 22;
Best Local Similarity 76.5%; Pred. No. 3e+05;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Best Local Similarity 72.2%; Pred. No. 5.6e+05;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 TTTCGCTTGCACCTCA 17
19 TTTCGCTTGCACCTCA 3

Oy 3 TTTCGCTTGCACCTCAG 20
2 TTTCGCTTGCACCTCAG 19

RESULT 6
A2625339 19 bp DNA linear GSS 13-DEC-2000
LOCUS 100464F13R Mouse 10kb plasmid UGCM library Mus musculus genomic
DEFINITION clone UGCM0464F13 R, DNA sequence.

RESULT 7
AU254819 21 bp mRNA linear EST 25-APR-2002
LOCUS AU254819 3'-directed mouse cDNA library Mus musculus cDNA clone
DEFINITION BED0003462 3', mRNA sequence.

ACCESSION A2625339 GI:11747529
VERSION A2625339
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

ACCESSION AU254819 GI:20316963
VERSION AU254819
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Kelly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A., and Wright, D., Weis, R.

REFERENCE Kato, K. and Matoba, R.
1 (bases 1 to 21)
Generation of expressed sequence tags from mouse brain
Unpublished (2002)
Contact: Rikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5581
Fax: 81-743-72-5589
Email: kkatobds.aist-nara.ac.jp, BED/index.html.
URL: http://love2.aist-nara.ac.jp/BED/index.html.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0464 row: F column: 13
Seq primer: CACACGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

TITLE Kikuya Kato
JOURNAL Unpublished (2002)
COMMENT Contact: Rikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5581
Fax: 81-743-72-5589
Email: kkatobds.aist-nara.ac.jp, BED/index.html.
URL: http://love2.aist-nara.ac.jp/BED/index.html.

FEATURES
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/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g14732114[g14732072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated

FEATURES
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/organism="Mus musculus"
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/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g14732114[g14732072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated

BASE COUNT 12 a 3 c 3 g 2 t 1 others

BASE COUNT 12 a 3 c 3 g 2 t 1 others

Query Match 50.0%; Score 10; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 50.0%; Score 10; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTTCGCTTGCACCTCA 17
13 TTTCGCTTGCACCTCA 4

Oy 1 TTTCGCTTGCACCTCAG 20
13 TTTCGCTTGCACCTCAG 19

RESULT 8
A2785704 21 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0029C21R Mouse 10kb plasmid UGCM library Mus musculus genomic
DEFINITION clone UGCM0029C21 R, DNA sequence.

RESULT 8
A2785704 21 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0029C21R Mouse 10kb plasmid UGCM library Mus musculus genomic
DEFINITION clone UGCM0029C21 R, DNA sequence.

ACCESSION A2785704 GI:12922730
VERSION A2785704
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

ACCESSION A2785704 GI:12922730
VERSION A2785704
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 21)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weis
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0029 row: C column: 21
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers
 1..21
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGC2W029C21"
 /clone_id="Mouse 10kb plasmid UGC1M library"
 /sex="Male"
 /lab_host="B. Coli strain XL10-Gold, TI-resistant, F-"
 /note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
 4 a 4 c 7 g 6 t
 ORIGIN
 Query Match 50.0%; Score 10; DB 17; Length 21;
 Best Local Similarity 72.2%; Pred. No. 5.8e+05;
 Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 3 TGGCTTGCCTCAGAG 20
 |||||
 1 TGGGTTTACACACGAG 18
 RESULT 9
 BH813511 24 bp DNA linear GSS 02-MAY-2002
 LOCUS BH813511
 DEFINITION SALK 064374 Arabidopsis thaliana TDNA insertion lines Arabidopsis
 accession BH813511 GI:20392116
 VERSION BH813511.1 GI:20392116
 KEYWORDS GSS.
 SOURCE chae cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

REFERENCE 1 (bases 1 to 24)
 AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadriind,C., Jeske,A., Kanes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J., and Ecker,J.R.
 TITLE A Sequence-indexed library of insertion Mutations in the Arabidopsis Genome
 JOURNAL Unpublished (2001)
 COMMENT Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated intron of At1g60590.
 Class: TDNA tagged.
 Location/Qualifiers
 1..24
 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_064374"
 /clone_id="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html.

BASE COUNT
 7 a 4 c 3 g 10 t
 ORIGIN
 Query Match 50.0%; Score 10; DB 17; Length 24;
 Best Local Similarity 72.2%; Pred. No. 6e+05;
 Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 3 TGGCTTGCCTCAGAG 20
 |||||
 3 TGGTTTACACACTG 20
 RESULT 10
 A2762000 24 bp DNA linear GSS 16-FEB-2001
 LOCUS A2762000
 DEFINITION IM0556F08R Mouse 10kb plasmid UGC1M library Mus musculus genomic
 clone UGC1M0556F08 R. DNA sequence.
 accession A2762000
 version A2762000.1 GI:12871547
 keywords GSS.
 source house mouse.
 organism Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 24)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weis
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0556 row: F column: 08

Seq primer: CACACAGGAAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 24.
 Location/Qualifiers

FEATURES

1..24
 source

/organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0556F08"
 /clone_1ib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: FMD2mV. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (G1473214|GB|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

7 a 7 c 5 g 5 t

Query Match 49.0%; Score 9.8; DB 17; Length 24;
 Best Local Similarity 84.6%; Pred. No. 7.6e+05;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 TTGGCACTCACA 19
 |||||
 DB 9 TCTGCCACACAGA 21

RESULT 11

TA259G080/c 24 bp DNA linear GSS 13-DEC-2000

LOCUS T. brucei sheared genomic DNA clone 259g08, reverse sequence,
 DEFINITION genomic survey sequence.
 ACCESSION AL488403
 VERSION AL488403.1 GI:11863797
 KEYWORDS GSS

SOURCE Trypanosoma brucei.
 ORGANISM Trypanosoma brucei
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.

REFERENCE 1 (bases 1 to 24)
 Hall N., Bowman S., Lennard N.J., Doggett J., Atkin R.,
 Chillingworth C., Ormond D., Harris B., El-Sayed N., Hou L.,
 Melville S.E., Rajandream M.A. and Barrett B.G.

TITLE Direct SubMISSION
 JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrett@anger.ac.uk and
 nhlsanger.ac.uk

COMMENT

Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vardan and B.
 Barrett, Oxford University Press, 1999).

Email: neilsayed@igr.org
 Details of T. brucei sequencing at the Sanger Centre are available
 at <http://www.sanger.ac.uk/projects/T-brucei/>.
 Location/Qualifiers

FEATURES

1..24
 source

/organism="Trypanosoma brucei"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="259g08"

BASE COUNT

9 a 5 c 7 g 3 t

Query Match 49.0%; Score 9.8; DB 17; Length 24;
 Best Local Similarity 84.6%; Pred. No. 7.6e+05;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGGCTTTCAC 14
 |||||
 DB 19 TTGGCTTTCAC 7

RESULT 12

AA916047/c 22 bp mRNA linear EST 29-APR-1998

LOCUS OG30401.s1 NCI CGAP Br7 Homo sapiens CDNA clone IMAGE:1441345 3'
 DEFINITION similar to SW:RL34_HUMAN P49207 60S RIBOSOMAL PROTEIN L34. ;, mRNA
 sequence.

ACCESSION AA916047
 VERSION AA916047.1 GI:3055439
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 22)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strauberg, Ph.D.
 Email: ggapbs-remail.nih.gov
 unknown library type
 Insert Length: 502
 Insert Length: 502
 Std Error: 0.00
 Seg primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES

1..22
 source

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1441345"
 /clone_1ib="NCI CGAP Br7"
 /lab_host="DH10B"
 /note="Organ: breast; Vector: pCMV-SPORT4; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.2 kb. Life technologies catalog
 #:10985-018"

BASE COUNT

5 a 5 c 7 g 5 t

Query Match 48.0%; Score 9.6; DB 9; Length 22;
 Best Local Similarity 75.0%; Pred. No. 9.3e+05;
 Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

COMMENT

4 GCGTTGGCACTCACA 19
 |||||
 DB 17 GCGTTGGCACTCACA 2

RESULT 13

A2592068 22 bp DNA linear GSS 13-DEC-2000

LOCUS IM0402H08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0402H08 R, DNA sequence.

ACCESSION A2592068
 VERSION A2592068.1 GI:11714258
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 22)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weis
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddu@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0402 row: H column: 08
 Seq primer: CACACAGCAACACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 22.
 Location/Qualifiers
 1..22
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCGCM0402H08"
 /clone_1lb="Mouse 10kb plasmid UUCGCM library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 6 a 6 c 3 g 7 t
 ORIGIN
 Query Match 48.0%; Score 9.6; DB 17; Length 22;
 Best Local Similarity 75.0%; Pred. No. 9.3e+05;
 Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 2 TTGGCTTGGCACTCA 17
 ||| ||||| ||
 Db 6 TTGATTTGCCAACA 21
 ||| ||||| ||
 RESULT 14
 A2771198 22 bp DNA linear GSS 16-FEB-2001
 LOCUS TA223E07P/c
 DEFINITION 1M0573M08F Mouse 10kb plasmid library Mus musculus genomic clone UUCGCM0573M08 F, DNA sequence.

ACCESSION A2771198
 VERSION A2771198.1 GI:12893200
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 22)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weis
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddu@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0573 row: M column: 08
 Seq primer: CGTTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 22.
 Location/Qualifiers
 1..22
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCGCM0573M08"
 /clone_1lb="Mouse 10kb plasmid UUCGCM library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 1 a 9 c 2 g 10 t
 ORIGIN
 Query Match 48.0%; Score 9.6; DB 17; Length 22;
 Best Local Similarity 75.0%; Pred. No. 9.3e+05;
 Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 TTGGCTTGGCACTC 16
 ||| ||||| ||
 Db 6 TTTCGTTTCTCTCAC 21
 ||| ||||| ||
 RESULT 15
 TA223E07P 22 bp DNA linear GSS 13-DEC-2000
 LOCUS TA223E07P/c
 DEFINITION T. brucei sheared genomic DNA clone 223e07, forward sequence, genomic survey sequence.

ACCESSION AL480269
 VERSION AL480269.1 GI:11846049
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei.
 ORGANISM Trypanosoma brucei
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.

REFERENCE
 AUTHORS 1 (bases 1 to 22)
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.
 Direct Submission
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA. E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk
 Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrell, Oxford University Press, 1999).
 Email: nh@sanger.ac.uk
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.
 Location/Qualifiers

FEATURES
 source
 1..22
 /organism="Trypanosoma brucei"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="223e07"

BASE COUNT
 ORIGIN 9 a 1 c 12 g 0 t

Query Match 48.0%; Score 9.6; DB 17; Length 22;
 Best Local Similarity 75.0%; Pred. No. 9.3e+05;
 Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 TTTCGTTGGCACTC 16
 |||||
 16 TTTCCTTTTCCTC 1

RESULT 16
 TA202H10/c
 LOCUS 23 bp DNA linear GSS 13-DEC-2000
 DEFINITION T. brucei sheared genomic DNA clone 202h11, reverse sequence,
 genomic survey sequence.
 ACCESSION AL477083
 VERSION AL477083.1 GI:11843538
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei.
 ORGANISM Trypanosoma brucei
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.

REFERENCE
 AUTHORS 1 (bases 1 to 23).
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.
 Direct Submission
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA. E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk
 Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small

Insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrell, Oxford University Press, 1999).
 Email: nh@sanger.ac.uk
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.
 Location/Qualifiers

FEATURES
 source
 1..23
 /organism="Trypanosoma brucei"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="202h11"

BASE COUNT
 ORIGIN 9 a 8 c 4 g 2 t

Query Match 48.0%; Score 9.6; DB 17; Length 23;
 Best Local Similarity 75.0%; Pred. No. 9.4e+05;
 Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 TTTCGTTGGCACTC 16
 |||||
 21 TTTCGATGCCATTC 6

RESULT 17
 BH864166
 LOCUS 25 bp DNA linear GSS 05-AUG-2002
 DEFINITION SALK_095483 Arabidopsis thaliana TDNA insertion lines Arabidopsis
 thaliana genomic clone SALK_095483, DNA sequence.
 ACCESSION BH864166
 VERSION BH864166.1 GI:22100064
 KEYWORDS GSS.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 25)
 Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadtrian,
 C., Jeske, A., Kames, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P.,
 Zimmerman, J., and Ecker, J.R.
 A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 Unpublished (2001)
 Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 556 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA.
 Class: TDNA tagged.
 Location/Qualifiers

FEATURES
 source
 1..25
 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_095483"
 /note="Arabidopsis thaliana TDNA insertion lines"
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html

BASE COUNT
 ORIGIN 6 a 3 c 3 g 13 t

Query Match 48.0%; Score 9.6; DB 17; Length 25;
 Best Local Similarity 75.0%; Pred. No. 9.7e+05;
 Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

ay	1	TTTGGCGTTGCCACTC	16
Db	5	TTTCCGTTGAATTC	20

RESULT 18	
LOCUS	BH864216
DEFINITION	BH864216 25 bp DNA linear GSS 05-AUG-2002 SALK_095576 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_095576, DNA sequence.

REFERENCE	1 (bases 1 to 25)
AUTHORS	Alonso, J. M., Lejse, T. J., Barajas, P., Chen, H., Cheuk, R., Gadtnab

FEATURES	Location/Qualifiers
SOURCE	1. .25

BASE COUNT	ORIGIN
6 a	3 c
3 g	13 c

	Query Match	48.0%	Score 9.6	DB 17	length 25
	Best Local Similarity	75.0%	Pred. No. 9.7e+05		
	Matches	12	Conservative	0	Mismatches 4
					Indels 0
					Gaps 0
QY	1 TTTGGGTTTGGCACTC	16			
Db	5 TTTCCGTTTGAATTC	20			

RESULT 19	
AZ589990/c	
LOCUS	20 bp DNA linear GSS 13-DEC-2000
DEFINITION	100399016 mouse 10kb plasmid U06C1M library Mus musculus genomic clone U06C1M039901 P, DNA sequence.
ACCESSION	AZ589990
VERSION	AZ589990.1
KEYWORDS	GI:11712180
SOURCE	GSS.
ORGANISM	house mouse. Mus musculus.
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE AUTHORS	1 (bases 1 to 20)
Dunn, D., Aoyagi, A.	

FEATURES	Location/Qualifiers
source	1. .20

BASE COUNT	3 a	5 c	7 g	5 e
------------	-----	-----	-----	-----

Query Match	97.0%;	Score 9.4;	DB 17;	Length 20;
Best Local Similarity	40.3%;	Pred. No. 1, 1e+06;		
Matches 10; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;
OY	10	GCACACTCAGAG	20	
db	14	GCACACTCAGAG	4	

RESULT	20
AZ812038/c	
LOCUS	
DEFINITION	21 bp DNA linear GSS 20-FEB-2001
ACCESSION	AZ812038
VERSION	ZK007802ZF Mouse 10kb plasmid UUCGIM library Mus musculus genomic
KEYWORDS	clone UUCG2M007802 F, DNA sequence.
SOURCE	AZ812038
ORGANISM	AZ812038.1 GI:12980869
	GSS.
	house mouse.
	Mus musculus.
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A., and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0078 row: 0 column: 22
 Seq primer: CGTTGTAAAACGACGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers
 1..21
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCGM0078022"
 /clone_lib="Mouse 10kb plasmid UUCGM library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 3 a 7 c 6 g 5 t
 ORIGIN
 Query Match 47.0%; Score 9.4; DB 17; Length 21;
 Best Local Similarity 90.9%; Pred. No. 1.2e+06;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 10 GCCACTCAGAG 20
 Db 14 GCCACTCAGAG 4

RESULT 21
 AZ662093/c 22 bp DNA linear GSS 14-DEC-2000
 LOCUS IM0541C05P Mouse 10kb plasmid UUCGM library Mus musculus genomic
 DEFINITION clone UUCGM0541C05 F, DNA sequence.
 ACCESSION AZ662093
 VERSION AZ662093.1 GI:11799239
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A., and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0541 row: C column: 05
 Seq primer: CGTTGTAAAACGACGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 22.
 Location/Qualifiers
 1..22
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCGM0541C05"
 /clone_lib="Mouse 10kb plasmid UUCGM library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 1 a 6 c 7 g 8 t
 ORIGIN
 Query Match 47.0%; Score 9.4; DB 17; Length 22;
 Best Local Similarity 90.9%; Pred. No. 1.2e+06;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 10 GCCACTCAGAG 20
 Db 22 GCCACTCAGAG 12

RESULT 22
 AZ612609 24 bp DNA linear GSS 13-DEC-2000
 LOCUS AZ612609
 DEFINITION IM0439P23P Mouse 10kb plasmid UUCGM library Mus musculus genomic
 clone UUCGM0439P23 F, DNA sequence.
 ACCESSION AZ612609
 VERSION AZ612609.1 GI:11734715
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 24)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamll,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A. and Wright,D., Weis,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0439 row: P column: 23
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 24.

FEATURES
source
1. 24
/organism="Mus musculus"
/strain="C57BL/6j"
/db_xref="taxon:10090"
/clone="U06C1M0439P23"
/clone_11b="Mouse 10kb plasmid U06C1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnars/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 [gi:4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 3 a 7 c 8 g 6 t

ORIGIN

Query Match 47.0%; Score 9.4; DB 17; Length 24;
Best Local Similarity 90.9%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 GCCACTCAGAG 20
|||||
3 GCCACTCTGAG 13

Db

RESULT 23
TA186D08P 24 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 186d08, forward sequence.
DEFINITION
ACCESSION AL475706
VERSION AL475706.1 GI:11841017
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.

REFERENCE 1 (bases 1 to 24)

AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harrie,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.

TITLE Direct Submision

JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Cambridge CB10 1SA. E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaubin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source
1. 24
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="186d08"

BASE COUNT 9 a 7 c 3 g 5 t

ORIGIN

Query Match 47.0%; Score 9.4; DB 17; Length 24;
Best Local Similarity 68.4%; Pred. No. 1.2e+06;
Matches 13; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 TTGGCTTGGCCACTCAGAG 20
|||||
6 TTGGCAAAACATCATAG 24

Db

RESULT 24
A2405188 21 bp DNA linear GSS 03-OCT-2000
LOCUS IM017G15R Mouse 10kb plasmid U06C1M library Mus musculus genomic clone U06C1M017G15 R, DNA sequence.
DEFINITION
ACCESSION A2405188
VERSION A2405188.1 GI:10529201
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamll,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A. and Wright,D., Weis,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0173 row: G column: 15
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
Location/Qualifiers

source	1. 21	/organism="Mus musculus"	
		/strain="C57BL/6J"	
		/db_xref="taxon:10090"	
		/clone="U06C1M0173G15"	
		/clone_idb="Mouse 10kb plasmid U06C1M library"	
		/sex="Male"	
		/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"	
		/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource	
		(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114[gB]AF12907.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."	
BASE COUNT	3 a 9 c 3 g 6 t		
ORIGIN			
Query Match	46.0%; Score 9.2; DB 17; Length 21;		
Best Local Similarity	78.6%; Pred. No. 1.5e+06;		
Matches	11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		
Qy	6 GTTGCACACTGAGA 19		
Dp	8 GTTCCCTCCCTCAA 21		
RESULT 25			
A2427688/c			
LOCUS			
DEFINITION	A2427688 21 bp DNA linear GSS 03-OCT-2000		
ACCESSION	U06209J15 Mouse 10kb plasmid U06C1M library Mus musculus genomic		
VERSION	A2427688		
KEYWORDS	A2427688.1 GI:10551701		
SOURCE	GSS.		
ORGANISM	house mouse.		
REFERENCE	Mus musculus.		
AUTHORS	Euhalyota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)		
TITLE	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A., and Wright, D., Weiss, R.		
JOURNAL	Mouse whole genome scaffolding with paired end reads from 10kb		
COMMENT	plasmid inserts		
	Unpublished (2000)		
	Contact: Robert B. Weiss		
	University of Utah Genome Center		
	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT		
	84112, USA		
	Tel: 801 585 5606		
	Fax: 801 585 7177		
	Email: ddunn@genetics.utah.edu		
	Insert Length: 10000 Std Error: 0.00		
	Plate: 0209 row: J column: 15		
	Seq primer: CACACAGAAACAGCTAGAC		
	Class: plasmid ends		
	High quality sequence stop: 21.		
	Location/Qualifiers		

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SOURCE
1. .21
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/collection="UGGCM0209J5"
/collection_1ib="Mouse 10kb plasmid UGGCM library"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, Ti-resistant, F-"/
note="Vector: PMD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repeated with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g[472214]gb/APR12972.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```


source 1. .21

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUCGM0211D23"

/clone.lib="Mouse 10kb plasmid UUCGM library"

/sex="Female"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 5 a 5 c 3 g 8 t

ORIGIN

Query Match 46.0%; Score 9.2; DB 17; Length 21;
Best Local Similarity 78.6%; Pred. No. 1.5e+06;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 GTTTCCTGCTCAGA 19
|||||
4 GTTTCCTGCTCATA 17

Db

RESULT 27

AZ583690 22 bp DNA linear GSS 13-DEC-2000

LOCUS 1M0378E1R Mouse 10kb plasmid UUCGM library Mus musculus genomic

DEFINITION clone UUCGM0378E16 R, DNA sequence.

ACCESSION AZ583690

VERSION AZ583690.1 GI:11703825

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)

REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A. and Wright,D.,Weiss,R.

AUTHORS

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0378 row: B column: 16
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

source 1. .22

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUCGM0378E16"

/clone.lib="Mouse 10kb plasmid UUCGM library"

/sex="Male"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 10 a 2 c 7 g 3 t

ORIGIN

Query Match 46.0%; Score 9.2; DB 17; Length 22;
Best Local Similarity 78.6%; Pred. No. 1.5e+06;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTCCTTGCCTC 14
|||||
22 TTTCCTTGCCTC 9

Db

RESULT 28

AZ634674 23 bp DNA linear GSS 13-DEC-2000

LOCUS 1M040A11R Mouse 10kb plasmid UUCGM library Mus musculus genomic

DEFINITION clone UUCGM040A11 R, DNA sequence.

ACCESSION AZ634674

VERSION AZ634674.1 GI:11756864

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23)

REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A. and Wright,D.,Weiss,R.

AUTHORS

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0490 row: A column: 11
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers

source
1. .23
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0490A11"
/clone_1lb="Mouse 10kb plasmid UUCG1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
2 a 7 c 3 g 11 t
ORIGIN

Query Match
Best Local Similarity 46.0%; Score 9.2; DB 17; Length 23;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTCGCTTGGCCAC 14
DB 9 TTTCGCTTGGCTC 22

RESULT 29
A2646716 23 bp DNA linear GSS 14-DEC-2000
DEFINITION 1M0512D23R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG1M0512D23 R, DNA sequence.
ACCESSION A2646716
VERSION A2646716.1 GI:11777462
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiser,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0512 row: D column: 23
Seq primer: CACACAGGAACGCTATACG
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers

FEATURES

source
1. .23
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0512D23"
/clone_1lb="Mouse 10kb plasmid UUCG1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
6 a 4 c 4 g 7 t
ORIGIN

Query Match
Best Local Similarity 46.0%; Score 9.2; DB 17; Length 23;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 TTTCGCTTGGCCAG 20
DB 3 TTTCGCTTGGCCAG 16

RESULT 30
A2418103 24 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0194L03F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG1M0194L03 F, DNA sequence.
ACCESSION A2418103
VERSION A2418103.1 GI:10542116
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiser,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0194 row: L column: 03
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers

FEATURES

Source

1.. 24
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCGCM0194L03"
/clone_1lb="Mouse 10kb plasmid UUCGCM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 [g1|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapored mouse DNA was annealed to
adapored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 10 a 4 c 4 g 6 t

ORIGIN

Query Match 46.0%; Score 9.2; DB 17; Length 24;
Best Local Similarity 78.6%; Pred. No. 1.5e+06;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 7 TTGGCACTGCAG 20
||| ||| |||
Db 23 TCTGCCATTAGAG 10

RESULT 31

AZ829689 24 bp DNA linear GSS 30-FEB-2001
LOCUS AZ829689
DEFINITION 2M0107C22F Mouse 10kb plasmid UUCGCM library Mus musculus genomic
clone UUCGCM0107C22 F, DNA sequence.

ACCESSION
AZ829689
A2829689.1 GI:12999513
GSS.

VERSION
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Dunn,D., Aoyagi,A., Barber,M., Beacom,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Kelly,
M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A.
and Wright,D., WeisB,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

JOURNAL COMMENT Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0107 row: C column: 22
Seq primer: CGTTGTAAACGACGCCACAT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers

FEATURES

1. .24
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCM2M0107C22"
/clone_lib="Mouse 10kb plasmid UGCM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnres/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The sheared DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g14732114[9b]AF29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN
6 a 7 c 6 g 5 t

Query Match 46.0%; Score 9.2; DB 17; Length 24;
Beet Local Similarity 78.6%; Pred. No. 1.5e+06;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 TTGGCCACTCAGAG 20
8 TTAGACACTGAGAG 21

Db 8 TTAGACACTGAGAG 21

RESULT 32
AZ379234/c 25 bp DNA linear GSS 02-OCT-2000
LOCUS 1M0134P16 Mouse 10kb plasmid UGCM library Mus musculus genomic
DEFINITION
ACCESSION AZ379234
VERSION
KEYWORDS
SOURCE
ORGANISM house mouse.
MUS musculus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)
Dunn,D., Aoyagi,A., Barber,M., Beacom,T., Duval,B., Hamli,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Kelly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weis,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., STC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0134 row: P column: 16
Seq primer: CGTTGTAAACGACGCGCACT
Clase: plasmid ends
High quality sequence scop: 25.
Location/Qualifiers

FEATURES

```

source
1..25
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="Mus musculus 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-".
/notes="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT      10 a      4 c      5 g      6 t
ORIGIN
Query Match      46.0%; Score 9.2; DB 17; Length 25;
Best Local Similarity 78.6%; Pred. No. 1.5e+06;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      7 TTTGCCACTCAGAG 20
      |||||
      22 TTGTCTTCAGAG 9

RESULT 33
BH759341      25 bp      DNA      linear      GSS 12-MAR-2002
LOCUS      KG02510-3prtime Drosophila melanogaster P[SuPor-P] P element
DEFINITION      insertion line Drosophila melanogaster genomic Sequence recovered
      from 3' end of P element, DNA sequence.
ACCESSION      BH759341
VERSION      BH759341.1 GI:19352580
KEYWORDS      GSS.
SOURCE      fruit fly.
ORGANISM      Drosophila melanogaster
      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
      Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
      Ephydroidea; Drosophilidae; Drosophila.
      1 (bases 1 to 25)
      Leiva, R., Hoskins, R., Liao, G., Morzen, N., Tsang, G., He, Y., Karpen
      G., Belter, H., Rubin, G. and Spradling, A.
      The Berkeley Drosophila Genome Project Gene Disruption Project
      Unpublished (2001).
      Contact: Gerald Rubin
      Berkeley Drosophila Genome Project
      University of California, Berkeley
      LSA Building, Berkeley, CA 94720-3200, USA
      Fax: 5106433947
      Email: gerry@fruitfly.berkeley.edu
      Sequence recovery method was inverse PCR.
      Sequence orientation is forward strand relative to 5' end of P
      element
      The P element insertion position is base 1 in the 25 bases. This
      insertion position refers to the first base of the 8 base target
      recognition sequence.
      Class: transposon-tagged.
      Location/Qualifiers
      1..25
FEATURES
source

```

```

/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="Drosophila melanogaster P[SuPor-P] P element
insertion lines"
/notes="Inverse PCR was performed on Drosophila
melanogaster strains each of which contains one or more
P[SuPor-P] P-element transposon insertion. The resultant
fragment for each strain was directly sequenced to
determine the genomic sequence at the site of insertion.
Details of the protocols used can be found at
http://www.fruitfly.org/about/methods/inverse.pcr.html."

BASE COUNT      1 a      9 c      6 g      9 t
ORIGIN
Query Match      46.0%; Score 9.2; DB 17; Length 25;
Best Local Similarity 78.6%; Pred. No. 1.5e+06;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      4 GCGTTGCCACTCA 17
      |||||
      7 GGGTTCCCTCTCA 20

RESULT 34
A2954781      19 bp      DNA      linear      GSS 27-APR-2001
LOCUS      A2954781/C
DEFINITION      clone UUGC2M0220C07 R, DNA sequence.
ACCESSION      A2954781
VERSION      A2954781.1 GI:13826008
KEYWORDS      GSS.
SOURCE      house mouse.
ORGANISM      Mus musculus
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
      1 (bases 1 to 19)
      Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
      Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
      M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.
      and Wright, D., Weiss, R.
      Mouse whole genome scaffolding with paired end reads from 10kb
      plasmid inserts
      Unpublished (2000)
      Contact: Robert B. Weiss
      University of Utah Genome Center
      University of Utah
      Km. 306, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
      84112, USA
      Tel: 801 585 5606
      Fax: 801 585 7177
      Email: ddunn@genetics.utah.edu
      Insert Length: 1000 Std. Error: 0.00
      Plate: 0220 Row: C Column: 07
      Seq primer: CACACGAGAAACAGCTATGACC
      Class: plasmid ends
      High quality sequence stop: 19.
      Location/Qualifiers
      1..19
FEATURES
source
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="UUGC2M0220C07"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-".
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were

```

ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E.coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN

8 a 6 c 4 g 1 t

Query Match 45.0%; Score 9; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTGCGTTTG 10
|||||
Db 11 TTGCGTTTG 3

RESULT 35
AZ435809 20 bp DNA linear GSS 03-OCT-2000
LOCUS 1M0223103F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0223103 F, DNA sequence.
ACCESSION AZ435809
VERSION AZ435809.1 GI:10559822
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islem,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weis,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT

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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0223 row: L column: 03
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.

FEATURES

source

1. 20

Location/Qualifiers

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0223103"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN

6 a 6 c 3 g 5 t

Query Match 45.0%; Score 9; DB 17; Length 20;
Best Local Similarity 70.6%; Pred. No. 1.8e+06;
Matches 12; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 TGC GTTGC CACTCAGA 19
|||||
Db 2 TACGATGCTCTCTCAA 18

RESULT 36
AZ991405 20 bp DNA linear GSS 27-APR-2001
LOCUS 2M0275004R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION clone UUGC2M0275004 R, DNA sequence.
ACCESSION AZ991405
VERSION AZ991405.1 GI:13862632
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islem,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weis,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT

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Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0275 row: O column: 04
Seq primer: CACACAGAAACACCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES

source

1. 20

Location/Qualifiers

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0275004"
/clone_1lb="Mouse 10kb plasmid UUGC2M library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD42nv, Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (g1473214|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent *E. coli* XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 7 a 6 c 5 t

Query Match 45.0%; Score 9; DB 17; Length 20;
 Best Local Similarity 70.6%; Pred. No. 1.8e+06;
 Matches 12; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TGGCTTGCACCTCAGA 19
 Db 3 TGGCATTCACCAACTA 19

RESULT 37 TA361P06P 20 bp DNA linear GSS 13-DEC-2000
 TA361P06P/c
 LOCUS T brucei sheared genomic DNA clone 361f06, forward sequence,
 DEFINITION genomic survey sequence.
 ACCESSION AL494520
 VERSION AL494520.1 GI:11870977
 KEYWORDS GSS.

SOURCE Trypanosoma brucei.
 ORGANISM Trypanosoma brucei.
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE 1 (bases 1 to 20)
 AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.

TITLE Direct Submission
 JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.
 Barrell, Oxford University Press, 1999).

DETAILS of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.
 Location/Qualifiers

FEATURES 1..20
 source /organism="Trypanosoma brucei"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="361f06"

BASE COUNT 6 a 9 c 3 g 2 t

Query Match 45.0%; Score 9; DB 17; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TGGCTTGC 11
 Db 17 TGGCTTGC 9

RESULT 38 TA62B07P 21 bp DNA linear GSS 16-DEC-2000
 TA62B07P/c
 LOCUS T. brucei sheared genomic DNA clone 62b07, forward sequence,
 DEFINITION genomic survey sequence.
 ACCESSION AL465023
 VERSION AL465023.1 GI:11877508
 KEYWORDS GSS.

SOURCE Trypanosoma brucei.
 ORGANISM Trypanosoma brucei.
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE 1 (bases 1 to 21)
 AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.

TITLE Direct Submission
 JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.
 Barrell, Oxford University Press, 1999).

DETAILS of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.
 Location/Qualifiers

FEATURES 1..21
 source /organism="Trypanosoma brucei"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="62b07"

BASE COUNT 7 a 5 c 4 g 5 t

Query Match 45.0%; Score 9; DB 17; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TTGGCACT 15
 Db 19 TTGGCACT 11

RESULT 39 A1186405 22 bp mRNA linear EST 28-OCT-1998
 A1186405/c
 LOCUS qd20605.x1 Soareg placenta 8to9weeks_2NBP8809W Homo sapiens CDNA
 clone IMAGE:1724288 3' similar to TR:015726 Q15726 MALIGNANT
 MELANOMA METASTASIS-SUPPRESSOR. /, mRNA sequence.
 ACCESSION A1186405
 VERSION A1186405.1 GI:3737043
 KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 22)
 AUTHORS NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph. D.
 Email: cgaaps-r@mail.nih.gov

This clone is available royalty-free through LML; contact the

FEATURES

SOURCE

IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 759 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers

1..22
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1724288"
/clone.lib="Soares placenta_8to9weeks_2NHP8to9g"
/dev_stage="two placentae: one from 8 weeks and another from 9 weeks post conception"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: placenta; Vector: pT73D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCACTCTGAAGTGGAGCGCGCGCATTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 8 a 4 c 8 g 2 t
ORIGIN

Query Match 45.0%; Score 9; DB 9; Length 22;
Best Local Similarity 70.6%; Pred. No. 1.9e+06;
Matches 12; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 TTGGCTTGGCACTCA 17
Db 22 TTCTCTGTGCACCCA 6

RESULT 40

A2367707/c

LOCUS

1M0117A08R Mouse 10kb plasmid UUCGM 1library Mus musculus genomic
clone UUCGM0117A08 R, DNA sequence.

ACCESSION

A2367707

VERSION

A2367707.1

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus

REFERENCE

A2367707

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausen,A. and Wright,D., Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

unpublished (2000)

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0117 row: A column: 08

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

FEATURES

SOURCE

1..22
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"

/clone="UUCGM0117A08"
/clone.lib="Mouse 10kb plasmid UUCGM 1library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 10 a 7 c 4 g 1 t
ORIGIN

Query Match 45.0%; Score 9; DB 17; Length 22;
Best Local Similarity 70.6%; Pred. No. 1.9e+06;
Matches 12; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 TTGGCTTGGCACTCAG 18
Db 18 TTGTGTTGGCTCTCTG 2

Search completed: June 7, 2003, 09:44:13
Job time: 1175.09 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 7, 2003, 07:20:34 ; Search time 391.418 Seconds

(without alignments)
1338.340 Million cell updates/sec

Title: US-10-080-959A-5

Sequence: 18
1 ctgcgccgcagccagc 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 521186

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1000 summaries

Database :

GenEmbl: *
1: gb_da: *
2: gb_hlg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pac: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *
15: em_da: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_pac: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *
29: em_vl: *
30: em_hlg_hum: *
31: em_hlg_inv: *
32: em_hlg_other: *
33: em_hlg_mus: *
34: em_hlg_pln: *
35: em_hlg_rdi: *
36: em_hlg_mam: *
37: em_hlg_vit: *
38: em_ey: *
39: em_higo_hum: *
40: em_higo_mus: *
41: em_higo_other: *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	6 AR210276	AR210276 Sequence
2	18	100.0	18	6 AX402704	AX402704 Sequence
3	13	72.2	21	6 AR159747	AR159747 Sequence
4	12.8	71.1	17	6 AR210194	AR210194 Sequence
5	12.8	71.1	17	6 AX402622	AX402622 Sequence
6	12.4	68.9	18	6 104828	104828 Sequence 7
7	12.4	67.8	22	6 171353	171353 Sequence 2
8	12.2	67.8	21	6 AX404363	AX404363 Sequence
9	12.2	67.8	21	6 AX404364	AX404364 Sequence
10	12	66.7	18	6 104832	104832 Sequence 11
11	12	66.7	21	6 AX096029	AX096029 Sequence
12	12	66.7	25	6 AR139910	AR139910 Sequence
13	12	66.7	25	6 AR167554	AR167554 Sequence
14	11.8	65.6	18	6 A38123	A38123 Sequence 3
15	11.8	65.6	18	6 A42267	A42267 Sequence 17
16	11.8	65.6	18	6 AR000469	AR000469 Sequence
17	11.8	65.6	18	6 AR044543	AR044543 Sequence
18	11.8	65.6	18	6 AR098234	AR098234 Sequence
19	11.8	65.6	18	6 AR127034	AR127034 Sequence
20	11.8	65.6	18	6 189306	189306 Sequence 3
21	11.8	65.6	18	6 189318	189318 Sequence 3
22	11.8	65.6	18	6 193614	193614 Sequence 3
23	11.8	65.6	24	6 A32651	A32651 Synthetic H
24	11.8	65.6	24	6 A32652	A32652 Synthetic H
25	11.8	65.6	24	6 AR097798	AR097798 Sequence
26	11.8	65.6	24	6 AR097799	AR097799 Sequence
27	11.8	65.6	24	6 191779	191779 Sequence 13
28	11.8	65.6	25	6 A75774	A75774 Sequence 43
29	11.8	65.6	19	6 AR085110	AR085110 Sequence
30	11.6	64.4	25	6 AX322593	AX322593 Sequence
31	11.6	64.4	21	6 AR021129	AR021129 Sequence
32	11.6	64.4	21	6 AX404361	AX404361 Sequence
33	11.6	64.4	21	6 AX404362	AX404362 Sequence
34	11.6	64.4	21	6 AX404365	AX404365 Sequence
35	11.6	64.4	21	6 AX404366	AX404366 Sequence
36	11.6	64.4	22	6 AR021109	AR021109 Sequence
37	11.6	64.4	22	6 AR021110	AR021110 Sequence
38	11.6	64.4	22	6 AR036253	AR036253 Sequence
39	11.6	64.4	22	6 AR036254	AR036254 Sequence
40	11.6	64.4	24	6 AX031299	AX031299 Sequence
41	11.6	64.4	24	13 AX031325	AX031325 Sequence
42	11.4	63.3	15	6 A15500	A15500 oligonucleo
43	11.4	63.3	15	6 A15500	A15500 oligonucleo
44	11.4	63.3	15	6 A15501	A15501 oligonucleo
45	11.4	63.3	15	6 A15501	A15501 oligonucleo
46	11.4	63.3	15	6 A32421	A32421 Synthetic P
47	11.4	63.3	19	6 BD011931	BD011931 Ameliorat
48	11.4	63.3	19	6 BD011987	BD011987 Therapeut
49	11.4	63.3	19	6 BD012048	BD012048 Therapeut
50	11.4	63.3	19	6 BD012935	BD012935 Inhibiti
51	11.4	63.3	19	6 E23331	E23331 Antibody ag
52	11.4	63.3	19	6 E27100	E27100 Remedy for
53	11.4	63.3	19	23 BD004411	BD004411 Ameliorat
54	11.4	63.3	19	23 BD004467	BD004467 Therapeut
55	11.4	63.3	19	23 BD004528	BD004528 Therapeut
56	11.4	63.3	19	23 BD008361	BD008361 Inhibiti
57	11.4	63.3	20	6 A81367	A81367 Sequence 12
58	11.4	63.3	20	6 AR163730	AR163730 Sequence
59	11.4	63.3	20	6 AX001587	AX001587 Sequence
60	11.4	63.3	22	6 AR023933	AR023933 Sequence
61	11.4	63.3	22	6 AR182249	AR182249 Sequence
62	11.4	63.3	24	6 A24897	A24897 oligonucleo
63	11.4	63.3	24	6 AR032196	AR032196 Sequence
64	11.2	62.2	16	6 AR196066	AR196066 Sequence
65	11.2	62.2	16	6 AX317642	AX317642 Sequence

C	66	11.2	62.2	18	6	AI1760	AI1760 Nucleotide	139	10.6	58.9	25	6	AX042502	AX042502 Sequence
C	67	11.2	62.2	18	6	AR196156	AR196156 Sequence	140	10.4	57.8	12	6	E08883	E08883 BamHI linker
C	68	11.2	62.2	19	6	AR210182	AR210182 Sequence	141	10.4	57.8	12	6	E08883	E08883 BamHI linker
C	69	11.2	62.2	19	6	AX026210	AX026210 Sequence	142	10.4	57.8	12	6	104862	104862 Sequence 2
C	70	11.2	62.2	20	6	AX296221	AX296221 Sequence	143	10.4	57.8	12	6	104862	104862 Sequence 2
C	71	11.2	62.2	21	6	AR138848	AR138848 Sequence	144	10.4	57.8	12	6	128840	128840 Sequence 78
C	72	11.2	62.2	22	6	AX317639	AX317639 Sequence	145	10.4	57.8	12	6	128840	128840 Sequence 78
C	73	11.2	62.2	23	6	AR144354	AR144354 Sequence	146	10.4	57.8	13	6	AI5498	AI5498 oligonucleo
C	74	11.2	62.2	24	6	AX291588	AX291588 Sequence	147	10.4	57.8	13	6	AI5498	AI5498 oligonucleo
C	75	11.2	62.2	24	6	AX095225	AX095225 Sequence	148	10.4	57.8	13	6	AI5499	AI5499 oligonucleo
C	76	11.2	62.2	24	6	AX342721	AX342721 Sequence	149	10.4	57.8	13	6	AI5499	AI5499 oligonucleo
C	77	11.2	62.2	24	6	AX031302	AX031302 Sequence	150	10.4	57.8	18	6	AR069001	AR069001 Sequence
C	78	11.2	62.2	24	13	AX031328	AX031328 Sequence	151	10.4	57.8	18	6	AR081196	AR081196 Sequence
C	79	11.2	62.2	25	6	AR068845	AR068845 Sequence	152	10.4	57.8	18	6	AR095514	AR095514 Sequence
C	80	11.2	62.2	25	6	AR070145	AR070145 Sequence	153	10.4	57.8	18	6	E05746	E05746 PCR primer
C	81	11.2	62.2	25	6	AR102902	AR102902 Sequence	154	10.4	57.8	19	6	AR009255	AR009255 Sequence
C	82	11.2	62.2	25	6	AR108081	AR108081 Sequence	155	10.4	57.8	19	6	AX259683	AX259683 Sequence
C	83	11.2	62.2	25	6	AR134729	AR134729 Sequence	156	10.4	57.8	19	6	178495	178495 Sequence 6
C	84	10.8	60.0	18	6	A05375	A05375 Synthetic p	157	10.4	57.8	20	6	AR125469	AR125469 Sequence
C	85	10.8	60.0	18	6	A05376	A05376 Synthetic p	158	10.4	57.8	20	6	AX195278	AX195278 Sequence
C	86	10.8	60.0	18	6	AR210276	AR210276 Sequence	159	10.4	57.8	20	6	AX477033	AX477033 Sequence
C	87	10.8	60.0	18	6	AX048142	AX048142 Sequence	160	10.4	57.8	22	6	103801	103801 Sequence 4
C	88	10.8	60.0	18	6	AX114959	AX114959 Sequence	161	10.4	57.8	23	6	AR061354	AR061354 Sequence
C	89	10.8	60.0	18	6	AX402704	AX402704 Sequence	162	10.4	57.8	23	6	AR061354	AR061354 Sequence
C	90	10.8	60.0	19	6	AX130852	AX130852 Sequence	163	10.4	57.8	23	6	AR108253	AR108253 Sequence
C	91	10.8	60.0	19	6	AX259683	AX259683 Sequence	164	10.4	57.8	23	6	AR108253	AR108253 Sequence
C	92	10.8	60.0	19	6	E15636	E15636 PCR primer	165	10.4	57.8	23	6	116210	116210 Sequence 36
C	93	10.8	60.0	20	6	A68406	A68406 Sequence 11	166	10.4	57.8	23	6	116210	116210 Sequence 36
C	94	10.8	60.0	20	6	AR136419	AR136419 Sequence	167	10.4	57.8	23	6	166696	166696 Sequence 36
C	95	10.8	60.0	20	6	AR212475	AR212475 Sequence	168	10.4	57.8	23	6	166696	166696 Sequence 36
C	96	10.8	60.0	20	6	AX027702	AX027702 Sequence	169	10.4	57.8	23	6	184790	184790 Sequence 36
C	97	10.8	60.0	20	6	AX080470	AX080470 Sequence	170	10.4	57.8	23	6	184790	184790 Sequence 36
C	98	10.8	60.0	20	6	AX462655	AX462655 Sequence	171	10.4	57.8	24	6	A82417	A82417 Sequence 5
C	99	10.8	60.0	21	6	A10825	A10825 PKX2 DNA fr	172	10.4	57.8	24	6	AR009211	AR009211 Sequence
C	100	10.8	60.0	21	6	A10825	A10825 PKX2 DNA fr	173	10.4	57.8	24	6	AR009211	AR009211 Sequence
C	101	10.8	60.0	21	6	A10825	A10825 PKX2 DNA fr	174	10.4	57.8	24	6	AR042594	AR042594 Sequence
C	102	10.8	60.0	21	6	A10825	A10825 PKX2 DNA fr	175	10.4	57.8	24	6	AR042594	AR042594 Sequence
C	103	10.8	60.0	21	6	AX172447	AX172447 Sequence	176	10.4	57.8	24	6	AR064727	AR064727 Sequence
C	104	10.8	60.0	24	6	AR146092	AR146092 Sequence	177	10.4	57.8	24	6	AR064727	AR064727 Sequence
C	105	10.8	60.0	24	6	AX149404	AX149404 Sequence	178	10.4	57.8	24	6	AR081548	AR081548 Sequence
C	106	10.8	60.0	24	6	AX444509	AX444509 Sequence	179	10.4	57.8	24	6	AR081548	AR081548 Sequence
C	107	10.8	60.0	24	6	115483	115483 Sequence 12	180	10.4	57.8	24	6	AR125661	AR125661 Sequence
C	108	10.8	60.0	24	6	127884	127884 Sequence 51	181	10.4	57.8	24	6	AR125661	AR125661 Sequence
C	109	10.8	60.0	25	6	A47526	A47526 Sequence 21	182	10.4	57.8	24	6	AX233483	AX233483 Sequence
C	110	10.8	60.0	25	6	AR097937	AR097937 Sequence	183	10.4	57.8	24	6	115483	115483 Sequence 12
C	111	10.8	60.0	25	6	AR198699	AR198699 Sequence	184	10.4	57.8	24	6	115955	115955 Sequence 56
C	112	10.8	60.0	25	6	AX014057	AX014057 Sequence	185	10.4	57.8	24	6	115955	115955 Sequence 56
C	113	10.8	60.0	25	6	AX042453	AX042453 Sequence	186	10.4	57.8	24	6	122454	122454 Sequence 3
C	114	10.8	60.0	25	6	AX042473	AX042473 Sequence	187	10.4	57.8	24	6	122454	122454 Sequence 3
C	115	10.8	60.0	25	6	AX236602	AX236602 Sequence	188	10.4	57.8	24	6	132477	132477 Sequence 59
C	116	10.8	60.0	25	6	AX236602	AX236602 Sequence	189	10.4	57.8	24	6	132477	132477 Sequence 59
C	117	10.8	60.0	25	6	AX236602	AX236602 Sequence	190	10.4	57.8	24	6	140672	140672 Sequence 3
C	118	10.8	60.0	20	6	AR124186	AR124186 Sequence	191	10.4	57.8	24	6	140672	140672 Sequence 3
C	119	10.8	60.0	20	6	AX459982	AX459982 Sequence	192	10.4	57.8	24	6	144740	144740 Sequence 3
C	120	10.6	58.9	21	6	AX096149	AX096149 Sequence	193	10.4	57.8	24	6	144740	144740 Sequence 3
C	121	10.6	58.9	23	10	MWTCB5	Z48997 M.musculus	194	10.4	57.8	24	6	144836	144836 Sequence 3
C	122	10.6	58.9	23	10	MWTC1902B	Z49043 M.musculus	195	10.4	57.8	24	6	144836	144836 Sequence 3
C	123	10.6	58.9	24	6	A25979	A25979 Artificial	196	10.4	57.8	24	6	145530	145530 Sequence 3
C	124	10.6	58.9	24	6	A30842	AR0842 Oligonucleo	197	10.4	57.8	24	6	145530	145530 Sequence 3
C	125	10.6	58.9	24	6	AR025330	AR025330 Sequence	198	10.4	57.8	24	6	145669	145669 Sequence 3
C	126	10.6	58.9	24	6	AR031724	AR031724 Sequence	199	10.4	57.8	24	6	145669	145669 Sequence 3
C	127	10.6	58.9	24	6	AR044652	AR044652 Sequence	200	10.4	57.8	24	6	147073	147073 Sequence 3
C	128	10.6	58.9	24	6	AR052057	AR052057 Sequence	201	10.4	57.8	24	6	147073	147073 Sequence 3
C	129	10.6	58.9	24	6	AR052106	AR052106 Sequence	202	10.4	57.8	24	6	155761	155761 Sequence 3
C	130	10.6	58.9	24	6	AR102724	AR102724 Sequence	203	10.4	57.8	24	6	155761	155761 Sequence 3
C	131	10.6	58.9	24	6	AR110444	AR110444 Sequence	204	10.4	57.8	24	6	159520	159520 Sequence 3
C	132	10.6	58.9	24	6	AR147375	AR147375 Sequence	205	10.4	57.8	24	6	159520	159520 Sequence 3
C	133	10.6	58.9	24	6	AX233483	AX233483 Sequence	206	10.4	57.8	24	6	196154	196154 Sequence 36
C	134	10.6	58.9	24	6	AX322595	AX322595 Sequence	207	10.4	57.8	24	6	196154	196154 Sequence 36
C	135	10.6	58.9	24	6	AX445602	AX445602 Sequence	208	10.4	57.8	25	6	AR062186	AR062186 Sequence
C	136	10.6	58.9	24	6	186292	186292 Sequence 27	209	10.4	57.8	25	6	AR135164	AR135164 Sequence
C	137	10.6	58.9	24	6	186341	186341 Sequence 76	210	10.2	56.7	16	6	A65270	A65270 Sequence 1
C	138	10.6	58.9	25	6	AX042476	AX042476 Sequence	211	10.2	56.7	16	6	AR134538	AR134538 Sequence

C 212	10.2	56.7	17	6	AR140170	AR140170 Sequence	285	10.2	56.7	21	6	I16140	I16140 Sequence 5
C 213	10.2	56.7	17	6	AR195708	AR195708 Sequence	286	10.2	56.7	21	6	I21311	I21311 Sequence 5
C 214	10.2	56.7	17	6	AR210194	AR210194 Sequence	C 287	10.2	56.7	21	6	I84721	I84721 Sequence 9
C 215	10.2	56.7	17	6	AX092740	AX092740 Sequence	C 288	10.2	56.7	22	6	AR066396	AR066396 Sequence
C 216	10.2	56.7	17	6	AX272862	AX272862 Sequence	C 289	10.2	56.7	22	6	AR200656	AR200656 Sequence
C 217	10.2	56.7	17	6	AX273293	AX273293 Sequence	C 290	10.2	56.7	22	6	AX188736	AX188736 Sequence
C 218	10.2	56.7	17	6	AX273294	AX273294 Sequence	C 291	10.2	56.7	22	6	AX188744	AX188744 Sequence
C 219	10.2	56.7	17	6	AX316104	AX316104 Sequence	C 292	10.2	56.7	24	6	A04371	A04371 Sequence fo
C 220	10.2	56.7	17	6	AX356933	AX356933 Sequence	C 293	10.2	56.7	24	6	A04371	A04371 Sequence fo
C 221	10.2	56.7	17	6	AX402622	AX402622 Sequence	C 294	10.2	56.7	24	6	A11769	A11769 Sequence fo
C 222	10.2	56.7	18	6	A87862	A87862 Sequence 10	C 295	10.2	56.7	24	6	AR019471	AR019471 Sequence
C 223	10.2	56.7	18	6	A89829	A89829 Sequence 10	C 296	10.2	56.7	24	6	AR028994	AR028994 Sequence
C 224	10.2	56.7	19	6	A70729	A70729 Sequence 50	C 297	10.2	56.7	24	6	AR065932	AR065932 Sequence
C 225	10.2	56.7	19	6	A79213	A79213 Sequence 50	C 298	10.2	56.7	24	6	AR095367	AR095367 Sequence
C 226	10.2	56.7	19	6	A93435	A93435 Sequence 1	C 299	10.2	56.7	24	6	AR176111	AR176111 Sequence
C 227	10.2	56.7	19	6	A96984	A96984 Sequence 62	C 300	10.2	56.7	24	6	AR201753	AR201753 Sequence
C 228	10.2	56.7	19	6	AR049021	AR049021 Sequence	C 301	10.2	56.7	24	6	AX289512	AX289512 Sequence
C 229	10.2	56.7	19	6	AR124122	AR124122 Sequence	C 302	10.2	56.7	24	6	AX290919	AX290919 Sequence
C 230	10.2	56.7	19	6	AR129881	AR129881 Sequence	C 303	10.2	56.7	24	6	AX291102	AX291102 Sequence
C 231	10.2	56.7	19	6	AR203412	AR203412 Sequence	C 304	10.2	56.7	24	6	AX292453	AX292453 Sequence
C 232	10.2	56.7	19	6	AX147709	AX147709 Sequence	C 305	10.2	56.7	24	6	AX406704	AX406704 Sequence
C 233	10.2	56.7	19	6	AX358553	AX358553 Sequence	C 306	10.2	56.7	24	6	AX445821	AX445821 Sequence
C 234	10.2	56.7	19	6	AX395002	AX395002 Sequence	C 307	10.2	56.7	24	6	AX447168	AX447168 Sequence
C 235	10.2	56.7	19	6	BD003443	BD003443 A Gene re	C 308	10.2	56.7	24	6	I16868	I16868 Sequence 6
C 236	10.2	56.7	20	6	AR012172	AR012172 Sequence	C 309	10.2	56.7	25	6	A00431	A00431 Nucleotide
C 237	10.2	56.7	20	6	AR012174	AR012174 Sequence	C 310	10.2	56.7	25	6	AR051207	AR051207 Sequence
C 238	10.2	56.7	20	6	AR062072	AR062072 Sequence	C 311	10.2	56.7	25	6	AR139910	AR139910 Sequence
C 239	10.2	56.7	20	6	AR086430	AR086430 Sequence	C 312	10.2	56.7	25	6	AR154075	AR154075 Sequence
C 240	10.2	56.7	20	6	AR093755	AR093755 Sequence	C 313	10.2	56.7	25	6	AR167554	AR167554 Sequence
C 241	10.2	56.7	20	6	AR093757	AR093757 Sequence	C 314	10.2	56.7	25	6	AX339699	AX339699 Sequence
C 242	10.2	56.7	20	6	AR104951	AR104951 Sequence	C 315	10.2	56.7	25	6	E28833	E28833 Human CC ty
C 243	10.2	56.7	20	6	AR147480	AR147480 Sequence	C 316	10.2	56.6	11	6	AR049483	AR049483 Sequence
C 244	10.2	56.7	20	6	AR162416	AR162416 Sequence	C 317	10.2	56.6	11	6	AR051634	AR051634 Sequence
C 245	10.2	56.7	20	6	AR163924	AR163924 Sequence	C 318	10.2	56.6	12	6	I68100	I68100 Sequence 4
C 246	10.2	56.7	20	6	AR167423	AR167423 Sequence	C 319	10.2	56.6	14	6	AR012001	AR012001 Sequence
C 247	10.2	56.7	20	6	AR206306	AR206306 Sequence	C 320	10.2	56.6	17	6	AR049484	AR049484 Sequence
C 248	10.2	56.7	20	6	AX139288	AX139288 Sequence	C 321	10.2	56.6	17	6	AR049485	AR049485 Sequence
C 249	10.2	56.7	20	6	AX155203	AX155203 Sequence	C 322	10.2	56.6	17	6	AR049486	AR049486 Sequence
C 250	10.2	56.7	20	6	AX284145	AX284145 Sequence	C 323	10.2	56.6	17	6	AR051635	AR051635 Sequence
C 251	10.2	56.7	20	6	AX295552	AX295552 Sequence	C 324	10.2	56.6	17	6	AR051636	AR051636 Sequence
C 252	10.2	56.7	20	6	AX295735	AX295735 Sequence	C 325	10.2	56.6	17	6	AR051637	AR051637 Sequence
C 253	10.2	56.7	20	6	BD012800	BD012800 A method	C 326	10.2	56.6	19	6	AR111513	AR111513 Sequence
C 254	10.2	56.7	20	6	BD013025	BD013025 Method of	C 327	10.2	56.6	19	6	AX068237	AX068237 Sequence
C 255	10.2	56.7	20	6	BD013028	BD013028 Method of	C 328	10.2	56.6	19	6	AX077196	AX077196 Sequence
C 256	10.2	56.7	20	6	E06986	E06986 5' primer to	C 329	10.2	56.6	20	6	AR126731	AR126731 Sequence
C 257	10.2	56.7	20	6	E10200	E10200 Synthetic O	C 330	10.2	56.6	20	6	AR201157	AR201157 Sequence
C 258	10.2	56.7	20	6	E15407	E15407 PCR primer.	C 331	10.2	56.6	20	6	AX034936	AX034936 Sequence
C 259	10.2	56.7	20	6	E27517	E27517 Modified ma	C 332	10.2	56.6	20	6	AX297368	AX297368 Sequence
C 260	10.2	56.7	20	6	E33496	E33496 Primer for	C 333	10.2	56.6	20	6	I30071	I30071 Sequence 23
C 261	10.2	56.7	20	6	E39114	E39114 Microorgan	C 334	10.2	56.6	21	6	AX095007	AX095007 Sequence
C 262	10.2	56.7	20	6	E39431	E39431 Method for	C 335	10.2	56.6	21	6	AX095198	AX095198 Sequence
C 263	10.2	56.7	20	6	I41052	I41052 Sequence 3	C 336	10.2	56.6	22	6	A24876	A24876 oligonucleo
C 264	10.2	56.7	20	6	I66222	I66222 Sequence 3	C 337	10.2	56.6	22	6	A24878	A24878 oligonucleo
C 265	10.2	56.7	20	23	BD008235	BD008235 A method	C 338	10.2	56.6	22	6	A79363	A79363 Sequence 12
C 266	10.2	56.7	20	23	BD010058	BD010058 Method of	C 339	10.2	56.6	22	6	A79365	A79365 Sequence 14
C 267	10.2	56.7	20	23	BD010061	BD010061 Method of	C 340	10.2	56.6	22	6	A91915	A91915 Sequence 2
C 268	10.2	56.7	21	6	A42348	A42348 Sequence 8	C 341	10.2	56.6	22	6	AR032175	AR032175 Sequence
C 269	10.2	56.7	21	6	A44379	A44379 Sequence 9	C 342	10.2	56.6	22	6	AR032177	AR032177 Sequence
C 270	10.2	56.7	21	6	A47166	A47166 Sequence 9	C 343	10.2	56.6	22	6	AX148322	AX148322 Sequence
C 271	10.2	56.7	21	6	A56642	A56642 Sequence 9	C 344	10.2	56.6	22	6	AX458675	AX458675 Sequence
C 272	10.2	56.7	21	6	A80363	A80363 Sequence 9	C 345	10.2	56.6	22	6	BD007603	BD007603 Nematoda-
C 273	10.2	56.7	21	6	AR111766	AR111766 Sequence	C 346	10.2	56.6	23	6	A87861	A87861 Sequence 9
C 274	10.2	56.7	21	6	AR179806	AR179806 Sequence	C 347	10.2	56.6	23	6	A89828	A89828 Sequence 9
C 275	10.2	56.7	21	6	AR193505	AR193505 Sequence	C 348	10.2	56.6	24	6	AR068161	AR068161 Sequence
C 276	10.2	56.7	21	6	AX036326	AX036326 Sequence	C 349	10.2	56.6	24	6	AR073355	AR073355 Sequence
C 277	10.2	56.7	21	6	AX081341	AX081341 Sequence	C 350	10.2	56.6	24	6	AX003631	AX003631 Sequence
C 278	10.2	56.7	21	6	AX093783	AX093783 Sequence	C 351	10.2	56.6	24	6	AX292735	AX292735 Sequence
C 279	10.2	56.7	21	6	AX097372	AX097372 Sequence	C 352	10.2	56.6	24	6	AX444889	AX444889 Sequence
C 280	10.2	56.7	21	6	AX145917	AX145917 Sequence	C 353	10.2	56.6	24	6	AX446255	AX446255 Sequence
C 281	10.2	56.7	21	6	AX201239	AX201239 Sequence	C 354	10.2	56.6	24	6	BD008078	BD008078 Novel pro
C 282	10.2	56.7	21	6	AX283171	AX283171 Sequence	C 355	10.2	56.6	25	6	A47536	A47536 Sequence 31
C 283	10.2	56.7	21	6	AX283300	AX283300 Sequence	C 356	10.2	56.6	25	6	AR036752	AR036752 Sequence
C 284	10.2	56.7	21	6	AX384637	AX384637 Sequence	C 357	10.2	56.6	25	6	AR097947	AR097947 Sequence

C 358	10	55.6	25	6	AX012372	AX012372 Sequence	C 431	9.8	54.4	23	6	E13387	E13387 PCR primer
C 359	10	55.6	25	6	E59978	E59978 Highly acti	C 432	9.8	54.4	24	6	A06972	A06972 Nucleotide
C 360	9.8	54.4	15	6	A07486	A07486 Nucleotide	C 433	9.8	54.4	24	6	A50031	A50031 Sequence 14
C 361	9.8	54.4	15	6	I35045	I35045 Sequence 13	C 434	9.8	54.4	24	6	AR151703	AR151703 Sequence
C 362	9.8	54.4	15	6	I35046	I35046 Sequence 14	C 435	9.8	54.4	24	6	AR151716	AR151716 Sequence
C 363	9.8	54.4	15	6	I35076	I35076 Sequence 44	C 436	9.8	54.4	24	6	AX080929	AX080929 Sequence
C 364	9.8	54.4	15	6	I35096	I35096 Sequence 64	C 437	9.8	54.4	24	6	AX290518	AX290518 Sequence
C 365	9.8	54.4	15	6	I35200	I35200 Sequence 16	C 438	9.8	54.4	24	6	AX117167	AX117167 Sequence
C 366	9.8	54.4	15	6	I75079	I75079 Sequence 9	C 439	9.8	54.4	24	6	AX322595	AX322595 Sequence
C 367	9.8	54.4	16	6	AR012039	AR012039 Sequence	C 440	9.8	54.4	24	6	AX444527	AX444527 Sequence
C 368	9.8	54.4	16	6	AX431360	AX431360 Sequence	C 441	9.8	54.4	24	6	AX444527	AX444527 Sequence
C 369	9.8	54.4	16	6	E27549	E27549 Probe for d	C 442	9.8	54.4	24	6	AX444527	AX444527 Sequence
C 370	9.8	54.4	17	6	AR191949	AR191949 Sequence	C 443	9.8	54.4	24	6	AX444527	AX444527 Sequence
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C 372	9.8	54.4	18	6	A26386	A26386 Probe no.4.	C 445	9.8	54.4	24	6	AX444527	AX444527 Sequence
C 373	9.8	54.4	18	6	A82098	A82098 Sequence 18	C 446	9.8	54.4	24	6	AX444527	AX444527 Sequence
C 374	9.8	54.4	18	6	A82102	A82102 Sequence 22	C 447	9.8	54.4	24	6	AX444527	AX444527 Sequence
C 375	9.8	54.4	18	6	A83186	A83186 Sequence 6	C 448	9.8	54.4	25	6	AX042861	AX042861 Sequence
C 376	9.8	54.4	18	6	AR034582	AR034582 Sequence	C 449	9.8	54.4	25	6	AX014053	AX014053 Sequence
C 377	9.8	54.4	18	6	AR051727	AR051727 Sequence	C 450	9.8	54.4	25	6	AX042861	AX042861 Sequence
C 378	9.8	54.4	18	6	AR054937	AR054937 Sequence	C 451	9.8	54.4	25	6	AX067200	AX067200 Sequence
C 379	9.8	54.4	18	6	AR069001	AR069001 Sequence	C 452	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 380	9.8	54.4	18	6	AR072241	AR072241 Sequence	C 453	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 381	9.8	54.4	18	6	AR081196	AR081196 Sequence	C 454	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 382	9.8	54.4	18	6	AR095514	AR095514 Sequence	C 455	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 383	9.8	54.4	18	6	AR121144	AR121144 Sequence	C 456	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 384	9.8	54.4	18	6	AR182918	AR182918 Sequence	C 457	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 385	9.8	54.4	18	6	AR196714	AR196714 Sequence	C 458	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 386	9.8	54.4	18	6	AR200050	AR200050 Sequence	C 459	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 387	9.8	54.4	18	6	AX001169	AX001169 Sequence	C 460	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 388	9.8	54.4	18	6	AX001173	AX001173 Sequence	C 461	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 389	9.8	54.4	18	6	BD002000	BD002000 Construct	C 462	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 390	9.8	54.4	18	6	E54927	E54927 Antibodies	C 463	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 391	9.8	54.4	18	6	I08750	I08750 Sequence 12	C 464	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 392	9.8	54.4	18	6	I26352	I26352 Sequence 44	C 465	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 393	9.8	54.4	18	6	I49673	I49673 Sequence 12	C 466	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 394	9.8	54.4	18	6	I92475	I92475 Sequence 5	C 467	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 395	9.8	54.4	19	6	A64793	A64793 Sequence 2	C 468	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 396	9.8	54.4	19	6	AR107967	AR107967 Sequence	C 469	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 397	9.8	54.4	19	6	AR199419	AR199419 Sequence	C 470	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 398	9.8	54.4	19	6	AR086224	AR086224 Sequence	C 471	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 399	9.8	54.4	20	6	AR107910	AR107910 Sequence	C 472	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 400	9.8	54.4	20	6	AR136419	AR136419 Sequence	C 473	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 401	9.8	54.4	20	6	AR136420	AR136420 Sequence	C 474	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 402	9.8	54.4	20	6	AR176790	AR176790 Sequence	C 475	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 403	9.8	54.4	20	6	AR195439	AR195439 Sequence	C 476	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 404	9.8	54.4	20	6	AR195439	AR195439 Sequence	C 477	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 405	9.8	54.4	20	6	AX045701	AX045701 Sequence	C 478	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 406	9.8	54.4	20	6	AX076689	AX076689 Sequence	C 479	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 407	9.8	54.4	20	6	AX356073	AX356073 Sequence	C 480	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 408	9.8	54.4	20	6	AX449252	AX449252 Sequence	C 481	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 409	9.8	54.4	20	6	E07460	E07460 Artificial	C 482	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 410	9.8	54.4	20	6	E25019	E25019 Oligonucleo	C 483	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 411	9.8	54.4	21	6	A36142	A36142 Sequence 7	C 484	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 412	9.8	54.4	21	6	AR085665	AR085665 Sequence	C 485	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 413	9.8	54.4	21	6	AR138932	AR138932 Sequence	C 486	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 414	9.8	54.4	21	6	AR208662	AR208662 Sequence	C 487	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 415	9.8	54.4	21	6	AX096936	AX096936 Sequence	C 488	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 416	9.8	54.4	21	6	AX145833	AX145833 Sequence	C 489	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 417	9.8	54.4	21	6	AX145917	AX145917 Sequence	C 490	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 418	9.8	54.4	21	6	I25727	I25727 Sequence 2	C 491	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 419	9.8	54.4	22	6	AR073294	AR073294 Sequence	C 492	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 420	9.8	54.4	22	6	AR130480	AR130480 Sequence	C 493	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 421	9.8	54.4	22	6	AR130480	AR130480 Sequence	C 494	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 422	9.8	54.4	22	6	AR130481	AR130481 Sequence	C 495	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 423	9.8	54.4	22	6	AR130481	AR130481 Sequence	C 496	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 424	9.8	54.4	22	6	AR182249	AR182249 Sequence	C 497	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 425	9.8	54.4	22	6	AR211321	AR211321 Sequence	C 498	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 426	9.8	54.4	22	6	E32640	E32640 Method for	C 499	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 427	9.8	54.4	23	6	A09945	A09945 probe. 1/19	C 500	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 428	9.8	54.4	23	6	A63614	A63614 Sequence 1	C 501	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 429	9.8	54.4	23	6	AR062462	AR062462 Sequence	C 502	9.8	54.4	25	6	BD006579	BD006579 Sequence
C 430	9.8	54.4	23	6	AR112392	AR112392 Sequence	C 503	9.8	54.4	25	6	BD006579	BD006579 Sequence

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505	9.6	53.3	21	6	AX154359	AX154359 Sequence	578	9.4	52.2	17	6	AX423238	AX423238 Sequence
506	9.6	53.3	21	6	AX460047	AX460047 Sequence	579	9.4	52.2	17	6	AX423462	AX423462 Sequence
507	9.6	53.3	21	6	E13821	E13821 PCR primer	580	9.4	52.2	17	6	AX423463	AX423463 Sequence
508	9.6	53.3	22	6	A00733	A00733 Nucleotide	581	9.4	52.2	17	6	E08804	E08804 PCR primer
509	9.6	53.3	22	6	A04814	A04814 Nucleotide	582	9.4	52.2	17	6	I36952	I36952 Sequence 38
510	9.6	53.3	22	6	A65666	A65666 Sequence 10	583	9.4	52.2	17	6	I52677	I52677 Sequence 41
511	9.6	53.3	22	6	AX038531	AX038531 Sequence	584	9.4	52.2	17	6	I56022	I56022 Sequence 3
512	9.6	53.3	22	6	AX320320	AX320320 Sequence	585	9.4	52.2	17	6	I95893	I95893 Sequence 3
513	9.6	53.3	23	6	A03039	A03039 Artificial	586	9.4	52.2	18	6	A15635	A15635 oligonucleo
514	9.6	53.3	23	6	A12831	A12831 Synthetic p	587	9.4	52.2	18	6	A15635	A15635 oligonucleo
515	9.6	53.3	23	6	AX038532	AX038532 Sequence	588	9.4	52.2	18	6	AR038242	AR038242 Sequence
516	9.6	53.3	23	6	I21873	I21873 Sequence 5	589	9.4	52.2	18	6	AR038243	AR038243 Sequence
517	9.6	53.3	23	6	I21879	I21879 Sequence 11	590	9.4	52.2	18	6	AR106850	AR106850 Sequence
518	9.6	53.3	24	6	A07961	A07961 oligonucleo	591	9.4	52.2	18	6	AR154196	AR154196 Sequence
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523	9.6	53.3	24	6	AR146080	AR146080 Sequence	596	9.4	52.2	18	6	AX377072	AX377072 Sequence
524	9.6	53.3	24	6	AX015311	AX015311 Sequence	597	9.4	52.2	18	6	E60063	E60063 Endonuclea
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527	9.6	53.3	24	6	AX151062	AX151062 Sequence	600	9.4	52.2	19	6	A05369	A05369 Synthetic p
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531	9.6	53.3	24	6	AX290739	AX290739 Sequence	604	9.4	52.2	19	6	AR074441	AR074441 Sequence
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533	9.6	53.3	24	6	AX292160	AX292160 Sequence	606	9.4	52.2	19	6	AR085318	AR085318 Sequence
534	9.6	53.3	24	6	AX292734	AX292734 Sequence	607	9.4	52.2	19	6	AR088066	AR088066 Sequence
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537	9.6	53.3	24	6	E05645	E05645 Primer. 9/1	610	9.4	52.2	19	6	AR143489	AR143489 Sequence
538	9.6	53.3	24	6	I89300	I89300 Sequence 12	611	9.4	52.2	19	6	AR171394	AR171394 Sequence
539	9.6	53.3	25	6	AR016269	AR016269 Sequence	612	9.4	52.2	19	6	AR171394	AR171394 Sequence
540	9.6	53.3	25	6	AR196785	AR196785 Sequence	613	9.4	52.2	19	6	I34613	I34613 Sequence 34
541	9.6	53.3	25	6	AX006970	AX006970 Sequence	614	9.4	52.2	20	6	A05195	A05195 oligonucleo
542	9.6	53.3	25	6	AX006971	AX006971 Sequence	615	9.4	52.2	20	6	A07131	A07131 Nucleotide
543	9.6	53.3	25	6	AX038534	AX038534 Sequence	616	9.4	52.2	20	6	A07131	A07131 Nucleotide
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545	9.6	53.3	25	6	I72154	I72154 Sequence 11	618	9.4	52.2	20	6	A90094	A90094 Sequence 27
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557	9.4	52.2	12	6	I14185	I14185 Sequence 17	630	9.4	52.2	20	6	AX355464	AX355464 Sequence
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561	9.4	52.2	15	6	AR166226	AR166226 Sequence	634	9.4	52.2	20	6	I32368	I32368 Sequence 37
562	9.4	52.2	15	6	E16786	E16786 PCR primer	635	9.4	52.2	21	6	A02284	A02284 Synthetic o
563	9.4	52.2	16	6	AR003524	AR003524 Sequence	636	9.4	52.2	21	6	A12128	A12128 oligonucleo
564	9.4	52.2	16	6	AX322719	AX322719 Sequence	637	9.4	52.2	21	6	A12128	A12128 oligonucleo
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568	9.4	52.2	17	6	AR057450	AR057450 Sequence	641	9.4	52.2	21	6	AX096301	AX096301 Sequence
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575	9.4	52.2	17	6	AX422207	AX422207 Sequence	648	9.4	52.2	21	6	AX395578	AX395578 Sequence
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C 655	9.4	52.2	22	6	AR069003	AR069003 Sequence	728	9.2	51.1	16	6	AR134539	AR134539 Sequence
C 656	9.4	52.2	22	6	AR081198	AR081198 Sequence	729	9.2	51.1	16	6	AX262386	AX262386 Sequence
C 657	9.4	52.2	22	6	AR095516	AR095516 Sequence	730	9.2	51.1	16	6	I55157	I55157 Sequence 6
C 658	9.4	52.2	22	6	AR099786	AR099786 Sequence	731	9.2	51.1	16	6	I68709	I68709 Sequence 9
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C 662	9.4	52.2	22	6	AX055385	AX055385 Sequence	735	9.2	51.1	17	6	AR160393	AR160393 Sequence
C 663	9.4	52.2	22	6	AX098407	AX098407 Sequence	736	9.2	51.1	17	6	AR160393	AR160393 Sequence
C 664	9.4	52.2	22	6	AX110876	AX110876 Sequence	737	9.2	51.1	17	6	AR189881	AR189881 Sequence
C 665	9.4	52.2	22	6	I32323	I32323 Sequence 4	738	9.2	51.1	17	6	AR196786	AR196786 Sequence
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C 667	9.4	52.2	23	6	A29942	A29942 Oligonucleo	740	9.2	51.1	17	6	AX001154	AX001154 Sequence
C 668	9.4	52.2	23	6	A31921	A31921 Synthetic C	741	9.2	51.1	17	6	AX014669	AX014669 Sequence
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C 680	9.4	52.2	23	6	AR102922	AR102922 Sequence	753	9.2	51.1	18	6	A36330	A36330 Sequence 33
C 681	9.4	52.2	23	6	AR103930	AR103930 Sequence	754	9.2	51.1	18	6	A42355	A42355 Sequence 15
C 682	9.4	52.2	23	6	AR108101	AR108101 Sequence	755	9.2	51.1	18	6	A44388	A44388 Sequence 18
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C 685	9.4	52.2	23	6	AR156396	AR156396 Sequence	758	9.2	51.1	18	6	A56649	A56649 Sequence 16
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C 687	9.4	52.2	23	6	AX100409	AX100409 Sequence	760	9.2	51.1	18	6	A80370	A80370 Sequence 16
C 688	9.4	52.2	23	6	AX235696	AX235696 Sequence	761	9.2	51.1	18	6	AR009966	AR009966 Sequence
C 689	9.4	52.2	23	6	E49137	E49137 Human large	762	9.2	51.1	18	6	AR009967	AR009967 Sequence
C 690	9.4	52.2	23	6	I12416	I12416 Sequence 20	763	9.2	51.1	18	6	AR032037	AR032037 Sequence
C 691	9.4	52.2	23	6	I23995	I23995 Sequence 7	764	9.2	51.1	18	6	AR032038	AR032038 Sequence
C 692	9.4	52.2	23	6	I58490	I58490 Sequence 18	765	9.2	51.1	18	6	AR083367	AR083367 Sequence
C 693	9.4	52.2	23	6	I67005	I67005 Sequence 1	766	9.2	51.1	18	6	AR111773	AR111773 Sequence
C 694	9.4	52.2	24	6	AX16123	AX16123 Oligonucleo	767	9.2	51.1	18	6	AR179813	AR179813 Sequence
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C 697	9.4	52.2	24	6	AX350849	AX350849 Sequence	770	9.2	51.1	18	6	AX009594	AX009594 Sequence
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C 700	9.4	52.2	24	6	I06726	I06726 Sequence 8	773	9.2	51.1	18	6	AX283179	AX283179 Sequence
C 701	9.4	52.2	25	6	A24887	A24887 Oligonucleo	774	9.2	51.1	18	6	AX283245	AX283245 Sequence
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C 703	9.4	52.2	25	6	AR032186	AR032186 Sequence	776	9.2	51.1	18	6	I30784	I30784 Sequence 22
C 704	9.4	52.2	25	6	AR086622	AR086622 Sequence	777	9.2	51.1	18	6	I46243	I46243 Sequence 22
C 705	9.4	52.2	25	6	AR086739	AR086739 Sequence	778	9.2	51.1	18	6	I78471	I78471 Sequence 32
C 706	9.4	52.2	25	6	AR137987	AR137987 Sequence	779	9.2	51.1	18	6	I78472	I78472 Sequence 33
C 707	9.4	52.2	25	6	AR160523	AR160523 Sequence	780	9.2	51.1	18	6	I84728	I84728 Sequence 16
C 708	9.4	52.2	25	6	AX049199	AX049199 Sequence	781	9.2	51.1	19	6	A22370	A22370 Oligonucleo
C 709	9.4	52.2	25	6	AX049804	AX049804 Sequence	782	9.2	51.1	19	6	A69625	A69625 Sequence 34
C 710	9.4	52.2	25	6	AX050802	AX050802 Sequence	783	9.2	51.1	19	6	A87312	A87312 Sequence 37
C 711	9.4	52.2	25	6	AX081601	AX081601 Sequence	784	9.2	51.1	19	6	AR076118	AR076118 Sequence
C 712	9.4	52.2	25	6	AX138771	AX138771 Sequence	785	9.2	51.1	19	6	AR119277	AR119277 Sequence
C 713	9.4	52.2	25	6	AX374782	AX374782 Sequence	786	9.2	51.1	19	6	AR136719	AR136719 Sequence
C 714	9.4	52.2	25	6	I42471	I42471 Sequence 1	787	9.2	51.1	19	6	AR164731	AR164731 Sequence
C 715	9.2	51.1	14	6	I42471	I42471 Sequence 1	788	9.2	51.1	19	6	AX079895	AX079895 Sequence
C 716	9.2	51.1	15	6	A08049	A08049 Oligonucleo	789	9.2	51.1	19	6	AX130668	AX130668 Sequence
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C 718	9.2	51.1	15	6	AR034030	AR034030 Sequence	791	9.2	51.1	19	6	AX136003	AX136003 Sequence
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C 800	9.2	51.1	20	6	A69631	A69631 Sequence 40	C 873	9.2	51.1	24	6	A51319	A51319 Sequence 4
C 801	9.2	51.1	20	6	AR000118	AR000118 Sequence	C 874	9.2	51.1	24	6	A95198	A95198 Sequence 16
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C 806	9.2	51.1	20	6	AR121000	AR121000 Sequence	C 879	9.2	51.1	24	6	AR201759	AR201759 Sequence
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C 817	9.2	51.1	20	6	AR208857	AR208857 Sequence	C 889	9.2	51.1	24	6	AX328824	AX328824 Sequence
C 818	9.2	51.1	20	6	AR211965	AR211965 Sequence	C 890	9.2	51.1	24	6	AX428849	AX428849 Sequence
C 819	9.2	51.1	20	6	AX038529	AX038529 Sequence	C 891	9.2	51.1	24	6	AX443606	AX443606 Sequence
C 820	9.2	51.1	20	6	AX055819	AX055819 Sequence	C 892	9.2	51.1	24	6	AX445111	AX445111 Sequence
C 821	9.2	51.1	20	6	AX193560	AX193560 Sequence	C 893	9.2	51.1	24	6	AX445111	AX445111 Sequence
C 822	9.2	51.1	20	6	AX193562	AX193562 Sequence	C 894	9.2	51.1	24	6	AX445426	AX445426 Sequence
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C 825	9.2	51.1	20	6	AX419736	AX419736 Sequence	C 897	9.2	51.1	24	6	BD003655	BD003655 Sequence
C 826	9.2	51.1	20	6	AX419752	AX419752 Sequence	C 898	9.2	51.1	24	6	106504	106504 Sequence 8
C 827	9.2	51.1	21	6	A10820	A10820 PKK1 DNA fr	C 899	9.2	51.1	24	6	116868	116868 Sequence 6
C 828	9.2	51.1	21	6	A10820	A10820 PKK1 DNA fr	C 900	9.2	51.1	24	6	124352	124352 Sequence 1
C 829	9.2	51.1	21	6	A10821	A10821 PKK1 DNA fr	C 901	9.2	51.1	24	6	133778	133778 Sequence 47
C 830	9.2	51.1	21	6	A10821	A10821 PKK1 DNA fr	C 902	9.2	51.1	24	9	HSR270369	HSR270369 Homo bap1
C 831	9.2	51.1	21	6	A46973	A46973 Sequence 13	C 903	9.2	51.1	25	6	A06321	A06321 Artificial
C 832	9.2	51.1	21	6	A79433	A79433 Sequence 7	C 904	9.2	51.1	25	6	A63691	A63691 Sequence 1
C 833	9.2	51.1	21	6	A98624	A98624 Sequence 18	C 905	9.2	51.1	25	6	A86784	A86784 Sequence 11
C 834	9.2	51.1	21	6	A98625	A98625 Sequence 19	C 907	9.2	51.1	25	6	AR019285	AR019285 Sequence
C 835	9.2	51.1	21	6	AR081653	AR081653 Sequence	C 908	9.2	51.1	25	6	AR053530	AR053530 Sequence
C 836	9.2	51.1	21	6	AR102342	AR102342 Sequence	C 909	9.2	51.1	25	6	AR076469	AR076469 Sequence
C 837	9.2	51.1	21	6	AR105838	AR105838 Sequence	C 910	9.2	51.1	25	6	AR089334	AR089334 Sequence
C 838	9.2	51.1	21	6	AX038530	AX038530 Sequence	C 911	9.2	51.1	25	6	AR093534	AR093534 Sequence
C 839	9.2	51.1	21	6	AX096489	AX096489 Sequence	C 912	9.2	51.1	25	6	AR129986	AR129986 Sequence
C 840	9.2	51.1	21	6	AX154225	AX154225 Sequence	C 913	9.2	51.1	25	6	AR137152	AR137152 Sequence
C 841	9.2	51.1	21	6	AX154375	AX154375 Sequence	C 914	9.2	51.1	25	6	AR140156	AR140156 Sequence
C 842	9.2	51.1	21	6	I15066	I15066 Sequence 22	C 915	9.2	51.1	25	6	AR141122	AR141122 Sequence
C 843	9.2	51.1	21	6	I17140	I17140 Sequence 22	C 916	9.2	51.1	25	6	AR145310	AR145310 Sequence
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C 845	9.2	51.1	21	6	I42165	I42165 Sequence 39	C 918	9.2	51.1	25	6	AX038534	AX038534 Sequence
C 846	9.2	51.1	22	6	A15292	A15292 linker mole	C 919	9.2	51.1	25	6	AX042482	AX042482 Sequence
C 847	9.2	51.1	22	6	A15292	A15292 linker mole	C 920	9.2	51.1	25	6	AX118798	AX118798 Sequence
C 848	9.2	51.1	22	6	A82573	A82573 Sequence 47	C 921	9.2	51.1	25	6	AX146521	AX146521 Sequence
C 849	9.2	51.1	22	6	A82573	A82573 Sequence 47	C 922	9.2	51.1	25	6	AX300566	AX300566 Sequence
C 850	9.2	51.1	22	6	AR073294	AR073294 Sequence	C 923	9.2	51.1	25	6	AX339699	AX339699 Sequence
C 851	9.2	51.1	22	6	AR081980	AR081980 Sequence	C 924	9.2	51.1	25	6	AX447588	AX447588 Sequence
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C 854	9.2	51.1	22	6	AX038531	AX038531 Sequence	C 927	9.2	51.1	25	6	I14574	I14574 Sequence 51
C 855	9.2	51.1	22	6	AX112485	AX112485 Sequence	C 928	9.2	51.1	25	6	I27887	I27887 Sequence 59
C 856	9.2	51.1	22	6	AX112487	AX112487 Sequence	C 929	9.2	51.1	25	6	I77237	I77237 Sequence 27
C 857	9.2	51.1	22	6	AX116310	AX116310 Sequence	C 930	9.2	51.1	10	6	BD007794	BD007794 LPS activ
C 858	9.2	51.1	22	6	AX322549	AX322549 Sequence	C 931	9.2	51.1	12	6	AX085035	AX085035 Sequence
C 859	9.2	51.1	23	6	A04135	A04135 Synthetic O	C 932	9.2	51.1	12	6	AX085049	AX085049 Sequence
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C 863	9.2	51.1	23	6	AX038532	AX038532 Sequence	C 936	9.2	51.1	15	6	AR139982	AR139982 Sequence
C 864	9.2	51.1	23	6	I29093	I29093 Sequence 14	C 937	9.2	51.1	15	6	AR139983	AR139983 Sequence
C 865	9.2	51.1	23	6	I42140	I42140 Sequence 14	C 938	9.2	51.1	15	6	AR140301	AR140301 Sequence
C 866	9.2	51.1	23	10	I89894	I89894 Sequence 3	C 939	9.2	51.1	15	6	AR140302	AR140302 Sequence
C 867	9.2	51.1	23	10	MMTCPS5	MMTCPS5 Sequence	C 940	9.2	51.1	15	6	AR140579	AR140579 Sequence
C 868	9.2	51.1	23	10	MMTC1902B	MMTC1902B Sequence	C 941	9.2	51.1	15	6	AR140580	AR140580 Sequence

942	9	50.0	15	6	AX362596	Sequence
943	9	50.0	17	6	AI0042	Nucleotide
944	9	50.0	17	6	AR185975	Sequence
945	9	50.0	17	6	AR191948	Sequence
946	9	50.0	17	6	AX139248	Sequence
947	9	50.0	17	6	AX206986	Sequence
948	9	50.0	17	6	AX265495	Sequence
949	9	50.0	17	6	AX265495	Sequence
950	9	50.0	17	6	AX265495	Sequence
951	9	50.0	17	6	AX475043	Sequence
952	9	50.0	17	6	126676	Sequence
953	9	50.0	17	6	126676	Sequence
954	9	50.0	17	6	126676	Sequence
955	9	50.0	18	6	A76033	Sequence
956	9	50.0	18	6	A88208	Sequence
957	9	50.0	18	6	A90175	Sequence
958	9	50.0	18	6	AR051728	Sequence
959	9	50.0	18	6	AR117171	Sequence
960	9	50.0	18	6	AR117181	Sequence
961	9	50.0	18	6	AR131564	Sequence
962	9	50.0	18	6	AR150496	Sequence
963	9	50.0	18	6	AR150506	Sequence
964	9	50.0	18	6	AR199498	Sequence
965	9	50.0	18	6	AR200051	Sequence
966	9	50.0	18	6	AR200969	Sequence
967	9	50.0	18	6	AR210288	Sequence
968	9	50.0	18	6	AX203102	Sequence
969	9	50.0	18	6	AX203104	Sequence
970	9	50.0	18	6	AX402716	Sequence
971	9	50.0	18	6	AX419720	Sequence
972	9	50.0	18	6	BD002001	Construct
973	9	50.0	18	6	E05750	PCR primer
974	9	50.0	18	6	126673	Sequence
975	9	50.0	19	6	149674	Sequence
976	9	50.0	19	6	A58116	Sequence
977	9	50.0	19	6	AR169677	Sequence
978	9	50.0	19	6	AR199419	Sequence
979	9	50.0	19	6	AX015897	Sequence
980	9	50.0	19	6	BD012978	Variant asc
981	9	50.0	19	6	E22961	Variant asc
982	9	50.0	19	6	HS010631	Homo sapi
983	9	50.0	20	6	BD006629	BD006629 A mutagen
984	9	50.0	20	6	AI6534	Oligonucleo
985	9	50.0	20	6	AR043512	Sequence
986	9	50.0	20	6	AR084362	Sequence
987	9	50.0	20	6	AR086213	Sequence
988	9	50.0	20	6	AR092920	Sequence
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990	9	50.0	20	6	AR124935	Sequence
991	9	50.0	20	6	AR124935	Sequence
992	9	50.0	20	6	AR136418	Sequence
993	9	50.0	20	6	AR136906	Sequence
994	9	50.0	20	6	AR144320	Sequence
995	9	50.0	20	6	AR144333	Sequence
996	9	50.0	20	6	AR144334	Sequence
997	9	50.0	20	6	AR144335	Sequence
998	9	50.0	20	6	AR144336	Sequence
999	9	50.0	20	6	AR144337	Sequence
1000	9	50.0	20	6	AR163904	Sequence
					AR164003	Sequence
					AR166697	Sequence

ALIGNMENTS

RESULT 1
LOCUS AR210276 18 bp DNA
DEFINITION Sequence 188 from patent US 6387652.
ACCESSION AR210276
VERSION AR210276.1 GI:21512465
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Haugland, R. and Vesper, S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: US 6387652-A 188 14-MAY-2002
FEATURES
SOURCE
1. 18
/organism="unknown"

BASE COUNT 2 a 8 c 6 g 2 t

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGCCCGGATCCAGGC 18
DB 1 CTGGCCCGGATCCAGGC 18

RESULT 2
LOCUS AX402704 18 bp DNA
DEFINITION Sequence 188 from Patent WO0196612.
ACCESSION AX402704
VERSION AX402704.1 GI:21387695
KEYWORDS
SOURCE
ORGANISM Stachybotrys chartarum.
Stachybotrys chartarum.
Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Stachybotrys.

REFERENCE 1
AUTHORS Haugland, R. and Vesper, S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: WO 0196612-A 188 20-DEC-2001
FEATURES
SOURCE
1. 18
/organism="Stachybotrys chartarum"
/db_xref="taxon:74722"

BASE COUNT 2 a 8 c 6 g 2 t

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGCCCGGATCCAGGC 18
DB 1 CTGGCCCGGATCCAGGC 18

RESULT 3
LOCUS AR169747 21 bp DNA
DEFINITION Sequence 2 from patent US 6291190.
ACCESSION AR169747
VERSION AR169747.1 GI:17907655
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 21)
AUTHORS Behr, M., Small, P., Schoolnik, G. and Wilson, M.A.
TITLE Molecular differences between species of the M. tuberculosis complex
JOURNAL Patent: US 6291190-A 2 18-SEP-2001;
FEATURES
SOURCE
1. 21
/organism="unknown"

BASE COUNT 4 a 11 c 5 g 1 t

Query Match 72.2%; Score 13; DB 6; Length 21;

Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCGCCGATCCAG 16
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Db 9 GCGCCGATCCAG 21
|||||

RESULT 4
AR210194/c AR210194 17 bp DNA linear PAT 20-JUN-2002
LOCUS AR210194
DEFINITION Sequence 106 from patent US 6387652.
ACCESSION AR210194
VERSION AR210194.1 GI:21512362
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Haugland R. and Vesper, S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: US 6387652-A 106 14-MAY-2002;
FEATURES Location/Qualifiers
source 1..17
BASE COUNT 0 a 8 c 6 g 3 t
ORIGIN

Query Match 71.1%; Score 12.8; DB 6; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.1e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCGCCGATCCAGGC 18
|||||
Db 17 GCGCCGATCCAGGC 2
|||||

RESULT 5
AX402622/c AX402622 17 bp DNA linear PAT 07-JUN-2002
LOCUS AX402622
DEFINITION Sequence 106 from Patent WO0196612.
ACCESSION AX402622
VERSION AX402622.1 GI:21387613
KEYWORDS
SOURCE Myrothecium verrucaria.
ORGANISM Myrothecium verrucaria
REFERENCE 1
AUTHORS Haugland R. and Vesper, S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: WO 0196612-A 106 20-DEC-2001;
FEATURES Location/Qualifiers
source 1..17
BASE COUNT 0 a 8 c 6 g 3 t
ORIGIN /db_xref="taxon:5532"

Query Match 71.1%; Score 12.8; DB 6; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.1e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCGCCGATCCAGGC 18
|||||
Db 17 GCGCCGATCCAGGC 2
|||||

RESULT 6
104828 104828 18 bp DNA linear PAT 02-DEC-1994
LOCUS 104828
DEFINITION Sequence 7 from Patent EP 0212532.
ACCESSION 104828

VERSION 104828.1 GI:591433
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Chan, H.W., Shelton, E.R., Baecker, P.A., Salazar, F.H., Martin, M.A.
TITLE Method for producing fusion proteins
JOURNAL Patent: EP 0212532-A1 7 04-MAR-1987;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 1 a 7 c 7 g 3 t
ORIGIN

Query Match 68.9%; Score 12.4; DB 6; Length 18;
Best Local Similarity 92.9%; Pred. No. 3.1e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCGCCGATCC 14
|||||
Db 1 CTGCGCCGATCC 14
|||||

RESULT 7
I71353/c I71353 22 bp DNA linear PAT 03-APR-1998
LOCUS I71353
DEFINITION Sequence 2 from patent US 5681725.
ACCESSION I71353
VERSION I71353.1 GI:3007488
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Jensen, E. Bech.
TITLE Process for producing heme proteins
JOURNAL Patent: US 5681725-A 2 28-OCT-1997;
FEATURES Location/Qualifiers
source 1..22
BASE COUNT 4 a 5 c 10 g 3 t
ORIGIN /organism="unknown"

Query Match 68.9%; Score 12.4; DB 6; Length 22;
Best Local Similarity 92.9%; Pred. No. 3e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCGCCGATCC 14
|||||
Db 16 CTGCGCCGATCC 3
|||||

RESULT 8
AX404363/c AX404363 21 bp DNA linear PAT 14-JUN-2002
LOCUS AX404363
DEFINITION Sequence 189 from Patent WO0224747.
ACCESSION AX404363
VERSION AX404363.1 GI:21437644
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Brinkmann, U. and Hoffmeyer, S.
TITLE Polymorphisms in human genes of cardiovascular regulators and their use in diagnostic and therapeutic applications
JOURNAL Patent: WO 0224747-A 189 28-MAR-2002;
FEATURES Location/Qualifiers
source 1..21
BASE COUNT 1 a 7 c 7 g 3 t
ORIGIN /organism="synthetic construct"

/db_xref="taxon:32630"
/note="artificial sequence-n=a or g"
BASE COUNT 5 a 3 c 9 g 3 t 1 others
ORIGIN

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Best Local Similarity 77.8%; Pred. No. 3.7e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGCGCCCGATCCAGCC 18
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20 CTGCGCCAGATCCAGCC 3

RESULT 9
LOCUS AX404364 21 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 190 from Patent WO0224747.
ACCESSION AX404364
VERSION AX404364.1 GI:21437645
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS
TITLE
JOURNAL
FEATURES
source
1.21
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="artificial sequence-n=t or c"

BASE COUNT 3 a 9 c 3 g 5 t 1 others
ORIGIN
Query Match 67.8%; Score 12.2; DB 6; Length 21;
Best Local Similarity 77.8%; Pred. No. 3.7e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGCGCCCGATCCAGCC 18
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2 CTGCGCCAGATCCAGCC 19

RESULT 10
LOCUS 104832 18 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 11 from Patent EP 0212532.
ACCESSION 104832
VERSION 104832.1 GI:591435
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 18)
AUTHORS
TITLE
JOURNAL
FEATURES
source
1.18
/organism="unknown"

BASE COUNT 1 a 8 c 6 g 3 t
ORIGIN
Query Match 66.7%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCGCCGATCC 14

|||||
DB 5 GCGCCGATCC 16

RESULT 11
LOCUS AX096029 21 bp DNA linear PAT 30-MAR-2001
DEFINITION Sequence 1207 from Patent WO0118250.
ACCESSION AX096029
VERSION AX096029.1 GI:13512256
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 21)
AUTHORS
TITLE
JOURNAL
FEATURES
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1.21
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 2 a 6 c 10 g 2 t 1 others
ORIGIN
Query Match 66.7%; Score 12; DB 6; Length 21;
Best Local Similarity 85.7%; Pred. No. 4.6e+05;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCGCCCGATCC 14
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18 CTGCGCCGATCC 5

RESULT 12
LOCUS AR139910 25 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 88 from patent US 6207416.
ACCESSION AR139910
VERSION AR139910.1 GI:14482406
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 25)
AUTHORS
TITLE
JOURNAL
FEATURES
source
1.25
/organism="unknown"

BASE COUNT 4 a 6 c 10 g 5 t
ORIGIN
Query Match 66.7%; Score 12; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCGATCCAGCC 18
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20 CCGATCCAGCC 9

RESULT 13
LOCUS AR167554 25 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 88 from patent US 6287759.
ACCESSION AR167554

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VERSION      AR167554.1  GI:17903340
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 25)
AUTHORS      Tearey,S.A., Emerson,S.U. and Purcell,R.H.
TITLE        Recombinant proteins of a Pakistani strain of hepatitis E and their
              use in diagnostic methods and vaccines
JOURNAL      Patent: US 6287759-A. 88 11-SEP-2001;
              Location/Qualifiers
FEATURES
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BASE COUNT   4 a      6 c      10 g      5 t
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Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCGGATCCAGGC 18
    |||||
Db 20 CCGGATCCAGGC 9

RESULT 14
LOCUS       A38123
DEFINITION Sequence 3 from Patent EP0605040.
ACCESSION  A38123
VERSION     A38123.1  GI:2294734
KEYWORDS
SOURCE      unidentified.
ORGANISM    unclassified.
REFERENCE    1 (bases 1 to 18)
AUTHORS      Deweer,P. and Amory,A.
TITLE        Pullulanase, micro-organisms producing the same, method for
              preparation thereof as well as its use
JOURNAL      Patent: EP 0605040-A 3 06-JUL-1994;
              SOLVAY (BE)
COMMENT      Other publication JP 6217770 940809
              Other publication CA 2112028 940629
              Other publication CN 1090325 940803
              Other publication AU 5275893 940707
              Other publication FI 935900 940629
              Other publication BE 1007723 951010
              Other publication BE 1007313 950516
              Other publication BE 1006483 940913.
FEATURES
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BASE COUNT   2 a      6 c      7 g      3 t
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Best Local Similarity 86.7%; Pred. No. 5.8e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGGCCCGGATCCA 15
    |||||
Db 16 CTGGCCCGGATCCA 2

RESULT 15
LOCUS       A42267/c
DEFINITION Sequence 17 from Patent EP0634490.
ACCESSION  A42267
VERSION     A42267.1  GI:2297757
KEYWORDS
SOURCE      unidentified.

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ORGANISM     unidentified
              unclassified.
REFERENCE    1 (bases 1 to 18)
AUTHORS      De,B.E., Lahaya,A., Ledoux,P., Amory,A., Detroz,R., Andre,C. and
              Vetter,R.
TITLE        Xylanase derived from a bacillus species, expression vectors for
              such xylanase and other proteins, host organisms therefor and use
              thereof
JOURNAL      Patent: EP 0634490-A 17 18-JAN-1995;
              SOLVAY (BE)
COMMENT      Other publication NZ 260989 950828
              Other publication BR 9402834 950613
              Other publication JP 7067637 950314
              Other publication FI 943389 950116
              Other publication CA 2128050 950116
              Other publication NO 942652 950116
              Other publication AU 6743284 950127
              Other publication GB 2279955 950118.
              Location/Qualifiers
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BASE COUNT   2 a      6 c      7 g      3 t
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Query Match 65.6%; Score 11.8; DB 6; Length 18;
Best Local Similarity 86.7%; Pred. No. 5.8e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGGCCCGGATCCA 15
    |||||
Db 16 CTGGCCCGGATCCA 2

RESULT 16
LOCUS       AR000469/c
DEFINITION Sequence 3 from patent US 5736375.
ACCESSION  AR000469
VERSION     AR000469.1  GI:3963000
KEYWORDS
SOURCE      Unknown.
ORGANISM    unclassified.
REFERENCE    1 (bases 1 to 18)
AUTHORS      Deweer,P. and Amory,A.
TITLE        Expression system for novel pullulanase
JOURNAL      Patent: US 5736375-A 3 07-APR-1998;
              Location/Qualifiers
FEATURES
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              /organism="unknown"
              /db_xref="taxon:32644"
BASE COUNT   2 a      6 c      7 g      3 t
ORIGIN
Query Match 65.6%; Score 11.8; DB 6; Length 18;
Best Local Similarity 86.7%; Pred. No. 5.8e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGGCCCGGATCCA 15
    |||||
Db 16 CTGGCCCGGATCCA 2

RESULT 17
LOCUS       AR044543/c
DEFINITION Sequence 3 from patent US 5817498.
ACCESSION  AR044543
VERSION     AR044543.1  GI:5966008
KEYWORDS
SOURCE      Unknown.
ORGANISM    unclassified.

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REFERENCE 1 (bases 1 to 18)
AUTHORS Deweer, P. and Amory, A.
TITLE Pullulanase producing microorganisms
JOURNAL Patent: US 5817498-A 3 06-OCT-1998;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 2 a 6 c 7 g 3 t
ORIGIN

Query Match 65.6%; Score 11.8; DB 6; Length 18;
Best Local Similarity 86.7%; Pred. No. 5.8e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CTGGCCCCGATCCA 15
16 CTGGCCCGAGAGCCA 2

RESULT 18
AR098234/c 18 bp DNA linear PAT 14-FEB-2001
LOCUS Sequence 3 from patent US 6074854.
DEFINITION AR098234
ACCESSION AR098234
VERSION AR098234.1 GI:12807491
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Deweer, P. and Amory, A.
TITLE Pullulanase, microorganisms which produce it, processes for the preparation of this pullulanase and the uses thereof
JOURNAL Patent: US 6074854-A 3 13-JUN-2000;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 2 a 6 c 7 g 3 t
ORIGIN

Query Match 65.6%; Score 11.8; DB 6; Length 18;
Best Local Similarity 86.7%; Pred. No. 5.8e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CTGGCCCCGATCCA 15
16 CTGGCCCGAGAGCCA 2

RESULT 19
ARI27034/c 18 bp DNA linear PAT 16-MAY-2001
LOCUS Sequence 17 from patent US 6180382.
DEFINITION ARI27034
ACCESSION ARI27034
VERSION ARI27034.1 GI:14113627
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS De Buy, E., Lahaye, A., Ledoux, P., Amory, A., Detroz, R., Andre, C. and Vetter, R.
TITLE Xylanase derived from a bacillus species, expression vectors for such xylanase and other proteins, host organisms therefor and use thereof
JOURNAL Patent: US 6180382-A 17 30-JAN-2001;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 2 a 6 c 7 g 3 t
ORIGIN

Query Match 65.6%; Score 11.8; DB 6; Length 13;

Best Local Similarity 86.7%; Pred. No. 5.8e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CTGGCCCCGATCCA 15
16 CTGGCCCGAGAGCCA 2

RESULT 20
189306/c 18 bp DNA linear PAT 10-AUG-1998
LOCUS Sequence 3 from patent US 5721127.
DEFINITION 189306
ACCESSION 189306
VERSION 189306.1 GI:3409246
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Deweer, P. and Amory, A.
TITLE Pullulanase
JOURNAL Patent: US 5721127-A 3 24-FEB-1998;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 2 a 6 c 7 g 3 t
ORIGIN

Query Match 65.6%; Score 11.8; DB 6; Length 18;
Best Local Similarity 86.7%; Pred. No. 5.8e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CTGGCCCCGATCCA 15
16 CTGGCCCGAGAGCCA 2

RESULT 21
189318/c 18 bp DNA linear PAT 10-AUG-1998
LOCUS Sequence 3 from patent US 5721128.
DEFINITION 189318
ACCESSION 189318
VERSION 189318.1 GI:3409258
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Deweer, P. and Amory, A.
TITLE Process for the production of novel pullulanase
JOURNAL Patent: US 5721128-A 3 24-FEB-1998;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 2 a 6 c 7 g 3 t
ORIGIN

Query Match 65.6%; Score 11.8; DB 6; Length 18;
Best Local Similarity 86.7%; Pred. No. 5.8e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CTGGCCCCGATCCA 15
16 CTGGCCCGAGAGCCA 2

RESULT 22
193614/c 18 bp DNA linear PAT 01-DEC-1998
LOCUS Sequence 3 from patent US 5731174.
DEFINITION 193614
ACCESSION 193614
VERSION 193614.1 GI:3938084
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Demeer, P. and Amory, A.
TITLE Process for the saccharification of starch
JOURNAL Patent: US 5731174-A 3 24-MAR-1998;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
BASE COUNT 2 a 6 c 7 g 3 t
ORIGIN
Query Match 65.6%; Score 11.8; DB 6; Length 18;
Best Local Similarity 86.7%; Pred. No. 5.6e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CTGCGCCCGATCCGA 15
Db 16 CTGCGCCGAGAGCCA 2
RESULT 23
A32651/c 24 bp DNA linear PAT 30-JUL-1996
LOCUS A32651
DEFINITION Synthetic HBBag gene adapter sequence.
ACCESSION A32651
VERSION A32651.1 GI:1567500
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
REFERENCE 1 (bases 1 to 24)
AUTHORS Thoma, H.A.D.
TITLE Peptide comprising hepatitis B surface antigen
JOURNAL Patent: EP 0304578-A 34 01-MAR-1989;
FEATURES Epitec Limited
source 1..24
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 7 a 6 c 5 g 6 t
ORIGIN
Query Match 65.6%; Score 11.8; DB 6; Length 24;
Best Local Similarity 86.7%; Pred. No. 5.6e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TGCGCCCGATCCAG 16
Db 24 TGAGCTCGATCCAG 10
RESULT 24
A32652 24 bp DNA linear PAT 30-JUL-1996
LOCUS A32652
DEFINITION Synthetic HBBag gene adapter sequence.
ACCESSION A32652
VERSION A32652.1 GI:1567501
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
REFERENCE 1 (bases 1 to 24)
AUTHORS Thoma, H.A.D.
TITLE Peptide comprising hepatitis B surface antigen
JOURNAL Patent: EP 0304578-A 35 01-MAR-1989;
FEATURES Epitec Limited
source 1..24
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 5 a 6 c 7 g 6 t

ORIGIN
Query Match 65.6%; Score 11.8; DB 6; Length 24;
Best Local Similarity 86.7%; Pred. No. 5.6e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TGCGCCCGATCCAG 16
Db 5 TGAGCTCGATCCAG 19
RESULT 25
AR097798/c 24 bp DNA linear PAT 14-FEB-2001
LOCUS AR097798
DEFINITION Sequence 25 from patent US 6072049.
ACCESSION AR097798
VERSION AR097798.1 GI:12806528
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Thoma, H.A.
TITLE Hepatitis B surface antigen vaccine
JOURNAL Patent: US 6072049-A 25 06-JUN-2000;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
BASE COUNT 7 a 6 c 5 g 6 t
ORIGIN
Query Match 65.6%; Score 11.8; DB 6; Length 24;
Best Local Similarity 86.7%; Pred. No. 5.6e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TGCGCCCGATCCAG 16
Db 24 TGAGCTCGATCCAG 10
RESULT 26
AR097799 24 bp DNA linear PAT 14-FEB-2001
LOCUS AR097799
DEFINITION Sequence 26 from patent US 6072049.
ACCESSION AR097799
VERSION AR097799.1 GI:12806529
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Thoma, H.A.
TITLE Hepatitis B surface antigen vaccine
JOURNAL Patent: US 6072049-A 26 06-JUN-2000;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
BASE COUNT 5 a 6 c 7 g 6 t
ORIGIN
Query Match 65.6%; Score 11.8; DB 6; Length 24;
Best Local Similarity 86.7%; Pred. No. 5.6e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TGCGCCCGATCCAG 16
Db 5 TGAGCTCGATCCAG 19
RESULT 27
I91779 24 bp DNA linear PAT 01-DEC-1998
LOCUS I91779
DEFINITION Sequence 13 from patent US 5726025.

ACCESSION 191779
 VERSION 191779.1 GI:3936249
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 24)
 AUTHORS Kirschner, M.W., King, R.W. and Peters, J.-M.
 TITLE Assay and reagents for detecting inhibitors of ubiquitin-dependent degradation of cell cycle regulatory proteins
 JOURNAL Patent: US 5726025-A 13 10-MAR-1998;
 FEATURES Location/Qualifiers
 source 1..24
 /organism="unknown"
 BASE COUNT 3 a 7 c 10 g 4 t
 ORIGIN
 Query Match 65.6%; Score 11.8; DB 6; Length 24;
 Best Local Similarity 86.7%; Pred. No. 5.6e+05;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 GCGCCGGATCCAGC 17
 Db 1 GCGCCGGATCCAGC 15
 RESULT 28
 A75774/c 25 bp DNA linear PAT 15-OCT-1999
 LOCUS Sequence 43 from Patent WO9322437.
 DEFINITION A75774
 ACCESSION A75774
 VERSION A75774.1 GI:6065722
 KEYWORDS
 ORGANISM human.
 SOURCE Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 25)
 AUTHORS Franssen, L. and Devos, K.
 TITLE NEW POLYPEPTIDES AND PEPTIDES, NUCLEIC ACIDS CODING FOR THEM, AND THEIR USE IN THE FIELD OF TUMOR THERAPY, INFLAMMATION OR IMMUNOLOGY
 JOURNAL Patent: WO 9322437-A 43 11-NOV-1993;
 INNOGENETICS NV (BE); FRANSSEN LUCIA (BE)
 FEATURES Location/Qualifiers
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 /db_xref="taxon:9606"
 /cell_line="THP-1"
 BASE COUNT 2 a 7 c 11 g 5 t
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 Best Local Similarity 86.7%; Pred. No. 5.5e+05;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 GCGCCGGATCCAGC 18
 Db 17 GCGCCGGATCCAGC 3
 RESULT 29
 AR085110/c 25 bp DNA linear PAT 01-SEP-2000
 LOCUS Sequence 43 from patent US 5981277.
 DEFINITION AR085110
 ACCESSION AR085110
 VERSION AR085110.1 GI:10011881
 KEYWORDS
 ORGANISM Unknown.
 SOURCE Unknown.
 REFERENCE 1 (bases 1 to 25)
 AUTHORS Franssen, L., Devos, K., Van De Voorde, A. and Van Heuverswyn, H.
 TITLE Polypeptides and peptides, nucleic acids coding for them, and their

use in the field of tumor therapy, inflammation or immunology
 JOURNAL Patent: US 5981277-A 43 09-NOV-1999;
 FEATURES Location/Qualifiers
 source 1..25
 /organism="unknown"
 BASE COUNT 2 a 7 c 11 g 5 t
 ORIGIN
 Query Match 65.6%; Score 11.8; DB 6; Length 25;
 Best Local Similarity 86.7%; Pred. No. 5.5e+05;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 GCGCCGGATCCAGC 18
 Db 17 GCGCCGGATCCAGC 3
 RESULT 30
 AX322593/c 19 bp DNA linear PAT 07-JUN-2002
 LOCUS Sequence 54 from Patent WO0192539.
 DEFINITION AX322593
 ACCESSION AX322593
 VERSION AX322593.1 GI:18093613
 KEYWORDS
 ORGANISM synthetic construct.
 SOURCE synthetic construct.
 ORGANISM artificial sequences.
 REFERENCE 1
 AUTHORS Ben-Bassat, A., Cattermole, M., Gatenby, A.A., Gibson, K.J.,
 Ramos-Gonzales, M.I., Ramos, D.L. and Sarislan, S.
 TITLE Method for the production of p-hydroxybenzoate in species of
 Pseudomonas and Agrobacterium
 JOURNAL Patent: WO 0192539-A 54 06-DEC-2001;
 E.I. DUPONT DE NEMOURS AND COMPANY, Legal Patent Records Center
 (US)
 FEATURES Location/Qualifiers
 source 1..19
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="primer-primer used for sequencing pcu"
 BASE COUNT 2 a 5 c 5 t
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 Query Match 64.4%; Score 11.6; DB 6; Length 19;
 Best Local Similarity 77.8%; Pred. No. 7.1e+05;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CTGGCCCGGATCCAGC 18
 Db 18 CAGCACCCGATCCAGC 1
 RESULT 31
 AR021129/c 21 bp DNA linear PAT 05-DEC-1998
 LOCUS Sequence 23 from patent US 5789248.
 DEFINITION AR021129
 ACCESSION AR021129
 VERSION AR021129.1 GI:3975744
 KEYWORDS
 ORGANISM Unknown.
 SOURCE Unknown.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Federad, O., Hovig, E., Engedraaten, O., Maelandsmo, G. and Agrawal, S.
 TITLE CAPL-specific oligonucleotides and method of inhibiting metastatic cancer
 JOURNAL Patent: US 5789248-A 23 04-AUG-1998;
 FEATURES Location/Qualifiers
 source 1..21
 /organism="unknown"
 BASE COUNT 5 a 3 c 10 g 3 t
 ORIGIN

Query Match 64.4%; Score 11.6; DB 6; Length 21;
Best Local Similarity 77.8%; Pred. No. 7e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CTGGCGCCGATCCAGGC 18
DB 18 CTGCTCCGAGATCCGAC 1

RESULT 32
LOCUS AX404361 21 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 187 from Patent WO0224747.
ACCESSION AX404361
VERSION AX404361.1 GI:21437642
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Brinkmann, U. and Hoffmeyer, S.
TITLE Polymorphisms in human genes of cardiovascular regulators and their use in diagnostic and therapeutic applications
JOURNAL Patent: WO 0224747-A 187 28-MAR-2002;
Epidaurus Biotechnology AG (DE)
FEATURES
source 1..21
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="artificial sequence"

BASE COUNT 6 a 3 c 9 g 3 t
ORIGIN

Query Match 64.4%; Score 11.6; DB 6; Length 21;
Best Local Similarity 77.8%; Pred. No. 7e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CTGGCGCCGATCCAGGC 18
DB 20 CTTCGCCAGATCCAGC 3

RESULT 33
LOCUS AX404362 21 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 188 from Patent WO0224747.
ACCESSION AX404362
VERSION AX404362.1 GI:21437643
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Brinkmann, U. and Hoffmeyer, S.
TITLE Polymorphisms in human genes of cardiovascular regulators and their use in diagnostic and therapeutic applications
JOURNAL Patent: WO 0224747-A 188 28-MAR-2002;
Epidaurus Biotechnology AG (DE)
FEATURES
source 1..21
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="artificial sequence"

BASE COUNT 3 a 9 c 3 g 6 t
ORIGIN

Query Match 64.4%; Score 11.6; DB 6; Length 21;
Best Local Similarity 77.8%; Pred. No. 7e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CTGGCGCCGATCCAGGC 18
DB 2 CTTCGCCAGATCCAGC 19

RESULT 34
LOCUS AX404365 21 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 191 from Patent WO0224747.
ACCESSION AX404365
VERSION AX404365.1 GI:21437646
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Brinkmann, U. and Hoffmeyer, S.
TITLE Polymorphisms in human genes of cardiovascular regulators and their use in diagnostic and therapeutic applications
JOURNAL Patent: WO 0224747-A 191 28-MAR-2002;
Epidaurus Biotechnology AG (DE)
FEATURES
source 1..21
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="artificial sequence"

BASE COUNT 5 a 3 c 10 g 3 t
ORIGIN

Query Match 64.4%; Score 11.6; DB 6; Length 21;
Best Local Similarity 77.8%; Pred. No. 7e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CTGGCGCCGATCCAGGC 18
DB 20 CTTCGCCAGATCCAGC 3

RESULT 35
LOCUS AX404366 21 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 192 from Patent WO0224747.
ACCESSION AX404366
VERSION AX404366.1 GI:21437647
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Brinkmann, U. and Hoffmeyer, S.
TITLE Polymorphisms in human genes of cardiovascular regulators and their use in diagnostic and therapeutic applications
JOURNAL Patent: WO 0224747-A 192 28-MAR-2002;
Epidaurus Biotechnology AG (DE)
FEATURES
source 1..21
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="artificial sequence"

BASE COUNT 3 a 10 c 3 g 5 t
ORIGIN

Query Match 64.4%; Score 11.6; DB 6; Length 21;
Best Local Similarity 77.8%; Pred. No. 7e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CTGGCGCCGATCCAGGC 18
DB 2 CTTCGCCAGATCCAGC 19

RESULT 36
LOCUS AR021109 22 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 3 from patent US 5769248.
ACCESSION AR021109

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VERSION      AR021109.1  GI:3975724
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 22)
AUTHORS     Foderstad,O., Hovig,E., Engebraaten,O., Maelandsmo,G. and Agrawal,S.
TITLE       CAPL-specific oligonucleotides and method of inhibiting metastatic
            cancer
JOURNAL     Patent: US 5789248-A 3 04-AUG-1998;
FEATURES
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BASE COUNT  5 a          3 c          11 g          3 t
ORIGIN
Query Match 64.4%; Score 11.6; DB 6; Length 22;
Best Local Similarity 77.8%; Pred. No. 6.9e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Cy          1 CTGGCGCCCGATCCAGGC 18
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Db          18 CTGCTCCAGATCCTGAC 1

RESULT 37
LOCUS       AR021110
DEFINITION Sequence 4 from patent US 5789248.
ACCESSION  AR021110
VERSION     AR021110.1  GI:3975725
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 22)
AUTHORS     Foderstad,O., Hovig,E., Engebraaten,O., Maelandsmo,G. and Agrawal,S.
TITLE       CAPL-specific oligonucleotides and method of inhibiting metastatic
            cancer
JOURNAL     Patent: US 5789248-A 4 04-AUG-1998;
FEATURES
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BASE COUNT  5 a          3 c          11 g          3 t
ORIGIN
Query Match 64.4%; Score 11.6; DB 6; Length 22;
Best Local Similarity 77.8%; Pred. No. 6.9e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Cy          1 CTGGCGCCCGATCCAGGC 18
            |||||
Db          18 CTGCTCCAGATCCTGAC 1

RESULT 38
LOCUS       AR036253/c
DEFINITION Sequence 3 from patent US 5872007.
ACCESSION  AR036253
VERSION     AR036253.1  GI:5952921
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 22)
AUTHORS     Foderstad,O., Hovig,E., Engebraaten,O., Maelandsmo,G. and Agrawal,S.
TITLE       CAPL-specific oligonucleotides and methods of inhibiting metastatic
            cancer
JOURNAL     Patent: US 5872007-A 3 16-FEB-1999;
FEATURES
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BASE COUNT  5 a          3 c          11 g          3 t
ORIGIN
Query Match 64.4%; Score 11.6; DB 6; Length 22;
Best Local Similarity 77.8%; Pred. No. 6.9e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Cy          1 CTGGCGCCCGATCCAGGC 18
            |||||
Db          18 CTGCTCCAGATCCTGAC 1

RESULT 39
LOCUS       AR036254
DEFINITION Sequence 4 from patent US 5872007.
ACCESSION  AR036254
VERSION     AR036254.1  GI:5952922
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 22)
AUTHORS     Foderstad,O., Hovig,E., Engebraaten,O., Maelandsmo,G. and Agrawal,S.
TITLE       CAPL-specific oligonucleotides and methods of inhibiting metastatic
            cancer
JOURNAL     Patent: US 5872007-A 4 16-FEB-1999;
FEATURES
source      1..22
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BASE COUNT  5 a          3 c          11 g          3 t
ORIGIN
Query Match 64.4%; Score 11.6; DB 6; Length 22;
Best Local Similarity 77.8%; Pred. No. 6.9e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Cy          1 CTGGCGCCCGATCCAGGC 18
            |||||
Db          18 CTGCTCCAGATCCTGAC 1

RESULT 40
LOCUS       AX031299/c
DEFINITION Sequence 21 from Patent WO9914321.
ACCESSION  AX031299
VERSION     AX031299.1  GI:10278627
KEYWORDS
SOURCE      unidentified.
ORGANISM    unidentified.
REFERENCE    1 (bases 1 to 24)
AUTHORS     O'Reilly,L., Puthalakath,H., Adams,J., O'Connor,L., Cory,S.,
            Huang,D.C. and Strasser,A.
TITLE       Novel therapeutic molecules
JOURNAL     Patent: WO 9914321-A 21 25-MAR-1999;
            INST MEDICAL W & B HALL (AU) ; PUTHALAKATH HANSA (AU) ; REILLY
            LORRAINE O (AU) ; ADAMS JERRY (AU) ; CONNOR LIAM O (AU) ; CORY
            SUZANNE (AU) ; HUANG DAVID C S (AU) ; STRASSER ANDREAS (AU)
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source      1..24
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            /db_xref="taxon:32644"
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ORIGIN
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Best Local Similarity 77.8%; Pred. No. 6.9e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Cy          1 CTGGCGCCCGATCCAGGC 18
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Db 18 CTGCGCCGGAAGCTTGC 1

Search completed: June 7, 2003, 08:51:19
Job time : 406.418 secs

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OM nucleic - nucleic search, using sw model

Run on: June 7, 2003, 08:05:49 / Search time 1030.58 Seconds

(without alignments)
282.868 Million cell updates/sec

Title: US-10-080-959A-5

Sequence: 1 ctgcgcgccgacccagc 18

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 18144

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
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8: em_hic:*
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16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
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23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	11.2	52.2	23 13 BM394673	BM394673 50072-2-5
2	10.6	58.9	23 13 BM394673	BM394673 50072-2-5
3	10.6	58.9	24 17 AZ634834	AZ634834 1M0490C19
4	10.4	57.8	23 17 AZ648503	AZ648503 2M0149H02
5	10	55.6	19 17 AZ685545	AZ685545 2M0159F09
6	10	55.6	21 17 AZ791884	AZ791884 2M043A02

C	7	9.6	53.3	20 17 AZ591658	AZ591658 1M040F19
C	8	9.6	53.3	21 17 AZ305158	AZ305158 1M0005K11
C	9	9.6	53.3	21 17 AZ834643	AZ834643 2M0117N24
C	10	9.6	53.3	24 17 AZ487506	AZ487506 1M0317P10
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C	21	8.6	47.8	23 13 BM395601	BM395601 5009-0-11
C	22	8.6	47.8	23 17 AZ410218	AZ410218 1M0182F23
C	23	8.6	47.8	23 17 AZ979817	AZ979817 2M0256F09
C	24	8.6	47.8	24 13 BM397860	BM397860 5009-0-38
C	25	8.6	47.8	24 17 TA368A07P	TA368A07P
C	26	8.6	47.8	25 14 L32061	L32061 HMXCP8D18.H
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C	28	8.4	46.7	19 17 AZ858446	AZ858446 2M0163D08
C	29	8.4	46.7	19 17 AZ858446	AZ858446 2M0163D08
C	30	8.4	46.7	20 17 AZ628022	AZ628022 1M0476A13
C	31	8.4	46.7	31 17 AZ657644	AZ657644 1M0534B02
C	32	8.4	46.7	20 17 AZ961140	AZ961140 2M0229P20
C	33	8.4	46.7	22 9 AA989077	AA989077 0788E03.8
C	34	8.4	46.7	22 9 A1086217	A1086217 0W90D12.8
C	35	8.4	46.7	25 9 AA878803	AA878803 0E86E04.8
C	36	8.4	46.7	25 9 A1119586	A1119586 c275A01.x
C	37	8.4	46.7	25 9 A1913416	A1913416 t277A09.x
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C	40	8.2	45.6	17 13 BM394186	BM394186 50072-2-2
C	41	8.2	45.6	19 13 BM394390	BM394390 50072-2-3
C	42	8.2	45.6	20 13 BM394004	BM394004 50072-2-1
C	43	8.2	45.6	20 17 AZ626475	AZ626475 1M0466B18
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C	54	8.2	45.6	23 17 AZ470337	AZ470337 1M0284D21
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C	57	8.2	45.6	24 17 AZ691546	AZ691546 2M0275O13
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C	67	8.2	44.4	20 17 AZ314365	AZ314365 1M0031G07
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C	71	8.2	44.4	22 17 AZ827350	AZ827350 2M0103C13
C	72	8.2	44.4	22 17 AZ976250	AZ976250 2M0251B10
C	73	8.2	44.4	23 17 AZ307616	AZ307616 1M0009H17
C	74	8.2	44.4	23 17 AZ629620	AZ629620 1M0482B14
C	75	8.2	44.4	24 17 AZ833999	AZ833999 2M016N24
C	76	8.2	44.4	24 13 BM395502	BM395502 50072-2-9
C	77	8.2	44.4	24 17 AZ309247	AZ309247 1M0031J14
C	78	8.2	44.4	25 9 A1206423	A1206423 q922h05.x
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C 81	7.8	43.3	19	17	A2444046	AZ444046	154	7.4	41.1	23	17	A2305600	A2305600	IM0006A19
C 82	7.8	43.3	20	17	AZ501483	IM0419H15	155	7.4	41.1	23	17	A2456925	A2456925	IM0260J06
C 83	7.8	43.3	20	17	AZ657644	IM0534B02	156	7.4	41.1	23	17	A2463102	A2463102	IM0271A15
C 84	7.8	43.3	21	17	AZ309721	IM0016P14	157	7.4	41.1	23	17	A2593454	A2593454	IM0405C03
C 85	7.8	43.3	22	17	AZ512467	IM0535B01	158	7.4	41.1	23	17	A2629873	A2629873	IM0483E10
C 86	7.8	43.3	23	17	AU256828	AU256828	159	7.4	41.1	23	17	A2639181	A2639181	IM0499D03
C 87	7.8	43.3	23	17	TA167D03P	TA167D03P	160	7.4	41.1	23	17	A2761953	A2761953	IM0556K06
C 88	7.8	43.3	24	17	A2324350	IM0046P14	161	7.4	41.1	23	17	A2785457	A2785457	2M0029A24
C 89	7.8	43.3	24	17	AZ248114	IM0210A01	162	7.4	41.1	23	17	A2848503	A2848503	2M0149H02
C 90	7.8	43.3	25	17	AZ813332	2M0080N04	163	7.4	41.1	24	9	AU257684	AU257684	AU257684
C 91	7.8	43.3	25	17	AZ772000	IM0547A06	164	7.4	41.1	24	9	AU258060	AU258060	AU258060
C 92	7.8	43.3	25	17	AZ810739	2M0076C02	165	7.4	41.1	24	17	A2446206	A2446206	IM0242I06
C 93	7.6	42.2	19	9	AI476315	AI476315	166	7.4	41.1	24	17	A2777167	A2777167	2M0011H19
C 94	7.6	42.2	19	17	AZ478277	IM0298B16	167	7.4	41.1	24	17	A2777167	A2777167	2M0011H19
C 95	7.6	42.2	19	17	AZ482050	IM0306H20	168	7.4	41.1	24	17	A2779051	A2779051	2M0014H20
C 96	7.6	42.2	19	17	AZ768918	IM0569F08	169	7.4	41.1	24	17	A2787029	A2787029	2M0032C23
C 97	7.6	42.2	20	17	AZ468517	IM0281N01	170	7.4	41.1	25	9	A2857110	A2857110	2M0161I24
C 98	7.6	42.2	20	17	AZ619289	IM0451M06	171	7.4	41.1	25	9	AA993070	AA993070	0001606.g
C 99	7.6	42.2	20	17	AZ809652	2M0073D18	172	7.4	41.1	25	9	AI620280	AI620280	0001606.g
C 100	7.6	42.2	21	17	AZ367152	IM0116M07	173	7.4	41.1	25	14	AA592718	AA592718	0029C12.f
C 101	7.6	42.2	22	9	AA879236	AA879236	174	7.4	41.1	25	17	W10809	W10809	0029C12.f
C 102	7.6	42.2	22	9	AA904202	AA904202	175	7.4	41.1	25	17	A2471181	A2471181	IM0285H11
C 103	7.6	42.2	22	9	AI708898	AI708898	176	7.4	41.1	25	17	A2606311	A2606311	IM0428G09
C 104	7.6	42.2	22	17	AZ659094	AZ659094	177	7.4	41.1	25	17	A2689660	A2689660	IM0569C07
C 105	7.6	42.2	22	17	AZ805989	2M0067C13	178	7.4	41.1	25	17	A2818242	A2818242	2M0088G12
C 106	7.6	42.2	22	17	AZ828017	2M0104H18	179	7.4	41.1	25	17	A2869367	A2869367	2M0181P03
C 107	7.6	42.2	22	17	TA1476B09P	TA1476B09P	180	7.2	40.0	13	13	BH790171	BH790171	SALK_0546
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C 110	7.6	42.2	23	13	AZ658085	IM0543J07	183	7.2	40.0	15	13	BM400586	BM400586	5009-0-0-76
C 111	7.6	42.2	23	17	AZ784767	2M0027P17	184	7.2	40.0	16	13	BM396817	BM396817	5009-0-0-45
C 112	7.6	42.2	23	17	AZ806883	2M0069B15	185	7.2	40.0	16	13	BM396718	BM396718	5009-0-0-24
C 113	7.6	42.2	24	17	AZ307544	IM0009H20	186	7.2	40.0	16	13	BM398358	BM398358	5009-0-0-45
C 114	7.6	42.2	24	17	AZ373306	IM0225D03	187	7.2	40.0	16	13	BM399771	BM399771	5009-0-0-61
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C 116	7.6	42.2	24	17	TA281E01P	TA281E01P	189	7.2	40.0	17	13	BM398023	BM398023	5009-0-0-4-
C 117	7.6	42.2	24	17	TA281E01P	TA281E01P	190	7.2	40.0	17	13	BM398024	BM398024	5009-0-0-4-
C 118	7.6	42.2	25	9	AA953687	AA953687	191	7.2	40.0	17	13	BM399768	BM399768	5009-0-0-61
C 119	7.6	42.2	25	9	AI1354591	AI1354591	192	7.2	40.0	18	13	BM396090	BM396090	5009-0-0-17
C 120	7.6	42.2	25	9	AI1359242	AI1359242	193	7.2	40.0	19	9	AA328295	AA328295	0160E07.g
C 121	7.6	42.2	25	9	AI1471126	AI1471126	194	7.2	40.0	19	17	AZ493714	AZ493714	IM0337J05
C 122	7.6	42.2	25	12	BF006798	BF006798	195	7.2	40.0	19	17	AZ5857450	AZ5857450	2M0162E17
C 123	7.6	42.2	25	14	BQ121142	BQ121142	196	7.2	40.0	20	14	D20001	D20001	HUMGS00971
C 124	7.6	42.2	25	14	AZ391369	IM0153K24	197	7.2	40.0	20	17	A2628022	A2628022	IM0476A13
C 125	7.6	42.2	25	17	AZ410566	IM0183E11	198	7.2	40.0	20	17	AZ789022	AZ789022	IM0397J05
C 126	7.6	42.2	25	17	AZ486714	IM0314J19	199	7.2	40.0	20	17	TA305802P	TA305802P	IM0397J05
C 127	7.6	42.2	25	17	AZ503541	IM0333A22	200	7.2	40.0	20	17	AU256378	AU256378	IM056378
C 128	7.6	42.2	25	17	AZ598912	IM0413P24	201	7.2	40.0	21	13	BM399017	BM399017	5009-0-0-51
C 129	7.6	42.2	25	17	AZ807246	2M0069N20	202	7.2	40.0	21	13	BM400884	BM400884	5009-0-0-6-
C 130	7.6	42.2	25	17	AZ968720	2M0241M10	203	7.2	40.0	21	17	AZ4307451	AZ4307451	IM0290E09
C 131	7.6	42.2	25	17	BM395358	50072-2-8	204	7.2	40.0	21	17	AZ474246	AZ474246	IM0290L08
C 132	7.6	42.2	25	17	HSM007775	HSM007775	205	7.2	40.0	21	17	AZ768059	AZ768059	IM0567302
C 133	7.6	42.2	25	17	HSM007775	HSM007775	206	7.2	40.0	21	17	AZ791884	AZ791884	2M00643A02
C 134	7.6	42.2	25	17	HSM007775	HSM007775	207	7.2	40.0	21	17	AZ791884	AZ791884	2M00643A02
C 135	7.6	42.2	25	17	AZ480102	IM0301A20	208	7.2	40.0	21	17	AZ803575	AZ803575	2M0064K04
C 136	7.6	42.2	25	17	AZ484303	IM0310K12	209	7.2	40.0	22	9	AA903686	AA903686	0K54901.g
C 137	7.6	42.2	25	17	AZ826361	2M0102H04	210	7.2	40.0	22	9	AI019069	AI019069	0018E10.x
C 138	7.6	42.2	25	17	AZ833844	2M0116C07	211	7.2	40.0	22	9	AI086217	AI086217	0000412.g
C 139	7.6	42.2	25	17	AU255294	AU255294	212	7.2	40.0	22	9	AI138264	AI138264	0003D12.x
C 140	7.6	42.2	25	17	AZ772893	IM0584D09	213	7.2	40.0	22	9	AI138264	AI138264	0003D12.x
C 141	7.6	42.2	25	17	AZ820516	2M0092C08	214	7.2	40.0	22	13	BM399045	BM399045	5009-0-0-52
C 142	7.6	42.2	25	17	AZ949545	2M0213E19	215	7.2	40.0	22	13	BM400176	BM400176	5009-0-0-68
C 143	7.6	42.2	25	17	BF984995	602287G05	216	7.2	40.0	22	14	D19582	D19582	MUGS00989
C 144	7.6	42.2	25	17	AZ405188	IM0173G15	217	7.2	40.0	22	17	AZ451708	AZ451708	IM0251P07
C 145	7.6	42.2	25	17	AZ460367	IM0265J10	218	7.2	40.0	22	17	AZ51708	AZ51708	IM0251P07
C 146	7.6	42.2	25	17	AI080445	0X82D10.8	219	7.2	40.0	22	17	AZ602332	AZ602332	IM0421I04
C 147	7.6	42.2	25	17	AI429547	mp22f03.x	220	7.2	40.0	22	17	AZ602332	AZ602332	IM0421I04
C 148	7.6	42.2	25	17	AI664440	ue62C03.x	221	7.2	40.0	23	13	BM399350	BM399350	5009-0-0-56
C 149	7.6	42.2	25	17	AI682443	wc53D06.x	222	7.2	40.0	23	17	AZ450598	AZ450598	IM0249H23
C 150	7.6	42.2	25	17	AI708898	aa86h07.f	223	7.2	40.0	23	17	AZ472899	AZ472899	IM0288L22
C 151	7.6	42.2	25	17	AZ442571	IM023611x	224	7.2	40.0	23	17	AZ610143	AZ610143	IM0435H17
C 152	7.6	42.2	25	17	AZ801946	2M0060E07	225	7.2	40.0	23	17	AZ761953	AZ761953	IM0556K06

C 226	7.2	40.0	23	17	AZ827973	AZ827973 2M0104P11	C 239	7	38.9	24	17	AZ314246	AZ314246 1M0031A01
C 227	7.2	40.0	23	17	AZ833999	AZ833999 2M0116N24	C 300	7	38.9	24	17	AZ328881	AZ328881 1M0052D20
C 228	7.2	40.0	23	17	TA151A11P	TA151A11P T. brucei	C 301	7	38.9	24	17	AZ43047	AZ43047 1M0237105
C 229	7.2	40.0	24	17	AZ402579	AZ402579 1M0169L21	C 302	7	38.9	24	17	AZ447201	AZ447201 1M0244D12
C 230	7.2	40.0	24	17	AZ834292	AZ834292 2M0116M23	C 303	7	38.9	24	17	AZ455814	AZ455814 1M0258B21
C 231	7.2	40.0	24	17	TA120F02P	TA120F02P T. brucei	C 304	7	38.9	24	17	AZ480758	AZ480758 1M0302G04
C 232	7.2	40.0	24	17	TA256H01Q	TA256H01Q T. brucei	C 305	7	38.9	24	17	AZ505483	AZ505483 1M0346M07
C 233	7.2	40.0	25	9	AA933337	AA933337 0144607.8	C 306	7	38.9	24	17	AZ762096	AZ762096 1M0556J18
C 234	7.2	40.0	25	9	AA970868	AA970868 0P1312.8	C 307	7	38.9	24	17	TA110D11P	TA110D11P T. brucei
C 235	7.2	40.0	25	9	AA119305	AA119305 0P72C06.x	C 308	7	38.9	25	9	AA921614	AA921614 1M021D09.T
C 236	7.2	40.0	25	9	AA1155015	AA1155015 0P72C06.x	C 309	7	38.9	25	9	AA926871	AA926871 0155C11.8
C 237	7.2	40.0	25	9	AA139242	AA139242 153H12.x	C 310	7	38.9	25	9	AA1002379	AA1002379 0Q87F02.8
C 238	7.2	40.0	25	9	AA159790	AA159790 0P04G06.x	C 311	7	38.9	25	9	AA149305	AA149305 0P72C06.x
C 239	7.2	40.0	25	9	AA160869	AA160869 0P26B02.x	C 312	7	38.9	25	9	AA1287253	AA1287253 0P06D12.x
C 240	7.2	40.0	25	9	AA172068	AA172068 0P70G12.x	C 313	7	38.9	25	9	AA1443365	AA1443365 0A31810.x
C 241	7.2	40.0	25	12	BF006798	BF006798 1160571.A	C 314	7	38.9	25	9	AA1458062	AA1458062 0P64C05.x
C 242	7.2	40.0	25	13	BM396165	BM396165 5009-0-18	C 315	7	38.9	25	9	AA1471126	AA1471126 0P90E05.x
C 243	7.2	40.0	25	13	BM399506	BM399506 5009-0-58	C 316	7	38.9	25	9	AA1624477	AA1624477 0P68E04.x
C 244	7.2	40.0	25	13	BM400776	BM400776 5009-0-79	C 317	7	38.9	25	9	AA1689424	AA1689424 0P83H02.x
C 245	7.2	40.0	25	17	AA025569	AA025569 0P(X)1654	C 318	7	38.9	25	9	AA1762402	AA1762402 0P65E10.x
C 246	7.2	40.0	25	17	AA2584819	AA2584819 1M0389A13	C 319	7	38.9	25	9	AA1256438	AA1256438 0P259472
C 247	7.2	40.0	25	17	AA2799437	AA2799437 2M0015B20	C 320	7	38.9	25	9	AA1259472	AA1259472 0P259472
C 248	7.2	40.0	25	17	AA2869367	AA2869367 2M0181P03	C 321	7	38.9	25	10	AA1246315	AA1246315 2821832.5
C 249	7.2	40.0	25	17	TA274G11Q	TA274G11Q HOA59-1-C	C 322	7	38.9	25	14	H30582	H30582 0P124612.r1
C 250	7.2	38.9	19	12	BC896949	BC896949 HOA59-1-C	C 323	7	38.9	25	14	N32966	N32966 0P10H07.81
C 251	7.2	38.9	19	17	AA2307686	AA2307686 1M0009B05	C 324	7	38.9	25	17	AA025268	AA025268 0P(3)3087
C 252	7.2	38.9	19	17	AA2323681	AA2323681 1M0045E13	C 325	7	38.9	25	17	AA2309210	AA2309210 1M0013P16
C 253	7.2	38.9	19	17	AA2372854	AA2372854 1M0124G22	C 326	7	38.9	25	17	AA2309210	AA2309210 1M0013P16
C 254	7.2	38.9	19	17	AA2410317	AA2410317 1M0182L02	C 327	7	38.9	25	17	AA2492371	AA2492371 1M0326P23
C 255	7.2	38.9	19	17	AA2441505	AA2441505 1M0233M13	C 328	7	38.9	25	17	AA2689384	AA2689384 2M0181C08
C 256	7.2	38.9	20	14	BO901238	BO901238 0P0002X4	C 329	7	38.9	25	17	BH740827	BH740827 0P04S06-5
C 257	7.2	38.9	20	14	BO901239	BO901239 0P0002X4	C 330	7	38.9	25	17	BH790171	BH790171 0P04S06-5
C 258	7.2	38.9	20	17	AA2308311	AA2308311 1M0011J12	C 331	7	38.9	25	17	BH840574	BH840574 0P04S06-5
C 259	7.2	38.9	20	17	AA2308311	AA2308311 1M0011J12	C 332	7	38.9	25	17	TA130E11P	TA130E11P T. brucei
C 260	7.2	38.9	20	17	AA2600447	AA2600447 1M0418H15	C 333	6.8	37.8	12	13	BM397357	BM397357 5009-0-31
C 261	7.2	38.9	20	17	AA2637794	AA2637794 1M0497D03	C 334	6.8	37.8	16	9	AA162040	AA162040 0P24A08.x
C 262	7.2	38.9	20	17	AA2662848	AA2662848 1M0542K07	C 335	6.8	37.8	16	13	AA1560058	AA1560058 0P38H11.x
C 263	7.2	38.9	20	17	AA2764505	AA2764505 1M0560M06	C 336	6.8	37.8	19	9	AA1885444	AA1885444 0P04S06-5
C 264	7.2	38.9	20	17	AA2764505	AA2764505 1M0560M06	C 337	6.8	37.8	19	9	AA1885444	AA1885444 0P04S06-5
C 265	7.2	38.9	20	17	AA2782314	AA2782314 2M0022D03	C 338	6.8	37.8	19	17	AA2345964	AA2345964 1M0081D01
C 266	7.2	38.9	20	17	AA2782314	AA2782314 2M0022D03	C 339	6.8	37.8	19	17	AA2480113	AA2480113 1M0301P20
C 267	7.2	38.9	20	17	AA2816586	AA2816586 2M0085H02	C 340	6.8	37.8	19	17	AA2763411	AA2763411 1M0558B24
C 268	7.2	38.9	20	17	AA2858804	AA2858804 2M0164P10	C 341	6.8	37.8	19	17	AA2803756	AA2803756 2M0064M15
C 269	7.2	38.9	21	17	AA2307451	AA2307451 1M0009B09	C 342	6.8	37.8	19	17	AA2821649	AA2821649 2M0094E05
C 270	7.2	38.9	21	17	AA2307929	AA2307929 1M0010P24	C 343	6.8	37.8	19	17	AA2948421	AA2948421 2M0211A01
C 271	7.2	38.9	21	17	AA2309714	AA2309714 1M0016M18	C 344	6.8	37.8	20	9	AA1695159	AA1695159 0P04S06-5
C 272	7.2	38.9	21	17	AA2341831	AA2341831 1M0074D02	C 345	6.8	37.8	20	17	AA2307483	AA2307483 1M0009P10
C 273	7.2	38.9	21	17	AA2405135	AA2405135 1M0173D14	C 346	6.8	37.8	20	17	AA2346745	AA2346745 1M0082D09
C 274	7.2	38.9	21	17	AA2420773	AA2420773 1M0198E18	C 347	6.8	37.8	20	17	AA2359918	AA2359918 1M0103A01
C 275	7.2	38.9	21	17	AA2607907	AA2607907 1M0430A12	C 348	6.8	37.8	20	17	AA2386570	AA2386570 1M0145C08
C 276	7.2	38.9	21	17	AA2816100	AA2816100 2M0084M11	C 349	6.8	37.8	20	17	AA2588120	AA2588120 1M0396A12
C 277	7.2	38.9	21	17	AA2838415	AA2838415 2M0134A10	C 350	6.8	37.8	20	17	AA2802218	AA2802218 2M0060J19
C 278	7.2	38.9	21	17	AA2956040	AA2956040 2M0222D02	C 351	6.8	37.8	20	17	AA2810573	AA2810573 2M0076K11
C 279	7.2	38.9	21	17	AA2981459	AA2981459 2M0258G21	C 352	6.8	37.8	20	17	AA2823598	AA2823598 2M0097B08
C 280	7.2	38.9	22	9	AA1444134	AA1444134 0P44A01.Y	C 353	6.8	37.8	20	17	AA18000404	AA18000404 2M0288A18
C 281	7.2	38.9	22	13	BM398650	BM398650 5009-0-48	C 354	6.8	37.8	20	17	AA18000404	AA18000404 2M0288A18
C 282	7.2	38.9	22	17	AA2425344	AA2425344 1M0205G19	C 355	6.8	37.8	21	10	AA1250310	AA1250310 2822017.5
C 283	7.2	38.9	22	17	AA2660257	AA2660257 1M0538F13	C 356	6.8	37.8	21	17	AA2305158	AA2305158 1M0005K11
C 284	7.2	38.9	22	17	AA2796591	AA2796591 2M0052G19	C 357	6.8	37.8	21	17	AA2313684	AA2313684 1M0030D08
C 285	7.2	38.9	22	17	AA455010	AA455010 T. brucei	C 358	6.8	37.8	21	17	AA2341757	AA2341757 1M0074P18
C 286	7.2	38.9	23	17	AA2307822	AA2307822 1M0010J11	C 359	6.8	37.8	21	17	AA2367152	AA2367152 1M0116M07
C 287	7.2	38.9	23	17	AA2336293	AA2336293 1M0066E02	C 360	6.8	37.8	21	17	AA2478651	AA2478651 1M0298E23
C 288	7.2	38.9	23	17	AA2433764	AA2433764 1M0219L14	C 361	6.8	37.8	21	17	AA2780316	AA2780316 2M0017J02
C 289	7.2	38.9	23	17	AA2448352	AA2448352 1M0246A06	C 362	6.8	37.8	21	17	AA2794033	AA2794033 2M0047D12
C 290	7.2	38.9	23	17	AA2781493	AA2781493 2M0019N20	C 363	6.8	37.8	21	17	AA2838415	AA2838415 2M0134A10
C 291	7.2	38.9	23	17	AA2819130	AA2819130 2M0089C03	C 364	6.8	37.8	21	17	AA2862607	AA2862607 2M0170C23
C 292	7.2	38.9	23	17	AA2822965	AA2822965 2M0096L11	C 365	6.8	37.8	21	17	AA2945150	AA2945150 2M0206P19
C 293	7.2	38.9	23	17	AA2869816	AA2869816 2M0182N06	C 366	6.8	37.8	22	9	AA1953755	AA1953755 0P04S06-5
C 294	7.2	38.9	23	17	AA2954677	AA2954677 2M0220C24	C 367	6.8	37.8	22	9	AA1174110	AA1174110 0P04S06-5
C 295	7.2	38.9	23	17	AA2954677	AA2954677 2M0220C24	C 368	6.8	37.8	22	9	AA1352536	AA1352536 0P04S06-5
C 296	7.2	38.9	23	17	AA2954677	AA2954677 2M0220C24	C 369	6.8	37.8	22	9	AA1352536	AA1352536 0P04S06-5
C 297	7.2	38.9	23	17	AA2954677	AA2954677 2M0220C24	C 370	6.8	37.8	22	13	AA1352536	AA1352536 0P04S06-5
C 298	7.2	38.9	24	10	AA1059812	AA1059812 0P701.Y9	C 371	6.8	37.8	22	13	AA1352536	AA1352536 0P04S06-5

372	6.8	37.8	22	17	AZ030912	AZ030912	1M0017P15	C 445	6.6	36.7	20	17	AZ659612	AZ659612	1M0537A07
373	6.8	37.8	22	17	AZ584779	AZ584779	1M0389112	C 446	6.6	36.7	20	17	AZ773092	AZ773092	1M0584K20
374	6.8	37.8	22	17	AZ788996	AZ788996	2M0036O22	C 447	6.6	36.7	20	17	AZ789755	AZ789755	2M0037O13
375	6.8	37.8	22	17	AZ984502	AZ984502	2M0265U05	C 448	6.6	36.7	20	17	AZ810573	AZ810573	2M0076K11
376	6.8	37.8	22	10	AM247451	AM247451	2819438.5	C 449	6.6	36.7	20	17	AZ832127	AZ832127	2M0112M17
377	6.8	37.8	23	17	AZ309657	AZ309657	1M0016C24	C 450	6.6	36.7	21	9	AL585450	AL585450	AL585450
378	6.8	37.8	23	17	AZ342826	AZ342826	1M0076C04	C 451	6.6	36.7	21	13	BM395436	BM395436	50072-2-9
379	6.8	37.8	23	17	AZ372664	AZ372664	1M0124E09	C 452	6.6	36.7	21	17	AZ309714	AZ309714	1M0016M18
380	6.8	37.8	23	17	AZ470337	AZ470337	1M0284D21	C 453	6.6	36.7	21	17	AZ443871	AZ443871	1M0238I07
381	6.8	37.8	23	17	AZ480676	AZ480676	1M0302P23	C 454	6.6	36.7	21	17	AZ466689	AZ466689	1M0227L03
382	6.8	37.8	23	17	AZ769548	AZ769548	1M0570I20	C 455	6.6	36.7	21	17	AZ466689	AZ466689	1M0227L03
383	6.8	37.8	23	17	AZ771520	AZ771520	1M0573H21	C 456	6.6	36.7	21	17	AZ511843	AZ511843	1M0357K05
384	6.8	37.8	23	17	AZ781778	AZ781778	2M0021E24	C 457	6.6	36.7	21	17	AZ785825	AZ785825	2M0030G05
385	6.8	37.8	23	17	AZ806883	AZ806883	2M0069B15	C 458	6.6	36.7	21	17	AZ794048	AZ794048	2M0047H07
C 386	6.8	37.8	23	17	HSMC03F05	X88494	H. sapiens D	C 459	6.6	36.7	21	17	AZ794048	AZ794048	2M0047H07
C 387	6.8	37.8	23	17	TR215B01P	AL473515	T. brucei	C 460	6.6	36.7	21	17	AZ801929	AZ801929	2M0060A09
C 388	6.8	37.8	24	17	AZ307299	AZ307299	1M0008D23	C 461	6.6	36.7	21	17	AZ819369	AZ819369	2M0089O21
C 389	6.8	37.8	24	17	AZ313141	AZ313141	1M0029D19	C 462	6.6	36.7	21	17	AZ830003	AZ830003	2M0109A04
C 390	6.8	37.8	24	17	AZ313141	AZ313141	1M0029D19	C 463	6.6	36.7	21	17	AZ841128	AZ841128	2M0138P22
C 391	6.8	37.8	24	17	AZ436588	AZ436588	1M0224H20	C 464	6.6	36.7	21	17	AZ841128	AZ841128	2M0138P22
C 392	6.8	37.8	24	17	AZ437306	AZ437306	1M0225D03	C 465	6.6	36.7	21	17	AZ873829	AZ873829	2M0187C15
C 393	6.8	37.8	24	17	AZ486765	AZ486765	1M0319P08	C 466	6.6	36.7	22	9	AA904202	AA904202	cg20E11.s
C 394	6.8	37.8	24	17	AZ608837	AZ608837	1M0433L14	C 467	6.6	36.7	22	9	AI035419	AI035419	ub46d05.r
C 395	6.8	37.8	24	17	AZ770304	AZ770304	1M0571K14	C 468	6.6	36.7	22	9	AI118718	AI118718	uc11h07.r
C 396	6.8	37.8	24	17	AZ77167	AZ77167	2M0011H19	C 469	6.6	36.7	22	9	AI267916	AI267916	qoz3h07.x
C 397	6.8	37.8	24	17	AZ805942	AZ805942	2M0067B10	C 470	6.6	36.7	22	9	AI739042	AI739042	w134f01.x
C 398	6.8	37.8	24	17	AZ807296	AZ807296	2M0070K03	C 471	6.6	36.7	22	13	BM399021	BM399021	5009-0-52
C 399	6.8	37.8	25	9	AA930851	AA930851	vz71b06.s	C 472	6.6	36.7	22	14	D21051	D21051	HUMGS02036
C 400	6.8	37.8	25	9	AI181643	AI181643	ub79h08.r	C 473	6.6	36.7	22	17	AZ402846	AZ402846	1M0170A20
C 401	6.8	37.8	25	9	AI299118	AI299118	gm14g07.x	C 474	6.6	36.7	22	17	AZ482065	AZ482065	1M0306M20
C 402	6.8	37.8	25	9	AI344221	AI344221	lc02h03.x	C 475	6.6	36.7	22	17	AZ623338	AZ623338	1M0460O19
C 403	6.8	37.8	25	9	AI594892	AI594892	vel2c06.x	C 476	6.6	36.7	22	17	AZ801946	AZ801946	2M0050E07
C 404	6.8	37.8	25	9	AI554281	AI554281	cg89f08.x	C 477	6.6	36.7	22	17	AZ822589	AZ822589	2M0095P21
C 405	6.8	37.8	25	9	AI914687	AI914687	ct26f09.x	C 478	6.6	36.7	22	17	AZ831937	AZ831937	2M0111P22
C 406	6.8	37.8	25	10	AM004243	BE732128	EST-NGR-1	C 479	6.6	36.7	22	17	AZ863707	AZ863707	2M0171N19
C 407	6.8	37.8	25	13	BI094828	BI094828	EST-CD34N	C 480	6.6	36.7	22	17	AZ963488	AZ963488	2M023J12
C 408	6.8	37.8	25	13	BM399506	BM399506	5009-0-58	C 481	6.6	36.7	22	17	AZ984948	AZ984948	2M0266F12
C 409	6.8	37.8	25	13	BM400580	BM400580	5009-0-76	C 482	6.6	36.7	22	17	TA205P05O	TA205P05O	
C 410	6.8	37.8	25	13	AZ510410	AZ510410	1M0354H21	C 483	6.6	36.7	22	17	TA259H01O	TA259H01O	
C 411	6.8	37.8	25	17	AZ584819	AZ584819	1M0389A13	C 484	6.6	36.7	23	13	BG927951	BG927951	HNC45-1-F
C 412	6.8	37.8	25	17	AZ760021	AZ760021	1M0535P20	C 485	6.6	36.7	23	13	BM397594	BM397594	5009-0-35
C 413	6.8	37.8	25	17	AZ781069	AZ781069	2M0018P19	C 486	6.6	36.7	23	13	AZ316049	AZ316049	1M0066G07
C 414	6.8	37.8	25	17	AZ799779	AZ799779	2M0057K19	C 487	6.6	36.7	23	17	AZ332483	AZ332483	1M0155D08
C 415	6.8	37.8	25	17	AZ803724	AZ803724	2M0073B21	C 488	6.6	36.7	23	17	AZ605022	AZ605022	1M0426G12
C 416	6.8	37.8	25	17	AZ861588	AZ861588	2M0168J04	C 489	6.6	36.7	23	17	AZ808080	AZ808080	2M0071I22
C 417	6.8	37.8	25	17	BH759431	BH759431	KG04006-5	C 490	6.6	36.7	23	17	AZ844206	AZ844206	2M0143I11
C 418	6.8	37.8	25	17	TA274G11Q	AL485967	T. brucei	C 491	6.6	36.7	23	17	TA134E10O	TA134E10O	
C 419	6.8	37.8	25	14	BE516032	BE516032	WH06f29.B	C 492	6.6	36.7	23	17	TA167C09Q	TA167C09Q	
C 420	6.6	36.7	15	12	BE219911	BE219911	601296879	C 493	6.6	36.7	23	17	TA67E07P	TA67E07P	
C 421	6.6	36.7	16	10	BE586084	BE586084	BEt#8PT7	C 494	6.6	36.7	24	13	BM393818	BM393818	
C 422	6.6	36.7	17	13	BM395525	BM395525	50072-2-5	C 495	6.6	36.7	24	13	BM396332	BM396332	5009-0-2
C 423	6.6	36.7	18	13	BM395302	BM395302	50072-2-8	C 496	6.6	36.7	24	13	BM396445	BM396445	5009-0-20
C 424	6.6	36.7	19	2	HSM007596	AL1042746	Homo sapi	C 497	6.6	36.7	24	13	BM397719	BM397719	5009-0-36
C 425	6.6	36.7	19	9	AI811474	AI811474	FW3G04.x	C 498	6.6	36.7	24	13	AZ314206	AZ314206	1M0030H19
C 426	6.6	36.7	19	17	AZ307864	AZ307864	1M0010F16	C 499	6.6	36.7	24	17	AZ341038	AZ341038	1M0073B16
C 427	6.6	36.7	19	17	AZ480062	AZ480062	1M0167K06	C 500	6.6	36.7	24	17	AZ379773	AZ379773	1M0135H09
C 428	6.6	36.7	19	17	AZ488204	AZ488204	1M0318B21	C 501	6.6	36.7	24	17	AZ428114	AZ428114	1M0210A01
C 429	6.6	36.7	19	17	AZ493833	AZ493833	1M0328P11	C 502	6.6	36.7	24	17	AZ424773	AZ424773	1M0292F21
C 430	6.6	36.7	19	17	AZ661787	AZ661787	1M0540T06	C 503	6.6	36.7	24	17	AZ492799	AZ492799	1M0327B10
C 431	6.6	36.7	19	17	AZ864822	AZ864822	2M0174C08	C 504	6.6	36.7	24	17	AZ500040	AZ500040	1M0338K07
C 432	6.6	36.7	19	17	AZ948421	AZ948421	2M0211A01	C 505	6.6	36.7	24	17	TA245F07P	TA245F07P	
C 433	6.6	36.7	19	17	AL1043349	AL1043349	Homo sapi	C 506	6.6	36.7	24	17	AA034350	AA034350	
C 434	6.6	36.7	20	12	BM393608	BM393608	50072-2-1	C 507	6.6	36.7	25	9	AA880161	AA880161	yy96h04.r
C 435	6.6	36.7	20	13	BM393369	BM393369	50072-2-3	C 508	6.6	36.7	25	9	AA908578	AA908578	cg84c09.s
C 436	6.6	36.7	20	13	BM394340	BM394340	50072-2-7	C 509	6.6	36.7	25	9	AI023012	AI023012	ow57f01.b
C 437	6.6	36.7	20	13	BM395025	BM395025	50072-2-9	C 510	6.6	36.7	25	9	AI025765	AI025765	ov94f03.s
C 438	6.6	36.7	20	13	BM395527	BM395527	1M0066U13	C 511	6.6	36.7	25	9	AI081705	AI081705	qwo1d01.s
C 439	6.6	36.7	20	14	CO1261	AZ497752	1M0234B14	C 512	6.6	36.7	25	9	AI133486	AI133486	
C 440	6.6	36.7	20	17	AZ442667	AZ442667	1M0234B14	C 513	6.6	36.7	25	9	BG896256	BG896256	
C 441	6.6	36.7	20	17	AZ442667	AZ442667	1M0234B14	C 514	6.6	36.7	25	9			
C 442	6.6	36.7	20	17	AZ442667	AZ442667	1M0234B14	C 515	6.6	36.7	25	9			
C 443	6.6	36.7	20	17	AZ442667	AZ442667	1M0234B14	C 516	6.6	36.7	25	9			
C 444	6.6	36.7	20	17	AZ442667	AZ442667	1M0234B14	C 517	6.6	36.7	25	12	BG896256	BG896256	

C 518	6.6	36.7	25	13	BM395408	BM395408 50072-2-8	C 591	6.4	35.6	21	9	AL585450
C 519	6.6	36.7	25	13	BM395454	BM395454 50072-2-9	C 592	6.4	35.6	21	13	BM395685
C 520	6.6	36.7	25	13	BM400880	BM400880 5009-0-8-	C 593	6.4	35.6	21	13	BM397213
C 521	6.6	36.7	25	14	D21049	D21049 HUMS02034	C 594	6.4	35.6	21	13	BM397525
C 522	6.6	36.7	25	14	AZ579573	AZ579573 1M0367M05	C 595	6.4	35.6	21	13	BM399000
C 523	6.6	36.7	25	17	AZ595024	AZ595024 1M0407D23	C 596	6.4	35.6	21	13	BM401202
C 524	6.6	36.7	25	17	AZ67918	AZ67918 1M0567B09	C 597	6.4	35.6	21	14	D42275
C 525	6.6	36.7	25	17	AZ785586	AZ785586 2M0029N04	C 598	6.4	35.6	21	17	AZ307929
C 526	6.6	36.7	25	17	AZ804762	AZ804762 2M0065N12	C 599	6.4	35.6	21	17	AZ309732
C 527	6.6	36.7	25	17	AZ807605	AZ807605 2M0070L05	C 600	6.4	35.6	21	17	AZ220581
C 528	6.6	36.7	25	17	AZ828517	AZ828517 2M0105J02	C 601	6.4	35.6	21	17	AZ220773
C 529	6.6	36.7	25	17	TA352B06	TA352B06 50072-2-8	C 602	6.4	35.6	21	17	AZ242046
C 530	6.4	35.6	11	13	BM395328	BM395328 50072-2-8	C 603	6.4	35.6	21	17	AZ400597
C 531	6.4	35.6	11	13	BM394028	BM394028 50072-2-1	C 604	6.4	35.6	21	17	AZ455471
C 532	6.4	35.6	14	13	BM392794	BM392794 50071-2-1	C 605	6.4	35.6	21	17	AZ455821
C 533	6.4	35.6	14	13	BM394089	BM394089 50072-2-1	C 606	6.4	35.6	21	17	AZ580960
C 534	6.4	35.6	14	13	BM395363	BM395363 50072-2-8	C 607	6.4	35.6	21	17	AZ581103
C 535	6.4	35.6	15	13	BM395188	BM395188 50072-2-7	C 608	6.4	35.6	21	17	AZ584607
C 536	6.4	35.6	16	9	AA939272	AA939272 CQ31B06.s	C 609	6.4	35.6	21	17	AZ598709
C 537	6.4	35.6	16	9	A1357296	A1357296 CQ15H01.x	C 610	6.4	35.6	21	17	AZ645766
C 538	6.4	35.6	16	9	A1648507	A1648507 LZ54C09.x	C 611	6.4	35.6	21	17	AZ775019
C 539	6.4	35.6	17	13	BM394186	BM394186 50072-2-2	C 612	6.4	35.6	21	17	AZ808124
C 540	6.4	35.6	18	13	BM395123	BM395123 50072-2-7	C 613	6.4	35.6	21	17	AZ813332
C 541	6.4	35.6	18	13	BM395697	BM395697 5009-0-60	C 614	6.4	35.6	21	17	AZ817328
C 542	6.4	35.6	19	9	AA878744	AA878744 CFB5A08.s	C 615	6.4	35.6	21	17	AZ967472
C 543	6.4	35.6	19	9	AA885697	AA885697 C134F01.s	C 616	6.4	35.6	22	9	AA894572
C 544	6.4	35.6	19	9	AA953971	AA953971 C088H01.s	C 617	6.4	35.6	22	9	AA908583
C 545	6.4	35.6	19	9	A1056541	A1056541 C98C11.x	C 618	6.4	35.6	22	9	AA933996
C 546	6.4	35.6	19	9	A1252235	A1252235 CQ78H03.x	C 619	6.4	35.6	22	9	A1039313
C 547	6.4	35.6	19	9	A1471695	A1471695 C199F04.x	C 620	6.4	35.6	22	9	A1160625
C 548	6.4	35.6	19	13	BM399684	BM399684 5009-0-60	C 621	6.4	35.6	22	9	A1219368
C 549	6.4	35.6	19	14	C00981	C00981 HUMS000337	C 622	6.4	35.6	22	9	A1566835
C 550	6.4	35.6	19	14	C01186	C01186 HUMS000788	C 623	6.4	35.6	22	9	AU256517
C 551	6.4	35.6	19	17	AZ403537	AZ403537 1M0171M05	C 624	6.4	35.6	22	9	AU259732
C 552	6.4	35.6	19	17	AZ424532	AZ424532 1M0204L07	C 625	6.4	35.6	22	17	AZ304010
C 553	6.4	35.6	19	17	AZ480415	AZ480415 1M0301K24	C 626	6.4	35.6	22	17	AZ309912
C 554	6.4	35.6	19	17	AZ514467	AZ514467 1M0361B19	C 627	6.4	35.6	22	17	AZ312636
C 555	6.4	35.6	19	17	AZ662546	AZ662546 1M0541P08	C 628	6.4	35.6	22	17	AZ313399
C 556	6.4	35.6	19	17	AZ761834	AZ761834 1M0556E19	C 629	6.4	35.6	22	17	AZ430045
C 557	6.4	35.6	19	17	AZ769235	AZ769235 1M0566I09	C 630	6.4	35.6	22	17	AZ623402
C 558	6.4	35.6	19	17	AZ771560	AZ771560 1M0574A03	C 631	6.4	35.6	22	17	AZ655018
C 559	6.4	35.6	19	17	AZ774950	AZ774950 2M0004M16	C 632	6.4	35.6	22	17	AZ655548
C 560	6.4	35.6	19	17	AZ791433	AZ791433 2M0004A24	C 633	6.4	35.6	22	17	AZ658507
C 561	6.4	35.6	19	17	AZ806669	AZ806669 2M0066G19	C 634	6.4	35.6	22	17	AZ786587
C 562	6.4	35.6	19	17	AZ807749	AZ807749 2M0070L17	C 635	6.4	35.6	22	17	AZ810548
C 563	6.4	35.6	19	17	AZ817291	AZ817291 2M0086P05	C 636	6.4	35.6	22	17	AZ829837
C 564	6.4	35.6	19	17	AZ825396	AZ825396 2M0100N04	C 637	6.4	35.6	22	17	AZ873093
C 565	6.4	35.6	19	17	AZ837373	AZ837373 2M0132C07	C 638	6.4	35.6	22	17	AZ950407
C 566	6.4	35.6	19	17	AZ861634	AZ861634 2M0168B18	C 639	6.4	35.6	22	17	AZ974353
C 567	6.4	35.6	19	17	AZ954781	AZ954781 2M0220C07	C 640	6.4	35.6	22	17	TA120D06P
C 568	6.4	35.6	19	17	AZ969805	AZ969805 2M0242O12	C 641	6.4	35.6	22	17	TA177177
C 569	6.4	35.6	19	17	AZ994163	AZ994163 2M0279F05	C 642	6.4	35.6	23	10	AM698813
C 570	6.4	35.6	20	12	BF966452	BF966452 602287066	C 643	6.4	35.6	23	13	BM396189
C 571	6.4	35.6	20	13	BM396970	BM396970 5009-0-27	C 644	6.4	35.6	23	13	BM397770
C 572	6.4	35.6	20	13	BM400174	BM400174 5009-0-68	C 645	6.4	35.6	23	13	BM398278
C 573	6.4	35.6	20	17	AZ307471	AZ307471 1M0009K12	C 646	6.4	35.6	23	14	D25865
C 574	6.4	35.6	20	17	AZ308410	AZ308410 1M0011A24	C 647	6.4	35.6	23	17	AZ336049
C 575	6.4	35.6	20	17	AZ309960	AZ309960 1M0017P23	C 648	6.4	35.6	23	17	AZ335054
C 576	6.4	35.6	20	17	AZ339816	AZ339816 1M0071M24	C 649	6.4	35.6	23	17	AZ380370
C 577	6.4	35.6	20	17	AZ368205	AZ368205 1M0181B07	C 650	6.4	35.6	23	17	AZ430197
C 578	6.4	35.6	20	17	AZ369092	AZ369092 1M0119B01	C 651	6.4	35.6	23	17	AZ471912
C 579	6.4	35.6	20	17	AZ499543	AZ499543 1M0337F19	C 652	6.4	35.6	23	17	AZ472899
C 580	6.4	35.6	20	17	AZ581146	AZ581146 1M0369G14	C 653	6.4	35.6	23	17	AZ475845
C 581	6.4	35.6	20	17	AZ583699	AZ583699 1M0378G15	C 654	6.4	35.6	23	17	AZ619403
C 582	6.4	35.6	20	17	AZ585902	AZ585902 1M0391M24	C 655	6.4	35.6	23	17	AZ661794
C 583	6.4	35.6	20	17	AZ622464	AZ622464 1M0459N13	C 656	6.4	35.6	23	17	AZ660176
C 584	6.4	35.6	20	17	AZ623068	AZ623068 1M0460C21	C 657	6.4	35.6	23	17	AZ666452
C 585	6.4	35.6	20	17	AZ775974	AZ775974 2M0009H14	C 658	6.4	35.6	23	17	AZ773601
C 586	6.4	35.6	20	17	AZ819520	AZ819520 2M0009I07	C 659	6.4	35.6	23	17	AZ785578
C 587	6.4	35.6	20	17	AZ822878	AZ822878 2M0009F02	C 660	6.4	35.6	23	17	AZ785661
C 588	6.4	35.6	20	17	AZ823598	AZ823598 2M00097B08	C 661	6.4	35.6	23	17	AZ808123
C 589	6.4	35.6	20	17	AZ861324	AZ861324 2M0167H13	C 662	6.4	35.6	23	17	AZ834608
C 590	6.4	35.6	21	2	HSM008113	AL0433263 Homo sapi	C 663	6.4	35.6	23	17	AZ991587

C 810	6.2	34.4	22	9	AI687266	tp94d10.x	C 883	6.2	34.4	25	9	AI262558	qk42e08.x
C 811	6.2	34.4	22	9	AI738559	AI738559 w339g02.x	C 884	6.2	34.4	25	9	AI276868	gv65a10.x
C 812	6.2	34.4	22	13	BM401155	BM401155 5009-0-83	C 885	6.2	34.4	25	9	AI277421	gm64e02.x
C 813	6.2	34.4	22	17	AZ331565	AZ331565 IM0059M06	C 886	6.2	34.4	25	9	AI298122	gm64e06.x
C 814	6.2	34.4	22	17	AZ339902	AZ339902 IM0071003	C 887	6.2	34.4	25	9	AI134358	tl41d09.x
C 815	6.2	34.4	22	17	AZ429020	AZ429020 IM0212F17	C 888	6.2	34.4	25	9	AI515120	lc64d05.x
C 816	6.2	34.4	22	17	AZ468023	AZ468023 IM0279L15	C 889	6.2	34.4	25	9	AI584521	lp95a407.x
C 817	6.2	34.4	22	17	AZ481923	AZ481923 IM0306L06	C 890	6.2	34.4	25	9	AI628239	lv93c04.x
C 818	6.2	34.4	22	17	AZ486633	AZ486633 IM0341I14	C 891	6.2	34.4	25	9	AI638719	tt24e01.x
C 819	6.2	34.4	22	17	AZ501345	AZ501345 IM0340I11	C 892	6.2	34.4	25	9	AI660931	wf20a11.x
C 820	6.2	34.4	22	17	AZ501345	AZ501345 IM0340I11	C 893	6.2	34.4	25	9	AA592718	vx229c12.x
C 821	6.2	34.4	22	17	AZ592201	AZ592201 IM0402K24	C 894	6.2	34.4	25	13	BM396446	BM396446 5009-0-20
C 822	6.2	34.4	22	17	AZ785866	AZ785866 IM0030002	C 895	6.2	34.4	25	13	BM400594	BM400594 5009-0-76
C 823	6.2	34.4	22	17	AZ828017	AZ828017 IM0104H18	C 896	6.2	34.4	25	13	BM400628	BM400628 5009-0-76
C 824	6.2	34.4	22	17	AZ958390	AZ958390 IM0225I07	C 897	6.2	34.4	25	13	BM400628	BM400628 5009-0-76
C 825	6.2	34.4	22	17	AZ976229	AZ976229 IM0251N06	C 898	6.2	34.4	25	17	AZ206874	AZ206874 IM0008E07
C 826	6.2	34.4	22	17	TA140A04P	TA140A04P T. brucei	C 899	6.2	34.4	25	17	AZ217298	AZ217298 IM0035N21
C 827	6.2	34.4	22	17	TA223E07P	TA223E07P T. brucei	C 900	6.2	34.4	25	17	AZ459569	AZ459569 IM0285D10
C 828	6.2	34.4	22	17	TA70B110	TA70B110 T. brucei	C 901	6.2	34.4	25	17	AZ491057	AZ491057 IM0324I24
C 829	6.2	34.4	23	2	HS0004279	HS0004279 Homo sapi	C 902	6.2	34.4	25	17	AZ776661	AZ776661 IM0010C05
C 830	6.2	34.4	23	2	HS0004394	HS0004394 Homo sapi	C 903	6.2	34.4	25	17	AZ794198	AZ794198 IM0047J13
C 831	6.2	34.4	23	10	AW246048	AW246048 2821453.5	C 904	6.2	34.4	25	17	AZ794198	AZ794198 IM0047J13
C 832	6.2	34.4	23	17	AZ330740	AZ330740 IM0056G07	C 905	6.2	34.4	25	17	AZ807031	AZ807031 IM0069B02
C 833	6.2	34.4	23	17	AZ343048	AZ343048 IM0076K17	C 906	6.2	34.4	25	17	AZ810739	AZ810739 IM0076C02
C 834	6.2	34.4	23	17	AZ388663	AZ388663 IM0148J15	C 907	6.2	34.4	25	17	AZ966613	AZ966613 IM0236C18
C 835	6.2	34.4	23	17	AZ463102	AZ463102 IM0271A15	C 908	6.2	34.4	25	17	BH852925	BH852925 SALK 0757
C 836	6.2	34.4	23	17	AZ480656	AZ480656 IM0302P23	C 909	6.2	34.4	25	17	TA114E04P	TA114E04P T. brucei
C 837	6.2	34.4	23	17	AZ593454	AZ593454 IM0405C03	C 910	6.2	34.4	25	17	TA17E020	TA17E020 T. brucei
C 838	6.2	34.4	23	17	AZ608730	AZ608730 IM0433E07	C 911	6.2	34.4	25	17	TA182C05P	TA182C05P T. brucei
C 839	6.2	34.4	23	17	AZ639181	AZ639181 IM0499D03	C 912	6.2	34.4	25	17	HS0008038	HS0008038 Homo sapi
C 840	6.2	34.4	23	17	AZ784767	AZ784767 IM0027P17	C 913	6.2	34.4	25	17	BH127401	BH127401 G-1c19.x
C 841	6.2	34.4	23	17	AZ808080	AZ808080 IM0071I22	C 914	6.2	34.4	25	17	BH169716	BH169716 SALK 0017
C 842	6.2	34.4	23	17	AZ821572	AZ821572 IM0094G21	C 915	6.2	34.4	25	17	BH169716	BH169716 SALK 0017
C 843	6.2	34.4	23	17	AZ822831	AZ822831 IM0096J21	C 916	6.2	34.4	25	17	BH169716	BH169716 SALK 0017
C 844	6.2	34.4	23	17	AZ844206	AZ844206 IM0131I11	C 917	6.2	34.4	25	17	BH169716	BH169716 SALK 0017
C 845	6.2	34.4	23	17	AZ869816	AZ869816 IM0182N06	C 918	6.2	34.4	25	17	BH169716	BH169716 SALK 0017
C 846	6.2	34.4	23	17	AZ971749	AZ971749 IM0245C21	C 919	6.2	34.4	25	17	BM395320	BM395320 H0A2-H-4
C 847	6.2	34.4	23	17	TA215B01P	TA215B01P T. brucei	C 920	6.2	34.4	25	17	BM395336	BM395336 50072-2-1
C 848	6.2	34.4	23	17	TA260H01P	TA260H01P T. brucei	C 921	6.2	34.4	25	17	AA545509	AA545509 0818d05.b
C 849	6.2	34.4	24	9	AL047412	AL047412 DFEZP586E	C 922	6.2	34.4	25	17	AI027323	AI027323 0w46a07.x
C 850	6.2	34.4	24	9	AL047412	AL047412 DFEZP586E	C 923	6.2	34.4	25	17	AI476315	AI476315 t415c09.x
C 851	6.2	34.4	24	9	AU258060	AU258060 AU258060	C 924	6.2	34.4	25	17	AI476315	AI476315 t415c09.x
C 852	6.2	34.4	24	10	AM059812	AM059812 LE7F01.YS	C 925	6.2	34.4	25	17	AI476315	AI476315 t415c09.x
C 853	6.2	34.4	24	13	BM395654	BM395654 50072-2-9	C 926	6.2	34.4	25	17	AI476315	AI476315 t415c09.x
C 854	6.2	34.4	24	13	BM396627	BM396627 5009-0-23	C 927	6.2	34.4	25	17	AI476315	AI476315 t415c09.x
C 855	6.2	34.4	24	13	BM398868	BM398868 5009-0-5-	C 928	6.2	34.4	25	17	AI476315	AI476315 t415c09.x
C 856	6.2	34.4	24	13	BM400107	BM400107 5009-0-66	C 929	6.2	34.4	25	17	AI476315	AI476315 t415c09.x
C 857	6.2	34.4	24	14	Z20614	Z20614 HSAACNVA.T	C 930	6.2	34.4	25	17	AI476315	AI476315 t415c09.x
C 858	6.2	34.4	24	17	AO050534	AO050534 nbxb0004b	C 931	6.2	34.4	25	17	AI476315	AI476315 t415c09.x
C 859	6.2	34.4	24	17	AZ317731	AZ317731 IM0035P22	C 932	6.2	34.4	25	17	AI476315	AI476315 t415c09.x
C 860	6.2	34.4	24	17	AZ318208	AZ318208 IM0037H08	C 933	6.2	34.4	25	17	AI476315	AI476315 t415c09.x
C 861	6.2	34.4	24	17	AZ392919	AZ392919 IM0155E16	C 934	6.2	34.4	25	17	AI476315	AI476315 t415c09.x
C 862	6.2	34.4	24	17	AZ405843	AZ405843 IM0174A20	C 935	6.2	34.4	25	17	AI476315	AI476315 t415c09.x
C 863	6.2	34.4	24	17	AZ428700	AZ428700 IM0212L16	C 936	6.2	34.4	25	17	AI476315	AI476315 t415c09.x
C 864	6.2	34.4	24	17	AZ443047	AZ443047 IM0237I06	C 937	6.2	34.4	25	17	AI476315	AI476315 t415c09.x
C 865	6.2	34.4	24	17	AZ617463	AZ617463 IM0448P15	C 938	6.2	34.4	25	17	AI476315	AI476315 t415c09.x
C 866	6.2	34.4	24	17	AZ655864	AZ655864 IM0547I04	C 939	6.2	34.4	25	17	AI476315	AI476315 t415c09.x
C 867	6.2	34.4	24	17	AZ780307	AZ780307 IM0017J04	C 940	6.2	34.4	25	17	AI476315	AI476315 t415c09.x
C 868	6.2	34.4	24	17	AZ812679	AZ812679 IM0079H03	C 941	6.2	34.4	25	17	AI476315	AI476315 t415c09.x
C 869	6.2	34.4	24	17	AZ956336	AZ956336 IM0222F13	C 942	6.2	34.4	25	17	AI476315	AI476315 t415c09.x
C 870	6.2	34.4	24	17	TA207E08P	TA207E08P T. brucei	C 943	6.2	34.4	25	17	AI476315	AI476315 t415c09.x
C 871	6.2	34.4	24	17	TA207E12Q	TA207E12Q T. brucei	C 944	6.2	34.4	25	17	AI476315	AI476315 t415c09.x
C 872	6.2	34.4	24	17	TA238D04Q	TA238D04Q T. brucei	C 945	6.2	34.4	25	17	AI476315	AI476315 t415c09.x
C 873	6.2	34.4	24	17	TA305G10P	TA305G10P T. brucei	C 946	6.2	34.4	25	17	AI476315	AI476315 t415c09.x
C 874	6.2	34.4	24	17	TA305G10P	TA305G10P T. brucei	C 947	6.2	34.4	25	17	AI476315	AI476315 t415c09.x
C 875	6.2	34.4	25	9	AA926871	AA926871 o155c11.b	C 948	6.2	34.4	25	17	AI476315	AI476315 t415c09.x
C 876	6.2	34.4	25	9	AI002379	AI002379 oq87f02.s	C 949	6.2	34.4	25	17	AI476315	AI476315 t415c09.x
C 877	6.2	34.4	25	9	AI024239	AI024239 oq87f02.s	C 950	6.2	34.4	25	17	AI476315	AI476315 t415c09.x
C 878	6.2	34.4	25	9	AI040331	AI040331 oq33b07.x	C 951	6.2	34.4	25	17	AI476315	AI476315 t415c09.x
C 879	6.2	34.4	25	9	AI127762	AI127762 qc31d01.x	C 952	6.2	34.4	25	17	AI476315	AI476315 t415c09.x
C 880	6.2	34.4	25	9	AI147073	AI147073 ok33c05.b	C 953	6.2	34.4	25	17	AI476315	AI476315 t415c09.x
C 881	6.2	34.4	25	9	AI147073	AI147073 ok33c05.b	C 954	6.2	34.4	25	17	AI476315	AI476315 t415c09.x
C 882	6.2	34.4	25	9	AI262558	AI262558 qk42e08.x	C 955	6.2	34.4	25	17	AI476315	AI476315 t415c09.x

956	6	33.3	20	17	AZ473322	AZ473322	1M0289H08
C 957	6	33.3	20	17	AZ473322	AZ473322	1M0289H08
C 958	6	33.3	20	17	AZ475852	AZ475852	1M0294A18
959	6	33.3	20	17	AZ484500	AZ484500	1M0311C01
C 960	6	33.3	20	17	AZ486007	AZ486007	1M0313E17
C 961	6	33.3	20	17	AZ491509	AZ491509	1M0325B09
C 962	6	33.3	20	17	AZ500772	AZ500772	1M0329N15
C 963	6	33.3	20	17	AZ512414	AZ512414	1M0357J21
C 964	6	33.3	20	17	AZ526355	AZ526355	1M0403M11
C 965	6	33.3	20	17	AZ600911	AZ600911	1M0418M21
C 966	6	33.3	20	17	AZ619289	AZ619289	1M0436E13
C 967	6	33.3	20	17	AZ619289	AZ619289	1M0436E13
968	6	33.3	20	17	AZ621188	AZ621188	1M0454G13
C 969	6	33.3	20	17	AZ628809	AZ628809	1M0481C17
C 970	6	33.3	20	17	AZ659612	AZ659612	1M0537A07
C 971	6	33.3	20	17	AZ780308	AZ780308	2M0017J05
C 972	6	33.3	20	17	AZ789090	AZ789090	2M0036C12
C 973	6	33.3	20	17	AZ808057	AZ808057	2M0071C22
C 974	6	33.3	20	17	AZ813013	AZ813013	2M0080P02
975	6	33.3	20	17	AZ828387	AZ828387	2M0105P13
C 976	6	33.3	20	17	AZ830457	AZ830457	2M0109P11
C 977	6	33.3	20	17	AZ833695	AZ833695	2M0115N20
C 978	6	33.3	20	17	AZ833695	AZ833695	2M0115N20
C 979	6	33.3	20	17	AZ835025	AZ835025	2M0129I02
C 980	6	33.3	20	17	AZ836069	AZ836069	2M0136P11
C 981	6	33.3	20	17	AZ839901	AZ839901	2M0136P11
C 982	6	33.3	20	17	AZ845320	AZ845320	2M0145M02
C 983	6	33.3	20	17	AZ859065	AZ859065	2M0164F06
984	6	33.3	20	17	AZ938837	AZ938837	2M0197L06
C 985	6	33.3	20	17	AZ949076	AZ949076	2M0212D23
C 986	6	33.3	20	17	AZ952391	AZ952391	2M0217P07
C 987	6	33.3	20	17	AZ953211	AZ953211	2M0218P15
C 988	6	33.3	20	17	AZ985308	AZ985308	2M0267D11
C 989	6	33.3	20	17	AZ995436	AZ995436	2M0281F18
C 990	6	33.3	20	17	AZ995535	AZ995535	2M0281F18
991	6	33.3	21	14	D20707	D20707	HUMCS01683
992	6	33.3	21	17	AZ306118	AZ306118	1M0007I06
993	6	33.3	21	17	AZ313630	AZ313630	1M0030I06
C 994	6	33.3	21	17	AZ313630	AZ313630	1M0030I06
995	6	33.3	21	17	AZ48213	AZ48213	1M0084N15
C 996	6	33.3	21	17	AZ442098	AZ442098	1M0234F12
C 997	6	33.3	21	17	AZ495585	AZ495585	1M0331H02
998	6	33.3	21	17	AZ526636	AZ526636	257PBH06
999	6	33.3	21	17	AZ581771	AZ581771	1M0370P10
1000	6	33.3	21	17	AZ594960	AZ594960	1M0407E16

ALIGNMENTS

RESULT 1
BM394673/c
LOCUS
DEFINITION
50072-2-5-D08.r.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
BM394673
BM394673.1 GI:18194726
EST.
Tetrahymena thermophila.
Tetrahymena thermophila.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
1 (bases 1 to 23)
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel
J., and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu
Seq primer: T3
Location/Qualifiers
1. 23
/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_1ib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT
1 a 11 c 8 g 3 t
ORIGIN
Query Match 62.2%; Score 11.2; DB 13; Length 23;
Best Local Similarity 81.2%; Pred. No. 3.4e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GCGCCGCGATCCAGGC 18
19 GGGCCCGGACCCATGC 4
Db
RESULT 2
BM394673/c
LOCUS
DEFINITION
50072-2-5-D08.r.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
BM394673
BM394673.1 GI:18194726
EST.
Tetrahymena thermophila.
Tetrahymena thermophila.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
1 (bases 1 to 23)
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel
J., and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1. 23
/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_1ib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT
1 a 11 c 8 g 3 t
ORIGIN
Query Match 58.9%; Score 10.6; DB 13; Length 23;
Best Local Similarity 76.5%; Pred. No. 6.2e+05;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TGGCGCCGATCCAGGC 18
1 TGGCGCATGGCTCGGCG 17
Db
RESULT 3
AZ634834/c
LOCUS
DEFINITION
1M0490C19R Mouse 10kb plasmid U9GCM library Mus musculus genomic
24 bp DNA linear GSS 13-DEC-2000

ACCESSION A2634834
 VERSION A2634834.1 GI:11757024
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 24)
 REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0490 row: C column: 19
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 24.
 Location/Qualifiers
 1..24
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCG1M0490C19"
 /clone_1lb="Mouse 10kb plasmid UUCG1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
 BASE COUNT 7 a 7 c 6 g 4 t
 ORIGIN
 Query Match 58.9%; Score 10.6; DB 17; Length 24;
 Best Local Similarity 76.5%; Pred. No. 6.2e+05;
 Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 2 TCGCCCGGATCCAGGC 18
 DB 22 TGTGCTCGATCCAGTC 6
 RESULT 4 A2648503 23 bp DNA 11near GSS 21-FEB-2001
 LOCUS A2648503
 DEFINITION 2M0149H02R Mouse 10kb plasmid UUCG1M library Mus musculus genomic

ACCESSION A2848503
 VERSION A2848503.1 GI:13031656
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23)
 REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0149 row: H column: 02
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 23.
 Location/Qualifiers
 1..23
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCG2M0149H02"
 /clone_1lb="Mouse 10kb plasmid UUCG1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD2 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
 BASE COUNT 2 a 10 c 6 g 5 t
 ORIGIN
 Query Match 57.8%; Score 10.4; DB 17; Length 23;
 Best Local Similarity 91.7%; Pred. No. 7.6e+05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 CGCCCGGATCCA 15
 DB 9 CTCCCGGATCCA 20
 RESULT 5 A2855545 19 bp DNA 11near GSS 21-FEB-2001
 LOCUS A2855545
 DEFINITION 2M0159F09R Mouse 10kb plasmid UUCG1M library Mus musculus genomic

clone UUGC2M0159F09 R, DNA sequence.

ACCESSION A2855545
 VERSION A2855545.1 GI:13045816
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0159 row: F column: 09
 Seq primer: CACACGAAACACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES
 source Location/Qualifiers
 1..19
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0159F09"
 /clone_lib="Mouse 10kb plasmid UUGCM library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptor and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 2 a 5 c 7 t
 5 g

ORIGIN
 Query Match 55.6%; Score 10; DB 17; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.1e+06;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GCCCGATCC 14
 |||||
 |||||

Db 3 GCCCGATCC 12

RESULT 6
 A2791884 21 bp DNA linear GSS 16-FEB-2001
 LOCUS
 DEFINITION 2M0043A02P Mouse 10kb plasmid UUGCM library Mus musculus genomic

clone UUGC2M0043A02 F, DNA sequence.

ACCESSION A2791884
 VERSION A2791884.1 GI:12935238
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0043 row: A column: 02
 Seq primer: CGTTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 21.

FEATURES
 source Location/Qualifiers
 1..21
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0043A02"
 /clone_lib="Mouse 10kb plasmid UUGCM library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptor and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 3 a 4 c 8 g
 6 t

ORIGIN
 Query Match 55.6%; Score 10; DB 17; Length 21;
 Best Local Similarity 72.2%; Pred. No. 1.1e+06;
 Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CTGCGCCCGATCCAGGC 18
 |||||
 |||||

Db 20 CAGCTTACGATCCAGAC 3

RESULT 7
 A2591658 20 bp DNA linear GSS 13-DEC-2000
 LOCUS
 DEFINITION 1M0401F19R Mouse 10kb plasmid UUGCM library Mus musculus genomic

clone UGCM0401P19 R, DNA sequence.

ACCESSION AZ591658
 VERSION AZ591658.1 GI:11713848
 GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Relilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)

JOURNAL COMMENT
 Contact: Robert B. Weis
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0401 row: F column: 19
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers

FEATURES
 source 1..20
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCM0401P19"
 /clone_1lb="Mouse 10kb plasmid UGCM library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 3 a 8 c 6 g 3 t
 ORIGIN

Query Match 53.3%; Score 9.6; DB 17; Length 20;
 Best Local Similarity 75.0%; Pred. No. 1.7e+06;
 Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CY 1 CTGGCCCGGATCCAG 16
 |||||
 DB 19 CAGCGCTCGCTCCAG 4

RESULT 8
 AZ305158 21 bp DNA linear GSS 29-SEP-2000
 LOCUS
 DEFINITION 1M0005K11R Mouse 10kb plasmid UGCM library Mus musculus genomic

clone UGCM0005K11 R, DNA sequence.

ACCESSION AZ305158
 VERSION AZ305158.1 GI:10341896
 GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Relilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)

JOURNAL COMMENT
 Contact: Robert B. Weis
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0005 row: K column: 11
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers

FEATURES
 source 1..21
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCM0005K11"
 /clone_1lb="Mouse 10kb plasmid UGCM library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 11 c 4 g 6 t
 ORIGIN

Query Match 53.3%; Score 9.6; DB 17; Length 21;
 Best Local Similarity 75.0%; Pred. No. 1.7e+06;
 Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CY 1 CTGGCCCGGATCCAG 16
 |||||
 DB 6 CTGCTCGCTCCG 21

RESULT 9
 AZ834643 21 bp DNA linear GSS 20-FEB-2001
 LOCUS
 DEFINITION 2M0117N24F Mouse 10kb plasmid UGCM library Mus musculus genomic

ACCESSION A2487506
 VERSION A2487506.1 GI:13004551
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0117 row: N column: 24
 Seq primer: CTTGTAAACGACGCCACT
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers
 1..21
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUC2M0117N24"
 /clone_1lb="Mouse 10kb plasmid UUC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /note="Vector: PMD42nv. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g114732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 1 a 5 c 10 g 5 t
 ORIGIN
 Query Match 53.3%; Score 9.6; DB 17; Length 21;
 Best Local Similarity 75.0%; Pred. No. 1.7e+06;
 Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 CTGCGCCCGATCCAG 16
 |||||
 Db 17 CTGAGCCCCCACCAG 2

RESULT 10
 A2487506 24 bp DNA linear GSS 05-OCT-2000
 LOCUS
 DEFINITION IM0317P10F Mouse 10kb plasmid UUC1M library Mus musculus genomic

ACCESSION A2487506
 VERSION A2487506.1 GI:10655316
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 24)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0317 row: P column: 10
 Seq primer: CTTGTAAACGACGCCACT
 Class: plasmid ends
 High quality sequence stop: 24.
 Location/Qualifiers
 1..24
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUC1M0317P10"
 /clone_1lb="Mouse 10kb plasmid UUC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /note="Vector: PMD42nv. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g114732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 4 a 5 c 9 g 6 t
 ORIGIN
 Query Match 53.3%; Score 9.6; DB 17; Length 24;
 Best Local Similarity 75.0%; Pred. No. 1.7e+06;
 Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 2 TGGCGCCCGATCCAG 17
 |||||
 Db 5 TGTGCCCCGTACAG 20

RESULT 11
 TAIL8G04P/c 25 bp DNA linear GSS 13-DEC-2000
 LOCUS
 DEFINITION T. brucei sheared genomic DNA clone 118g04, forward sequence,

genomic survey sequence.

ACCESSION AL463737 GI:11832909
 VERSION AL463737.1 GI:11832909
 KEYWORDS Trypanosoma brucei.
 SOURCE Trypanosoma brucei
 ORGANISM Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.

REFERENCE 1 (bases 1 to 25)
 AUTHORS Hall, N., Bowman, S., Lennard, N. J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S. E., Rajandream, M. A. and Barrell, B. G.
 TITLE Direct Substitution
 JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA. E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk
 COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + 1 method used for the library construction is described in detail in Smith, H. and Venter, J. C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
 Location/Qualifiers
 1..25
 /organism="Trypanosoma brucei"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="118904"

BASE COUNT 10 a 6 c 4 g 5 t
 ORIGIN

Query Match 53.3%; Score 9.6; DB 17; Length 25;
 Best Local Similarity 75.0%; Pred. No. 1.7e+06;
 Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TGCGCCGATCCAGG 17
 Db 25 TGTGACCGATCAAGG 10

RESULT 12
 LOCUS AZ314246 24 bp DNA linear GSS 29-SEP-2000
 DEFINITION IM0031A01F Mouse 10kb plasmid UGCCIM library Mus musculus genomic clone UGCCIM0031A01 F, DNA sequence.
 ACCESSION AZ314246
 VERSION AZ314246.1 GI:10359945
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 24)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
 Tel: 801 585 5606

Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0031 row: A column: 01
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 24.
 Location/Qualifiers
 1..24
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCCIM0031A01"
 /clone_lib="Mouse 10kb plasmid UGCCIM library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: pMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 3 a 6 c 9 g 6 t
 ORIGIN

Query Match 51.1%; Score 9.2; DB 17; Length 24;
 Best Local Similarity 78.6%; Pred. No. 2.5e+06;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 GCCCGATCCAGG 18
 Db 6 GCCCGATCCAGG 19

RESULT 13
 LOCUS AZ634834 24 bp DNA linear GSS 13-DEC-2000
 DEFINITION IM0490C19R Mouse 10kb plasmid UGCCIM library Mus musculus genomic clone UGCCIM0490C19 R, DNA sequence.
 ACCESSION AZ634834
 VERSION AZ634834.1 GI:11757024
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 24)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
 Tel: 801 585 5606

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN
8 a 7 c 5 g 3 t

Query Match 50.0%; Score 9; DB 17; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.1e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 GATCCAGGC 18
|||||
Db 15 GATCCAGGC 23

RESULT 16
LOCUS A2342826 23 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0076C04F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
clone UGCG1M076C04 F, DNA sequence.

ACCESSION A2342826
VERSION A2342826.1 GI:10420451
KEYWORDS GSS.

SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamli,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiser,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Plasmid inserts
COMMENT Unpublished (2000)
Contact: Robert B. Weiser
University of Utah Genome Center
Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0076 row: C column: 04
Seq primer: CGTGTAAACGACGCGCACT
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers

FEATURES
SOURCE

1. 23
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG1M076C04"
/clone_1lb="Mouse 10kb plasmid UGCG1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN
5 a 7 c 6 g 5 t

Query Match 48.9%; Score 8.8; DB 17; Length 23;
Best Local Similarity 83.3%; Pred. No. 3.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 GCGCCCGATCC 14
|||||
Db 12 GTGCCCGATCC 1

RESULT 17
LOCUS A2827973 23 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0104P1R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
clone UGCG2M0104P1 R, DNA sequence.

ACCESSION A2827973
VERSION A2827973.1 GI:12997881
KEYWORDS GSS.

SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamli,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiser,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Plasmid inserts
COMMENT Unpublished (2000)
Contact: Robert B. Weiser
University of Utah Genome Center
Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0104 row: F column: 11
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers

FEATURES
SOURCE

1. 23
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M0104P1"
/clone_1lb="Mouse 10kb plasmid UGCG1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

Query Match 48.9%; Score 8.8; DB 17; Length 25;
 Best Local Similarity 83.3%; Pred. No. 3.8e+06;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCGCCCGATCC 14
 19 GCGCCGCTATCC 8

RESULT 20
 AA954509/c 19 bp mRNA linear EST 23-JUN-1998
 LOCUS
 DEFINITION
 AA954509
 c881405.61 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
 IMAGE:1563081 3' similar to TR:Q24035 Q24035 ENA POLYPEPTIDE.
 /contains element MSRI repetitive element /, mRNA sequence.
 AA954509
 AA954509.1 GI:3118204
 EST.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 19)
 NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaaps-r@mail.nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Trace considered overall poor quality
 Insert Length: 754 Std Error: 0.00
 Seq primer: -40m13 fwd. ST from Amerisham
 High quality sequence stop: 1.
 Location/Qualifiers
 1..19
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1563081"
 /clone_1fb="Soares_NFL_T_GBC_S1"
 /lab_host="DH10B"
 /note="Organ: pooled; Vector: pT7SD-Pac (pharmacia) with
 a modified polylinker; Site 1: Not I; Site 2: Eco RI;
 Equal amounts of plasmid DNA from three normalized
 libraries (fetal lung MbHL19W, testis NHT, and B-cell
 NCI-CCAP GCB1) were mixed and 88 circles were made in
 vitro. Following HAP purification, this DNA was used as
 tracer in a subtractive hybridization reaction. The driver
 was PCR-amplified cDNAs from pools of 5,000 clones made
 from the same 3 libraries. The pools consisted of
 I.M.A.G.E. clones 297480-302087 682632-687239,
 726408-728711, and 729096-731393. Subtraction by Bento
 Soares and M. Fatima Bonaldo."

BASE COUNT
 ORIGIN
 1 a 11 c 7 g 0 t

Query Match 47.8%; Score 8.6; DB 9; Length 19;
 Best Local Similarity 73.3%; Pred. No. 4.6e+06;
 Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GCGCCCGATCCAGG 17
 16 GCGCCCGGCGCTGG 2

RESULT 21
 BM395601/c 23 bp mRNA linear EST 17-JAN-2002
 LOCUS
 DEFINITION
 5009-0-1-C04.c.1 Chilcoat/Turkewitz cDNA (large fraction)
 Tetrahymena thermophila cDNA, mRNA sequence.
 ACCESSION
 BM395601

VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

BM395601.1 GI:18195654
 EST.
 Tetrahymena thermophila.
 Tetrahymena thermophila
 Tetrahymena thermophila
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
 Hymenostomatida; Tetrahymenina; Tetrahymena.
 1 (bases 1 to 23)
 Turkewitz A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E., Frankel
 J., and Klobutcher, L.
 EST from Tetrahymena thermophila, strain CU428.1, growing cells
 Unpublished (2002)
 Contact: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3

FEATURES
 source
 Location/Qualifiers
 1..23
 /organism="Tetrahymena thermophila"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_1fb="Chilcoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript SK+; Details on library
 preparation can be found in Chilcoat and Turkewitz (2001)
 Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT
 ORIGIN
 9 a 6 c 6 g 2 t

Query Match 47.8%; Score 8.6; DB 13; Length 23;
 Best Local Similarity 73.3%; Pred. No. 4.6e+06;
 Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 CGCCCGATCCAGGC 18
 23 CGCGTGGCTCCAGC 9

RESULT 22
 AZ410218/c 23 bp DNA linear GSS 03-OCT-2000
 LOCUS
 DEFINITION
 AZ410218
 1M0182F23F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 clone UGCGIM0182F23 F, DNA sequence.
 AZ410218
 AZ410218.1 GI:10534231
 GSS.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 23)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmood, M., Meenen, B., Pedersen, T., Kelly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.
 and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts.
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0182 row: F column: 23
 Seq primer: CGTTGTAACACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 23.

FEATURES
SOURCE

Location/Qualifiers
1. .23

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0182F23"
/clone_1lb="Mouse 10kb plasmid UUC1M library"
/sex="Male"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN

2 a 0 c 14 g 7 t

Query Match 47.8%; Score 8.6; DB 17; Length 23;
Best Local Similarity 73.3%; Pred. No. 4.6e+06;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Cy 1 CTGCGCCCGATCCA 15
Db 19 CTCACCCCATCCA 5

RESULT 23
LOCUS 23 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0256F09R Mouse 10kb plasmid UUC2M library Mus musculus genomic
ACCESSION A2979817
VERSION A2979817
KEYWORDS A2979817.1 GI:13851044
SOURCE GSS.
ORGANISM house mouse.
Mammalia; Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0256 row: F column: 09
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.

FEATURES
SOURCE

Location/Qualifiers
1. .23

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M0256F09"
/clone_1lb="Mouse 10kb plasmid UUC2M library"
/sex="Female"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN

5 a 8 c 3 g 7 t

Query Match 47.8%; Score 8.6; DB 17; Length 23;
Best Local Similarity 73.3%; Pred. No. 4.6e+06;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Cy 4 CGCCCGATCCAGGC 18
Db 3 CTCCTTATCCAGGC 17

RESULT 24
LOCUS BM397860/c 24 bp mRNA linear EST 17-JAN-2002
DEFINITION 5009-0-38-B08.t.1 Chilcoat/Turkewitz cDNA (large fraction)
ACCESSION BM397860
VERSION BM397860.1 GI:18197913
KEYWORDS EST.
SOURCE EST.
ORGANISM Tetrahymena thermophila.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.
1 (bases 1 to 24)
Turkewitz, A.P., Karier, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel, J., and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
SOURCE

Location/Qualifiers
1. .24

/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_1lb="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript 2 SK+, Details on library preparation can be found in Chilcoat and Turkewitz (2001)


```
/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114[gb|AF129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

BASE COUNT 2 a 5 c 5 g 7 t
ORIGIN

Query Match 46.7%; Score 8.4; DB 17; Length 19;
Best Local Similarity 90.0%; Pred. No. 5.7e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 GGATCCAGGC 18
|||||
12 GGATCCGGGC 3

Db 12 GGATCCGGGC 3

RESULT 28
A2858446 19 bp DNA linear GSS 21-FEB-2001
LOCUS 2M0163D08R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0163D08 R, DNA sequence.

ACCESSION A2858446
VERSION A2858446.1 GI:13051622
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0163 row: D column: 08
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1..19
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0163D08"
/clone_1kb="Mouse 10kb plasmid UUGCIM library"

FEATURES
SOURCE

```
/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114[gb|AF129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

BASE COUNT 3 a 5 c 5 g 6 t
ORIGIN

Query Match 46.7%; Score 8.4; DB 17; Length 19;
Best Local Similarity 90.0%; Pred. No. 5.7e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 GGATCCAGGC 18
|||||
10 GGATCTGGGC 19

Db 10 GGATCTGGGC 19

RESULT 29
A2858446 19 bp DNA linear GSS 21-FEB-2001
LOCUS A2858446/C
DEFINITION 2M0163D08R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0163D08 R, DNA sequence.

ACCESSION A2858446
VERSION A2858446.1 GI:13051622
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0163 row: D column: 08
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1..19
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0163D08"
/clone_1kb="Mouse 10kb plasmid UUGCIM library"

FEATURES
SOURCE

/sex="Male"
/lab host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g1|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT
ORIGIN
3 a 5 c 5 g 6 t

Query Match
Best Local Similarity 46.7%; Score 8.4; DB 17; Length 19;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCCCGGATCC 14
Db 19 GCCAGGATCC 10

RESULT 30
AZ628022 20 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0476A13F Mouse 10kb plasmid UGCM library Mus musculus genomic
DEFINITION clone UGCM0476A13 F, DNA sequence.
ACCESSION AZ628022
VERSION AZ628022.1 GI:11750212
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausen,A.
and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0476 row: A column: 13
Seq primer: CGTGTGAAACGACGCGCACT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1..20
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCM0476A13"
/clone_1lb="Mouse 10kb plasmid UGCM library"

/sex="Male"
/lab host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g1|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT
ORIGIN
8 a 6 c 4 g 2 t

Query Match
Best Local Similarity 46.7%; Score 8.4; DB 17; Length 20;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 GGATCCAGGC 18
Db 17 GGTTCCAGGC 8

RESULT 31
AZ657644 20 bp DNA linear GSS 14-DEC-2000
LOCUS 1M0534B02F Mouse 10kb plasmid UGCM library Mus musculus genomic
DEFINITION clone UGCM0534B02 F, DNA sequence.
ACCESSION AZ657644
VERSION AZ657644.1 GI:11794790
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausen,A.
and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0534 row: B column: 02
Seq primer: CGTGTGAAACGACGCGCACT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1..20
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCM0534B02"
/clone_1lb="Mouse 10kb plasmid UGCM library"

```
/sex="Male"
/lab host="E. coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

BASE COUNT
ORIGIN
2 a 11 c 4 g 3 t

Query Match 46.7%; Score 8.4; DB 17; Length 20;
Best Local Similarity 90.0%; Pred. No. 5.7e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 3; Gaps 0;

OY 5 GCCCGGATCC 14
Db 3 GCCCGGATCC 12

RESULT 32
AZ961140 20 bp DNA linear GSS 27-APR-2001
LOCUS
DEFINITION 2M0229P20F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0229P20 F, DNA sequence.
ACCESSION
AZ961140
VERSION
AZ961140.1 GI:13832367
KEYWORDS
GSS.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Telam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weis
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0229 row: P column: 20
Seq primer: CATTGTAAACGACGCCACT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. 20
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0229P20"
/clone_lib="Mouse 10kb plasmid UUGC2M library"

FEATURES
source

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/sex="Female"
/lab host="E. coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD2 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

BASE COUNT
ORIGIN
1 a 8 c 7 g 4 t

Query Match 46.7%; Score 8.4; DB 17; Length 20;
Best Local Similarity 90.0%; Pred. No. 5.7e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CTGCGCCCGG 10
Db 9 CTGCGCTCGG 18

RESULT 33
AA989077/c 22 bp mRNA linear EST 27-JUN-1998
LOCUS
DEFINITION cr88a03.s1 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1602940.3,
similar to TR:015816 015816 TRANSMEMBRANE PROTEIN UNGED 1. [2]
TR:014902; contains TR1.b2 MSRI repetitive element ;, mRNA
sequence.
ACCESSION
AA989077
VERSION
AA989077.1 GI:3174648
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 22)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Christopher Morkaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNLT at:
www.bio.lnl.gov/bdrp/image/image.html

Trace considered overall poor quality
Insert Length: 760 Std Error: 0.00
Seq primer: -40m3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. 22
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1602940"
/clone_lib="NCI-CGAP_Lu5"

FEATURES
source

TITLE
The WashU-HMI Mouse EST Project
JOURNAL
Unpublished (1996)
COMMENT
Contact: Maria M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63138
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu

This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:910701

Trace considered overall poor quality
Possible reversed clone; similarity on wrong strand
Seq primer: -28m3 rev2 ET from Amerham
High quality sequence stop: 1.
Location/Qualifiers

FEATURES

SOURCE

1..25
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1398985"
/clone_1lb="Soares_mammary_gland_NBMG"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Organ: mammary gland; Vector: p773D-Pac (Pharmacia
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
primer (5',
TGTTACCAATCTGAGTGAGAGCGCCGATGTTTCTTTTCTTTTCTTTT
T 3'); double-stranded cDNA was ligated to Eco RI
adaptor (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified p773 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M. Fatima
Bonaldo."

BASE COUNT

8 a 4 c 8 g 5 t

ORIGIN

Query Match 46.7%; Score 8.4; DB 9; Length 25;
Best Local Similarity 90.0%; Pred. No. 5.7e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TGCCGCCGGA 11
16 TGCTCCCGA 25

RESULT 37 25 bp mRNA linear EST 16-DEC-1999
A1913416
LOCUS t277803.x1 NCI CGAP Panl Homo sapiens cDNA clone IMAGE:2294584.3
DEFINITION similar to SW-PRP HUMAN P81489 SALIVARY PROLINE-RICH PROTEIN 11-1
; contains PTH5.c2 MSRI repetitive element ; mRNA sequence.

ACCESSION A1913416
VERSION A1913416.1 GI:5633271
KEYWORDS EST.

SOURCE

human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 25)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbbs-remail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.llnl.gov/bdrrp/image/image.html

Trace considered overall poor quality
Insert Length: 1741 Std Error: 0.00
Seq primer: -400P from Glibco
High quality sequence stop: 1.
Location/Qualifiers

FEATURES

SOURCE

1..25
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2294584"
/clone_1lb="NCI CGAP Panl"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/note="Organ: pancreas; Vector: pCMV-Sport6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 Kb. Life Technologies catalog #:
11548-013"

BASE COUNT

3 a 16 c 6 g 0 t

ORIGIN

Query Match 46.7%; Score 8.4; DB 9; Length 25;
Best Local Similarity 90.0%; Pred. No. 5.7e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 CGCCCGATC 13
12 CGCCCGACC 21

RESULT 38 25 bp DNA linear GSS 29-SEP-2000
A2307545/c
LOCUS H0009H22F Mouse 10kb plasmid UUC1M library Mus musculus genomic
DEFINITION clone UUC1M0009H22 F, DNA sequence.

ACCESSION A2307545
VERSION A2307545.1 GI:1034652
KEYWORDS GSS.

SOURCE

house mouse.

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)
Dunn, D., Aoyagi, A., Barber, M., Beaconn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

ACCESSION A2307545

VERSION A2307545.1 GI:1034652

KEYWORDS

GSS.

FEATURES

High quality sequence stop: 25.
Location/Qualifiers

SOURCE

1..25

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0009H22"
/clone_1lb="Mouse 10kb plasmid UUC1M library"
/sex="Male"

/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 3 a 8 c 5 g 9 t

ORIGIN

Query Match 46.7%; Score 8.4; DB 17; Length 25;
Best Local Similarity 90.0%; Pred. No. 5.7e+06;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGCCCGGAT 12
Db 13 GCGCCCGGAT 4

RESULT 39

BM393804 15 bp mRNA linear EST 17-JAN-2002
LOCUS 50072-2-11-B12.r.1 Chlcoat/Turkewitz cDNA (large fraction)

DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION BM393804
VERSION BM393804.1 GI:18193857

KEYWORDS EST.

ORGANISM Tetrahymena thermophila.

REFERENCE 1 (bases 1 to 15)
Turkewitz, A.P., Karre, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel

Tetrahymena thermophila.
Hymenostomatida; Tetrahymenina; Tetrahymena.

Turkewitz, A.P., Karre, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel
J. and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)

COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES Location/Qualifiers

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/strain="CU428.1"

/db_xref="taxon:5911"
/clone_lib="Chlcoat/Turkewitz cDNA (large fraction)"
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preparation can be found in Chlcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT 2 a 4 c 7 g 2 t

ORIGIN

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Best Local Similarity 76.9%; Pred. No. 6.9e+06;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GCGCCCGGATCCA 15
Db 15 GCGCCCGGATCCA 3

RESULT 40

BM394186 17 bp mRNA linear EST 17-JAN-2002
LOCUS 50072-2-2-D09.r.1 Chlcoat/Turkewitz cDNA (large fraction)

DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION BM394186
VERSION BM394186.1 GI:18194239

KEYWORDS EST.

ORGANISM Tetrahymena thermophila.

REFERENCE 1 (bases 1 to 17)
Turkewitz, A.P., Karre, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel

Tetrahymena thermophila.
Hymenostomatida; Tetrahymenina; Tetrahymena.

Turkewitz, A.P., Karre, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel
J. and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
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COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES Location/Qualifiers

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preparation can be found in Chlcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT 1 a 4 c 8 g 4 t

ORIGIN

Query Match 45.6%; Score 8.2; DB 13; Length 17;
Best Local Similarity 76.9%; Pred. No. 6.9e+06;

Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GCGCCCGGATCCA 15
Db 17 GCGCCCGGATCCA 5

Search completed: June 7, 2003, 09:44:33
Job time: 1050.58 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 7, 2003, 08:51:24 ; Search time 68.7273 Seconds

(without alignments)
366.546 Million cell updates/sec

Title: US-10-080-959a-5

Perfect score: 18
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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 870385 seqs, 699768693 residues

Total number of hits satisfying chosen parameters: 359952

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	11.4	63.3	19	9	US-09-423-800-34
7	11.4	63.3	19	9	US-10-182-018-34
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C 103	10.2	56.7	20	10	US-09-891-517-76	Sequence 76, Appl	C 176	9.8	54.4	17	9	US-09-848-754A-1015	Sequence 1015, App
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C 135	10.2	56.7	25	10	US-09-866-108-11296	Sequence 11296, App	C 208	9.8	54.4	22	9	US-09-990-385-20	Sequence 20, Appl
C 136	10.2	56.7	25	10	US-09-866-108-11297	Sequence 11297, App	C 209	9.8	54.4	22	9	US-10-131-591A-76	Sequence 76, Appl
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C 138	10.2	56.7	25	10	US-09-972-467-5	Sequence 5, Appl	C 211	9.8	54.4	22	9	US-10-161-025-6	Sequence 6, Appl
C 139	10.2	56.7	25	10	US-09-963-285-12	Sequence 12, Appl	C 212	9.8	54.4	23	9	US-09-520-338-15	Sequence 15, Appl
C 140	10.2	56.7	15	9	US-09-877-705A-107	Sequence 107, App	C 213	9.8	54.4	23	9	US-09-507-362-75	Sequence 75, Appl
C 141	10.2	56.7	15	9	US-09-877-705A-108	Sequence 108, App	C 214	9.8	54.4	23	10	US-09-016-139-1	Sequence 1, Appl
C 142	10.2	56.7	15	9	US-09-877-738A-107	Sequence 107, App	C 215	9.8	54.4	23	12	US-10-101-747-3	Sequence 3, Appl
C 143	10.2	56.7	15	9	US-09-877-738A-108	Sequence 108, App	C 216	9.8	54.4	24	9	US-10-211-673-14	Sequence 14, Appl
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C 145	10.2	56.7	20	10	US-09-848-696-9	Sequence 9, Appl	C 218	9.8	54.4	24	9	US-09-940-185-1424	Sequence 1424, App
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C 147	10.2	56.7	21	9	US-10-012-898-22	Sequence 22, Appl	C 220	9.8	54.4	24	10	US-09-777-430A-79	Sequence 79, Appl
C 148	10.2	56.7	22	10	US-09-899-980A-32	Sequence 32, Appl	C 221	9.8	54.4	24	10	US-09-285-355C-18	Sequence 18, Appl
C 149	10.2	56.7	22	10	US-09-940-185-1344	Sequence 1344, App	C 222	9.8	54.4	24	10	US-09-997-664-56	Sequence 56, Appl
C 150	10.2	56.7	24	9	US-09-940-185-2710	Sequence 2710, App	C 223	9.8	54.4	25	9	US-09-847-101B-26	Sequence 26, Appl
C 151	10.2	56.7	25	10	US-10-061-943A-24	Sequence 24, Appl	C 224	9.8	54.4	25	9	US-10-215-112-8440	Sequence 8440, App
C 152	10.2	56.7	25	10	US-09-866-108-3582	Sequence 3582, App	C 225	9.8	54.4	25	9	US-09-507-362-78	Sequence 78, Appl
C 153	10.2	56.7	25	10	US-09-866-108-3583	Sequence 3583, App	C 226	9.8	54.4	25	10	US-09-866-108-5518	Sequence 5518, App
C 154	10.2	56.7	25	10	US-09-866-108-3584	Sequence 3584, App	C 227	9.8	54.4	25	10	US-09-866-108-5519	Sequence 5519, App
C 155	10.2	56.7	25	10	US-09-866-108-3585	Sequence 3585, App	C 228	9.8	54.4	25	10	US-09-866-108-5520	Sequence 5520, App
C 156	10.2	56.7	25	10	US-09-866-108-3586	Sequence 3586, App	C 229	9.8	54.4	25	10	US-09-866-108-5521	Sequence 5521, App
C 157	10.2	56.7	25	10	US-09-866-108-3587	Sequence 3587, App	C 230	9.8	54.4	17	9	US-09-961-077-80	Sequence 80, Appl
C 158	10.2	56.7	25	10	US-09-866-108-3588	Sequence 3588, App	C 231	9.8	54.4	17	9	US-09-961-077-82	Sequence 82, Appl
C 159	10.2	56.7	25	10	US-09-866-108-3589	Sequence 3589, App	C 232	9.8	54.4	17	9	US-09-780-533A-647	Sequence 647, App
C 160	9.8	54.4	15	9	US-09-880-313A-211	Sequence 211, App	C 233	9.6	53.3	17	9	US-09-848-754A-1759	Sequence 1759, App
C 161	9.8	54.4	15	9	US-09-880-313A-217	Sequence 217, App	C 234	9.6	53.3	17	9	US-09-848-754A-1014	Sequence 1014, App
C 162	9.8	54.4	15	9	US-09-880-313A-223	Sequence 223, App	C 235	9.6	53.3	17	9	US-09-848-754A-1068	Sequence 1068, App
C 163	9.8	54.4	15	9	US-09-880-313A-225	Sequence 225, App	C 236	9.6	53.3	17	9	US-09-848-754A-1069	Sequence 1069, App
C 164	9.8	54.4	15	9	US-09-880-313A-235	Sequence 235, App	C 237	9.6	53.3	17	9	US-09-930-423-1483	Sequence 1483, App
C 165	9.8	54.4	15	9	US-09-880-313A-247	Sequence 247, App	C 238	9.6	53.3	17	9		

239	9.6	53.3	17	10	US-09-866-108-651	Sequence 651, App	C 312	9.4	52.2	22	9	US-09-307-824-92	Sequence 92, Appl
240	9.6	53.3	17	10	US-09-866-108-652	Sequence 652, App	C 313	9.4	52.2	22	9	US-09-307-841-92	Sequence 92, Appl
241	9.6	53.3	17	10	US-09-866-108-2579	Sequence 2579, Ap	C 314	9.4	52.2	22	9	US-09-304-011-92	Sequence 92, Appl
C 242	9.6	53.3	18	9	US-10-253-408-21	Sequence 21, Appl	C 315	9.4	52.2	22	9	US-09-306-742-92	Sequence 92, Appl
C 243	9.6	53.3	19	9	US-10-251-482-17	Sequence 17, Appl	C 316	9.4	52.2	22	9	US-09-306-838-92	Sequence 92, Appl
C 244	9.6	53.3	20	9	US-09-964-261-286	Sequence 286, App	C 317	9.4	52.2	22	9	US-09-307-613-92	Sequence 92, Appl
C 245	9.6	53.3	20	9	US-09-949-427-144	Sequence 144, App	C 318	9.4	52.2	22	9	US-09-307-942-92	Sequence 92, Appl
C 246	9.6	53.3	20	9	US-09-906-158-42	Sequence 42, Appl	C 319	9.4	52.2	22	9	US-09-304-820-92	Sequence 92, Appl
C 248	9.6	53.3	20	9	US-10-123-434-9	Sequence 9, Appl	C 320	9.4	52.2	22	9	US-09-304-859-92	Sequence 92, Appl
C 249	9.6	53.3	20	9	US-09-953-047-62	Sequence 62, Appl	C 321	9.4	52.2	22	9	US-09-309-204-92	Sequence 92, Appl
C 250	9.6	53.3	20	10	US-09-899-440-10	Sequence 10, Appl	C 322	9.4	52.2	22	9	US-09-304-786-92	Sequence 92, Appl
C 251	9.6	53.3	20	10	US-09-734-847A-63	Sequence 63, Appl	C 323	9.4	52.2	22	9	US-09-306-646-92	Sequence 92, Appl
C 252	9.6	53.3	20	10	US-09-734-847A-64	Sequence 64, Appl	C 324	9.4	52.2	22	9	US-09-306-700-92	Sequence 92, Appl
C 253	9.6	53.3	20	10	US-09-800-629A-172	Sequence 172, App	C 325	9.4	52.2	22	9	US-09-302-903-92	Sequence 92, Appl
C 254	9.6	53.3	21	9	US-09-964-261-287	Sequence 287, App	C 326	9.4	52.2	22	9	US-09-303-748A-92	Sequence 92, Appl
C 255	9.6	53.3	21	9	US-09-093-972C-985	Sequence 95, App	C 327	9.4	52.2	22	9	US-09-303-786-92	Sequence 92, Appl
C 256	9.6	53.3	21	10	US-09-728-466-39	Sequence 39, Appl	C 328	9.4	52.2	22	9	US-09-302-736-92	Sequence 92, Appl
C 257	9.6	53.3	21	10	US-09-765-081-259	Sequence 259, App	C 329	9.4	52.2	22	9	US-09-304-119-92	Sequence 92, Appl
C 258	9.6	53.3	22	9	US-09-964-261-288	Sequence 288, App	C 330	9.4	52.2	22	9	US-09-304-956-92	Sequence 92, Appl
C 259	9.6	53.3	23	9	US-09-144-886-7	Sequence 7, Appl	C 331	9.4	52.2	22	9	US-09-307-794-92	Sequence 92, Appl
C 259	9.6	53.3	23	9	US-09-964-261-289	Sequence 289, App	C 332	9.4	52.2	22	9	US-09-302-692-92	Sequence 92, Appl
C 260	9.6	53.3	24	8	US-08-887-505-48	Sequence 48, Appl	C 333	9.4	52.2	22	9	US-09-303-520-92	Sequence 92, Appl
C 261	9.6	53.3	24	9	US-09-964-261-290	Sequence 290, App	C 334	9.4	52.2	22	9	US-09-303-843-92	Sequence 92, Appl
C 262	9.6	53.3	24	9	US-09-940-185-1518	Sequence 1518, Ap	C 335	9.4	52.2	22	9	US-09-304-462-92	Sequence 92, Appl
C 263	9.6	53.3	25	9	US-09-773-559-9	Sequence 9, Appl	C 336	9.4	52.2	22	9	US-09-305-056-92	Sequence 92, Appl
C 264	9.6	53.3	25	9	US-09-964-261-291	Sequence 291, App	C 337	9.4	52.2	22	9	US-09-307-925-92	Sequence 92, Appl
C 265	9.6	53.3	25	9	US-09-961-077-1250	Sequence 1250, Ap	C 338	9.4	52.2	22	9	US-09-304-553-92	Sequence 92, Appl
C 266	9.6	53.3	25	9	US-10-215-112-1196	Sequence 1196, A	C 339	9.4	52.2	22	9	US-09-305-381-92	Sequence 92, Appl
C 267	9.6	53.3	25	10	US-09-866-108-3580	Sequence 3580, Ap	C 340	9.4	52.2	22	9	US-09-309-064-92	Sequence 92, Appl
C 268	9.6	53.3	25	10	US-09-866-108-3581	Sequence 3581, Ap	C 341	9.4	52.2	22	9	US-09-305-088-92	Sequence 92, Appl
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C 270	9.4	52.2	15	10	US-09-866-108-5508	Sequence 7, Appl	C 343	9.4	52.2	22	9	US-09-302-759-92	Sequence 92, Appl
C 271	9.4	52.2	15	10	US-09-919-758-7	Sequence 7, Appl	C 344	9.4	52.2	22	9	US-09-305-075-92	Sequence 92, Appl
C 272	9.4	52.2	16	10	US-09-873-075A-4	Sequence 4, Appl	C 345	9.4	52.2	22	9	US-09-302-534-92	Sequence 92, Appl
C 273	9.4	52.2	17	9	US-09-864-785-668	Sequence 668, App	C 346	9.4	52.2	22	9	US-09-302-713-92	Sequence 92, Appl
C 274	9.4	52.2	17	9	US-09-982-658A-3	Sequence 3, Appl	C 347	9.4	52.2	22	9	US-09-307-979-92	Sequence 92, Appl
C 275	9.4	52.2	17	9	US-09-971-631-3	Sequence 3, Appl	C 348	9.4	52.2	22	9	US-09-302-615-92	Sequence 92, Appl
C 276	9.4	52.2	17	10	US-09-848-754A-2230	Sequence 2230, Ap	C 349	9.4	52.2	22	9	US-09-303-925-92	Sequence 92, Appl
C 277	9.4	52.2	17	10	US-09-866-108-6772	Sequence 6772, Ap	C 350	9.4	52.2	22	9	US-09-309-320-92	Sequence 92, Appl
C 278	9.4	52.2	17	10	US-09-866-108-6773	Sequence 6773, Ap	C 351	9.4	52.2	22	10	US-09-309-320-92	Sequence 92, Appl
C 279	9.4	52.2	17	10	US-09-866-108-6774	Sequence 6774, Ap	C 352	9.4	52.2	22	10	US-09-309-088B-92	Sequence 92, Appl
C 280	9.4	52.2	17	10	US-09-866-108-6775	Sequence 6775, Ap	C 353	9.4	52.2	23	9	US-10-084-686-1	Sequence 1, Appl
C 281	9.4	52.2	17	10	US-09-866-108-6776	Sequence 6776, Ap	C 354	9.4	52.2	23	9	US-09-507-362-76	Sequence 76, Appl
C 282	9.4	52.2	17	10	US-09-866-108-6777	Sequence 6777, Ap	C 355	9.4	52.2	23	10	US-09-725-112-2486	Sequence 2486, Ap
C 283	9.4	52.2	17	10	US-09-866-108-6778	Sequence 6778, Ap	C 356	9.4	52.2	24	9	US-09-859-854-10	Sequence 10, Appl
C 284	9.4	52.2	18	9	US-09-954-594A-36	Sequence 36, Appl	C 357	9.4	52.2	24	9	US-09-852-416-10	Sequence 10, Appl
C 285	9.4	52.2	18	9	US-09-974-685-36	Sequence 36, Appl	C 358	9.4	52.2	24	9	US-09-839-446-49	Sequence 49, Appl
C 286	9.4	52.2	18	9	US-09-093-972C-4	Sequence 4, Appl	C 359	9.4	52.2	24	9	US-09-940-185-1524	Sequence 1524, Ap
C 287	9.4	52.2	18	10	US-09-865-807-36	Sequence 36, Appl	C 360	9.4	52.2	24	10	US-09-940-185-2509	Sequence 2509, Ap
C 288	9.4	52.2	18	10	US-09-774-414-4	Sequence 4, Appl	C 361	9.4	52.2	24	10	US-09-859-854-10	Sequence 10, Appl
C 289	9.4	52.2	18	10	US-09-959-373-2911	Sequence 2911, Ap	C 362	9.4	52.2	25	9	US-09-898-570-49	Sequence 49, Appl
C 290	9.4	52.2	19	9	US-09-967-237-4	Sequence 4, Appl	C 363	9.4	52.2	25	9	US-09-887-145-48	Sequence 48, Appl
C 291	9.4	52.2	19	10	US-09-772-719-4	Sequence 4, Appl	C 364	9.4	52.2	25	9	US-10-215-112-2486	Sequence 2486, Ap
C 292	9.4	52.2	19	10	US-09-918-951-12	Sequence 12, Appl	C 365	9.4	52.2	25	9	US-10-215-112-2850	Sequence 2850, Ap
C 293	9.4	52.2	20	9	US-09-888-326-492	Sequence 492, App	C 366	9.4	52.2	25	9	US-10-215-112-4114	Sequence 4114, Ap
C 294	9.4	52.2	20	9	US-10-057-550-78	Sequence 78, Appl	C 367	9.4	52.2	25	10	US-10-215-112-8314	Sequence 8314, Ap
C 295	9.4	52.2	20	9	US-10-112-653-511	Sequence 511, App	C 368	9.4	52.2	25	10	US-09-866-108-11664	Sequence 11664, A
C 296	9.4	52.2	20	9	US-10-017-995-534	Sequence 534, App	C 369	9.4	52.2	25	10	US-09-866-108-11665	Sequence 11665, A
C 297	9.4	52.2	20	9	US-10-067-125-51	Sequence 51, Appl	C 370	9.4	52.2	25	10	US-09-866-108-11666	Sequence 11666, A
C 298	9.4	52.2	20	9	US-09-776-479-534	Sequence 534, App	C 371	9.4	52.2	25	10	US-09-866-108-11667	Sequence 11667, A
C 299	9.4	52.2	20	9	US-10-001-076-38	Sequence 38, Appl	C 372	9.4	52.2	25	10	US-09-866-108-11668	Sequence 11668, A
C 300	9.4	52.2	20	10	US-09-758-881-56	Sequence 56, Appl	C 373	9.4	52.2	25	10	US-09-866-108-11669	Sequence 11669, A
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C 302	9.4	52.2	20	10	US-09-854-883-203	Sequence 203, Appl	C 375	9.4	52.2	25	10	US-09-866-108-11671	Sequence 11671, A
C 303	9.4	52.2	20	10	US-09-752-639-79	Sequence 79, Appl	C 376	9.4	52.2	25	10	US-09-866-108-11672	Sequence 11672, A
C 304	9.4	52.2	20	10	US-09-984-198-79	Sequence 79, Appl	C 377	9.4	52.2	25	10	US-09-866-108-11673	Sequence 11673, A
C 305	9.4	52.2	20	10	US-09-809-545A-83	Sequence 83, Appl	C 378	9.4	52.2	25	10	US-09-866-108-11674	Sequence 11674, A
C 306	9.4	52.2	21	9	US-09-808-602-40	Sequence 40, Appl	C 379	9.4	52.2	25	10	US-09-866-108-11675	Sequence 11675, A
C 307	9.4	52.2	21	9	US-09-808-602-41	Sequence 41, Appl	C 380	9.4	52.2	25	10	US-09-866-108-11676	Sequence 11676, A
C 308	9.4	52.2	21	9	US-10-158-160A-86	Sequence 26, Appl	C 381	9.4	52.2	25	10	US-09-866-108-11677	Sequence 11677, A
C 309	9.4	52.2	21	9	US-09-952-213D-8	Sequence 8, Appl	C 382	9.4	52.2	25	10	US-09-866-108-11678	Sequence 11678, A
C 310	9.4	52.2	22	9	US-09-905-291A-92	Sequence 92, Appl	C 383	9.4	52.2	25	10	US-09-911-346-12	Sequence 12, Appl
C 311	9.4	52.2	22	9	US-09-902-853-92	Sequence 92, Appl	C 384	9.2	51.1	14	9	US-10-076-106-1	Sequence 1, Appl

C 385	9.2	51.1	14	9	US-10-076-106-1	Sequence 1, Appl1	458	9.2	51.1	20	9	US-10-181-107-120	Sequence 120, App
386	9.2	51.1	15	9	US-09-864-785-3720	Sequence 3720, Ap	C 459	9.2	51.1	20	9	US-10-228-443-87	Sequence 87, Appl
387	9.2	51.1	15	9	US-10-118-100-38	Sequence 38, Appl	C 460	9.2	51.1	20	9	US-10-007-076-170	Sequence 170, Appl
388	9.2	51.1	15	10	US-09-953-242-14	Sequence 14, Appl	C 461	9.2	51.1	20	9	US-10-016-149-19	Sequence 19, Appl
389	9.2	51.1	16	8	US-08-591-486B-39	Sequence 39, Appl	C 462	9.2	51.1	20	9	US-10-166-841-3	Sequence 3, Appl1
390	9.2	51.1	16	9	US-09-821-278-5	Sequence 2, Appl1	C 463	9.2	51.1	20	10	US-09-758-881-21	Sequence 21, Appl
391	9.2	51.1	16	9	US-09-760-294-2	Sequence 5, Appl1	C 464	9.2	51.1	20	10	US-09-735-995-50	Sequence 50, Appl
392	9.2	51.1	17	9	US-09-978-295A-544	Sequence 544, App	C 465	9.2	51.1	20	10	US-09-802-669-70	Sequence 70, Appl
393	9.2	51.1	17	9	US-09-978-697-544	Sequence 544, App	C 466	9.2	51.1	20	10	US-09-874-847A-62	Sequence 62, Appl
394	9.2	51.1	17	9	US-09-864-785-333	Sequence 333, App	C 467	9.2	51.1	20	10	US-09-852-053-21	Sequence 21, Appl
395	9.2	51.1	17	9	US-09-864-785-467	Sequence 467, App	C 468	9.2	51.1	20	10	US-09-932-448-7	Sequence 7, Appl1
396	9.2	51.1	17	9	US-09-864-785-468	Sequence 468, App	C 469	9.2	51.1	20	10	US-09-932-448-23	Sequence 23, Appl
397	9.2	51.1	17	9	US-09-864-785-2101	Sequence 2101, Ap	C 470	9.2	51.1	20	10	US-09-791-406-21	Sequence 21, Appl
398	9.2	51.1	17	9	US-09-864-785-2864	Sequence 2864, App	C 471	9.2	51.1	20	10	US-09-964-261-87	Sequence 267, Appl
399	9.2	51.1	17	9	US-09-999-832A-544	Sequence 544, App	C 472	9.2	51.1	21	9	US-10-101-461-9	Sequence 9, Appl1
400	9.2	51.1	17	9	US-09-825-805-387	Sequence 387, App	C 473	9.2	51.1	21	9	US-09-984-842-19	Sequence 19, Appl
401	9.2	51.1	17	9	US-09-825-805-857	Sequence 857, App	C 474	9.2	51.1	21	9	US-09-765-081-434	Sequence 105, App
402	9.2	51.1	17	9	US-09-978-189-544	Sequence 544, App	C 475	9.2	51.1	21	9	US-09-860-788C-116	Sequence 116, Appl
403	9.2	51.1	17	9	US-09-961-077-1251	Sequence 1251, Ap	C 476	9.2	51.1	21	9	US-09-984-842-18	Sequence 18, Appl
404	9.2	51.1	17	9	US-09-961-077-1251	Sequence 1251, Ap	C 477	9.2	51.1	21	9	US-10-206-839-105	Sequence 105, App
405	9.2	51.1	17	9	US-09-978-608A-544	Sequence 544, App	C 478	9.2	51.1	21	10	US-09-776-874A-18	Sequence 434, App
406	9.2	51.1	17	9	US-09-818-875-467	Sequence 467, App	C 479	9.2	51.1	21	10	US-10-066-151-43	Sequence 43, Appl
407	9.2	51.1	17	9	US-09-818-875-468	Sequence 468, App	C 480	9.2	51.1	21	10	US-09-964-261-288	Sequence 288, App
408	9.2	51.1	17	9	US-09-978-191A-544	Sequence 544, App	C 481	9.2	51.1	22	9	US-09-739-843-6	Sequence 36, Appl
409	9.2	51.1	17	9	US-09-978-403A-544	Sequence 544, App	C 482	9.2	51.1	22	10	US-09-899-980A-32	Sequence 6, Appl1
410	9.2	51.1	17	9	US-09-978-564A-544	Sequence 544, App	C 483	9.2	51.1	22	10	US-09-417-791-9	Sequence 9, Appl1
411	9.2	51.1	17	9	US-09-978-565A-544	Sequence 544, App	C 484	9.2	51.1	22	10	US-09-417-791-11	Sequence 11, Appl
412	9.2	51.1	17	9	US-09-978-585A-544	Sequence 544, App	C 485	9.2	51.1	22	10	US-09-934-332-14	Sequence 14, Appl
413	9.2	51.1	17	9	US-10-017-081A-544	Sequence 544, App	C 486	9.2	51.1	22	10	US-09-997-664-10	Sequence 10, Appl
414	9.2	51.1	17	9	US-09-978-82A-544	Sequence 544, App	C 487	9.2	51.1	22	10	US-08-812-933A-37	Sequence 37, Appl
415	9.2	51.1	17	9	US-09-981-915A-544	Sequence 544, App	C 488	9.2	51.1	23	8	US-08-812-933A-38	Sequence 38, Appl
416	9.2	51.1	17	9	US-09-999-833A-544	Sequence 544, App	C 489	9.2	51.1	23	9	US-09-964-261-289	Sequence 289, App
417	9.2	51.1	17	9	US-10-167-749-544	Sequence 544, App	C 490	9.2	51.1	23	9	US-10-124-038-13	Sequence 13, Appl
418	9.2	51.1	17	9	US-09-918-585A-544	Sequence 544, App	C 491	9.2	51.1	23	10	US-09-871-615-3	Sequence 3, Appl1
419	9.2	51.1	17	9	US-09-877-478-455	Sequence 455, App	C 492	9.2	51.1	23	9	US-09-860-784-74	Sequence 74, Appl
420	9.2	51.1	17	9	US-09-877-478-2391	Sequence 2391, Ap	C 493	9.2	51.1	23	9	US-09-964-261-290	Sequence 290, App
421	9.2	51.1	17	9	US-09-877-478-2392	Sequence 2392, Ap	C 494	9.2	51.1	23	10	US-10-027-661A-1	Sequence 1, Appl1
422	9.2	51.1	17	9	US-10-013-921A-544	Sequence 544, App	C 495	9.2	51.1	23	10	US-09-860-784-74	Sequence 74, Appl
423	9.2	51.1	17	9	US-09-978-423A-544	Sequence 544, App	C 496	9.2	51.1	24	9	US-09-964-261-290	Sequence 290, App
424	9.2	51.1	17	9	US-09-848-754A-824	Sequence 824, App	C 497	9.2	51.1	24	9	US-10-027-661A-1	Sequence 1, Appl1
425	9.2	51.1	17	9	US-09-978-193A-544	Sequence 544, App	C 498	9.2	51.1	24	9	US-10-175-268-1	Sequence 1, Appl1
426	9.2	51.1	17	9	US-10-016-177A-544	Sequence 544, App	C 499	9.2	51.1	24	9	US-10-121-058-42	Sequence 42, Appl
427	9.2	51.1	17	9	US-10-016-177A-544	Sequence 544, App	C 500	9.2	51.1	24	9	US-10-121-058-42	Sequence 42, Appl
428	9.2	51.1	17	9	US-09-999-830A-544	Sequence 544, App	C 501	9.2	51.1	24	9	US-10-124-038-17	Sequence 17, Appl
429	9.2	51.1	17	9	US-09-978-757A-544	Sequence 544, App	C 502	9.2	51.1	24	9	US-09-992-665-308	Sequence 308, App
430	9.2	51.1	17	9	US-10-055-719-10	Sequence 10, Appl	C 503	9.2	51.1	24	9	US-09-940-185-61	Sequence 61, Appl
431	9.2	51.1	17	9	US-09-930-423-1484	Sequence 1484, Ap	C 504	9.2	51.1	24	9	US-09-940-185-1566	Sequence 1566, App
432	9.2	51.1	17	9	US-09-930-423-1485	Sequence 1485, Ap	C 505	9.2	51.1	24	9	US-09-940-185-1566	Sequence 1566, App
433	9.2	51.1	17	10	US-09-978-187B-544	Sequence 544, App	C 506	9.2	51.1	24	9	US-09-940-185-1566	Sequence 1566, App
434	9.2	51.1	17	10	US-09-866-108-649	Sequence 649, App	C 507	9.2	51.1	24	9	US-09-940-185-1566	Sequence 1566, App
435	9.2	51.1	17	10	US-09-866-108-649	Sequence 649, App	C 508	9.2	51.1	24	9	US-09-940-185-1566	Sequence 1566, App
436	9.2	51.1	17	10	US-09-866-108-649	Sequence 649, App	C 509	9.2	51.1	24	9	US-09-940-185-1566	Sequence 1566, App
437	9.2	51.1	17	10	US-09-866-108-649	Sequence 649, App	C 510	9.2	51.1	24	10	US-09-940-185-1566	Sequence 1566, App
438	9.2	51.1	18	9	US-09-835-370-17	Sequence 17, Appl	C 511	9.2	51.1	24	10	US-09-803-347-1	Sequence 1, Appl1
439	9.2	51.1	18	9	US-09-835-370-17	Sequence 17, Appl	C 512	9.2	51.1	24	10	US-09-803-347-1	Sequence 1, Appl1
440	9.2	51.1	18	10	US-09-858-616-3	Sequence 3, Appl1	C 513	9.2	51.1	24	10	US-09-803-347-1	Sequence 1, Appl1
441	9.2	51.1	18	10	US-09-858-616-3	Sequence 3, Appl1	C 514	9.2	51.1	24	10	US-09-803-347-1	Sequence 1, Appl1
442	9.2	51.1	18	10	US-09-858-616-3	Sequence 3, Appl1	C 515	9.2	51.1	24	10	US-09-803-347-1	Sequence 1, Appl1
443	9.2	51.1	18	10	US-09-858-616-3	Sequence 3, Appl1	C 516	9.2	51.1	24	10	US-09-803-347-1	Sequence 1, Appl1
444	9.2	51.1	19	9	US-10-000-512-26	Sequence 26, Appl	C 517	9.2	51.1	24	10	US-09-803-347-1	Sequence 1, Appl1
445	9.2	51.1	19	9	US-10-138-316-42	Sequence 42, Appl	C 518	9.2	51.1	24	10	US-09-803-347-1	Sequence 1, Appl1
446	9.2	51.1	19	10	US-09-754-949-16	Sequence 16, Appl	C 519	9.2	51.1	24	12	US-10-066-151-89	Sequence 89, Appl
447	9.2	51.1	19	10	US-09-754-949-16	Sequence 16, Appl	C 520	9.2	51.1	24	12	US-10-066-151-89	Sequence 89, Appl
448	9.2	51.1	19	10	US-09-754-949-16	Sequence 16, Appl	C 521	9.2	51.1	25	9	US-09-860-784-76	Sequence 76, Appl
449	9.2	51.1	19	10	US-09-754-949-16	Sequence 16, Appl	C 522	9.2	51.1	25	9	US-09-860-784-76	Sequence 76, Appl
450	9.2	51.1	20	9	US-09-860-784-73	Sequence 73, Appl	C 523	9.2	51.1	25	9	US-09-860-784-76	Sequence 76, Appl
451	9.2	51.1	20	9	US-09-860-784-73	Sequence 73, Appl	C 524	9.2	51.1	25	9	US-09-860-784-76	Sequence 76, Appl
452	9.2	51.1	20	9	US-09-860-784-73	Sequence 73, Appl	C 525	9.2	51.1	25	9	US-09-860-784-76	Sequence 76, Appl
453	9.2	51.1	20	9	US-09-860-784-73	Sequence 73, Appl	C 526	9.2	51.1	25	9	US-09-860-784-76	Sequence 76, Appl
454	9.2	51.1	20	9	US-09-860-784-73	Sequence 73, Appl	C 527	9.2	51.1	25	9	US-09-860-784-76	Sequence 76, Appl
455	9.2	51.1	20	9	US-09-860-784-73	Sequence 73, Appl	C 528	9.2	51.1	25	9	US-09-860-784-76	Sequence 76, Appl
456	9.2	51.1	20	9	US-09-860-784-73	Sequence 73, Appl	C 529	9.2	51.1	25	9	US-09-860-784-76	Sequence 76, Appl
457	9.2	51.1	20	9	US-09-860-784-73	Sequence 73, Appl	C 530	9.2	51.1	25	9	US-09-860-784-76	Sequence 76, Appl

C 531	9.2	51.1	25	9	US-10-215-112-9042	Sequence 9042, Ap	C 604	9	50.0	20	10	US-09-832-648-7	Sequence 7, Appl
C 532	9.2	51.1	25	9	US-10-215-112-11993	Sequence 11993, A	C 605	9	50.0	20	10	US-09-832-648-23	Sequence 23, Appl
C 533	9.2	51.1	25	9	US-10-264-361-14	Sequence 14, Appl	C 606	9	50.0	20	10	US-09-965-662-10	Sequence 10, Appl
C 534	9.2	51.1	25	9	US-09-940-185-4043	Sequence 4043, Ap	C 607	9	50.0	21	9	US-09-978-299A-584	Sequence 584, App
C 535	9.2	51.1	25	10	US-09-866-108-3578	Sequence 3578, Ap	C 608	9	50.0	21	9	US-09-978-697-584	Sequence 584, App
C 536	9.2	51.1	25	10	US-09-866-108-3591	Sequence 3591, Ap	C 609	9	50.0	21	9	US-09-978-192A-584	Sequence 584, App
C 537	9.2	51.1	25	10	US-09-866-108-11287	Sequence 11287, A	C 610	9	50.0	21	9	US-09-999-832A-584	Sequence 584, App
C 538	9.2	51.1	25	10	US-09-866-108-11299	Sequence 11299, A	C 611	9	50.0	21	9	US-09-978-189-584	Sequence 584, App
C 539	9.2	51.1	25	10	US-09-452-599-93	Sequence 93, Appl	C 612	9	50.0	21	9	US-10-132-605-25	Sequence 25, Appl
C 540	9.2	51.1	25	10	US-09-815-330A-8	Sequence 8, Appl	C 613	9	50.0	21	9	US-09-978-608A-584	Sequence 584, App
C 541	9.2	51.1	25	10	US-09-956-998A-6	Sequence 6, Appl	C 614	9	50.0	21	9	US-09-978-191A-584	Sequence 584, App
C 542	9.2	51.1	25	10	US-09-956-998A-6	Sequence 13, Appl	C 615	9	50.0	21	9	US-09-978-403A-584	Sequence 584, App
C 543	9.2	51.1	25	10	US-09-990-186-2245	Sequence 2245, Ap	C 616	9	50.0	21	9	US-09-978-588A-584	Sequence 584, App
C 544	9.2	51.1	9	10	US-09-989-789-2245	Sequence 2245, Ap	C 617	9	50.0	21	9	US-10-167-744-584	Sequence 584, App
C 545	9.2	51.1	11	10	US-09-813-031-10	Sequence 10, Appl	C 618	9	50.0	21	9	US-10-017-081A-584	Sequence 584, App
C 546	9.2	51.1	11	10	US-09-813-031-18	Sequence 18, Appl	C 619	9	50.0	21	9	US-09-949-427-402	Sequence 402, App
C 547	9.2	51.1	11	10	US-09-813-990A-10	Sequence 10, Appl	C 620	9	50.0	21	9	US-09-978-824-584	Sequence 584, App
C 548	9.2	51.1	11	10	US-09-813-990A-18	Sequence 18, Appl	C 621	9	50.0	21	9	US-09-981-912A-584	Sequence 584, App
C 549	9.2	51.1	15	9	US-09-879-813-67	Sequence 67, Appl	C 622	9	50.0	21	9	US-09-999-833A-584	Sequence 584, App
C 550	9.2	51.1	15	9	US-10-118-100-28	Sequence 28, Appl	C 623	9	50.0	21	9	US-10-167-744-584	Sequence 584, App
C 551	9.2	51.1	15	10	US-09-005-243-91	Sequence 91, Appl	C 624	9	50.0	21	9	US-09-918-588A-584	Sequence 584, App
C 552	9.2	51.1	15	10	US-09-005-243-92	Sequence 92, Appl	C 625	9	50.0	21	9	US-09-978-423A-584	Sequence 584, App
C 553	9.2	51.1	15	10	US-09-224-683-91	Sequence 91, Appl	C 626	9	50.0	21	9	US-10-013-921A-584	Sequence 584, App
C 554	9.2	51.1	15	10	US-09-224-683-92	Sequence 92, Appl	C 627	9	50.0	21	9	US-09-978-193A-584	Sequence 584, App
C 555	9.2	51.1	16	9	US-09-880-113A-213	Sequence 213, App	C 628	9	50.0	21	9	US-10-013-929A-584	Sequence 584, App
C 556	9.2	51.1	16	9	US-09-880-113A-219	Sequence 219, App	C 629	9	50.0	21	9	US-10-016-172A-584	Sequence 584, App
C 557	9.2	51.1	16	9	US-09-880-113A-225	Sequence 225, App	C 630	9	50.0	21	9	US-09-999-830A-584	Sequence 584, App
C 558	9.2	51.1	16	9	US-09-880-113A-231	Sequence 231, App	C 631	9	50.0	21	9	US-09-978-757A-584	Sequence 584, App
C 559	9.2	51.1	16	9	US-09-880-113A-237	Sequence 237, App	C 632	9	50.0	21	9	US-09-978-187B-584	Sequence 584, App
C 560	9.2	51.1	16	9	US-09-880-113A-249	Sequence 249, App	C 633	9	50.0	21	10	US-09-765-061-151	Sequence 151, App
C 561	9.2	51.1	17	9	US-09-880-113A-273	Sequence 273, App	C 634	9	50.0	21	10	US-09-923-246-16	Sequence 16, Appl
C 562	9.2	51.1	17	9	US-09-825-805-317	Sequence 317, App	C 635	9	50.0	21	10	US-09-889-238-89	Sequence 89, Appl
C 563	9.2	51.1	17	9	US-09-825-805-360	Sequence 360, App	C 636	9	50.0	22	10	US-09-880-253A-37	Sequence 37, Appl
C 564	9.2	51.1	17	9	US-09-818-875-2886	Sequence 2886, Ap	C 637	9	50.0	22	10	US-09-862-027-67	Sequence 67, Appl
C 565	9.2	51.1	17	9	US-09-818-875-2887	Sequence 2887, Ap	C 638	9	50.0	23	9	US-10-101-461-11	Sequence 11, Appl
C 566	9.2	51.1	17	10	US-09-768-436-9	Sequence 9, Appl	C 639	9	50.0	23	9	US-10-138-316-53	Sequence 53, Appl
C 567	9.2	51.1	17	10	US-09-866-108-653	Sequence 653, App	C 640	9	50.0	23	9	US-10-247-287-6	Sequence 23, Appl
C 568	9.2	51.1	17	10	US-09-866-108-2449	Sequence 2449, Ap	C 641	9	50.0	23	10	US-09-416-234A-23	Sequence 23, Appl
C 569	9.2	51.1	17	10	US-09-866-108-9969	Sequence 9969, Ap	C 642	9	50.0	24	9	US-09-978-299A-486	Sequence 486, App
C 570	9.2	51.1	18	9	US-09-910-483-64	Sequence 483, Ap	C 643	9	50.0	24	9	US-09-978-697-486	Sequence 486, App
C 571	9.2	51.1	18	9	US-10-096-986-67	Sequence 67, Appl	C 644	9	50.0	24	9	US-10-112-797-2	Sequence 2, Appl
C 572	9.2	51.1	18	10	US-09-766-113-10	Sequence 10, Appl	C 645	9	50.0	24	9	US-09-978-191A-486	Sequence 486, App
C 573	9.2	51.1	18	10	US-09-766-113-12	Sequence 12, Appl	C 646	9	50.0	24	9	US-09-978-812A-486	Sequence 486, App
C 574	9.2	51.1	19	9	US-10-117-983-5	Sequence 5, Appl	C 647	9	50.0	24	9	US-09-999-813A-486	Sequence 486, App
C 575	9.2	51.1	19	9	US-09-880-113A-253	Sequence 253, App	C 648	9	50.0	24	9	US-09-978-189-486	Sequence 486, App
C 576	9.2	51.1	19	10	US-09-920-552-90	Sequence 90, Appl	C 649	9	50.0	24	9	US-09-852-411-8	Sequence 411, Appl
C 577	9.2	51.1	19	10	US-09-832-648-24	Sequence 24, Appl	C 650	9	50.0	24	9	US-09-978-608A-486	Sequence 486, App
C 578	9.2	51.1	20	9	US-10-060-301-35	Sequence 35, Appl	C 651	9	50.0	24	9	US-09-978-403A-486	Sequence 486, App
C 579	9.2	51.1	20	9	US-10-099-704-3	Sequence 3, Appl	C 652	9	50.0	24	9	US-09-978-562A-486	Sequence 486, App
C 580	9.2	51.1	20	9	US-10-219-248-26	Sequence 26, Appl	C 653	9	50.0	24	9	US-09-978-588A-486	Sequence 486, App
C 581	9.2	51.1	20	9	US-10-077-219-3	Sequence 3, Appl	C 654	9	50.0	24	9	US-10-017-081A-486	Sequence 486, App
C 582	9.2	51.1	20	9	US-10-219-247-26	Sequence 26, Appl	C 655	9	50.0	24	9	US-09-978-824-486	Sequence 486, App
C 583	9.2	51.1	20	9	US-09-880-113A-207	Sequence 207, App	C 656	9	50.0	24	9	US-09-981-912A-486	Sequence 486, App
C 584	9.2	51.1	20	9	US-09-880-113A-243	Sequence 243, App	C 657	9	50.0	24	9	US-09-999-813A-486	Sequence 486, App
C 585	9.2	51.1	20	9	US-09-880-113A-261	Sequence 261, App	C 658	9	50.0	24	9	US-10-167-744-486	Sequence 486, App
C 586	9.2	51.1	20	9	US-09-948-002-55	Sequence 55, Appl	C 659	9	50.0	24	9	US-09-918-588A-486	Sequence 486, App
C 587	9.2	51.1	20	9	US-09-948-002-69	Sequence 69, Appl	C 660	9	50.0	24	9	US-09-978-423A-486	Sequence 486, App
C 588	9.2	51.1	20	9	US-10-222-334-13	Sequence 13, Appl	C 661	9	50.0	24	9	US-10-013-929A-486	Sequence 486, App
C 589	9.2	51.1	20	9	US-10-118-100-29	Sequence 29, Appl	C 662	9	50.0	24	9	US-09-978-193A-486	Sequence 486, App
C 590	9.2	51.1	20	9	US-10-304-136-6	Sequence 6, Appl	C 663	9	50.0	24	9	US-10-013-929A-486	Sequence 486, App
C 591	9.2	51.1	20	9	US-10-300-616-8	Sequence 8, Appl	C 664	9	50.0	24	9	US-10-016-172A-486	Sequence 486, App
C 592	9.2	51.1	20	9	US-09-898-556A-15	Sequence 15, Appl	C 665	9	50.0	24	9	US-09-999-830A-486	Sequence 486, App
C 593	9.2	51.1	20	9	US-09-915-814-65	Sequence 65, Appl	C 666	9	50.0	24	9	US-09-952-522B-10	Sequence 10, Appl
C 594	9.2	51.1	20	10	US-09-734-846-46	Sequence 46, Appl	C 667	9	50.0	24	9	US-09-978-757A-486	Sequence 486, App
C 595	9.2	51.1	20	10	US-09-752-983-124	Sequence 124, App	C 668	9	50.0	24	9	US-10-184-732-29	Sequence 29, Appl
C 596	9.2	51.1	20	10	US-09-825-922-6	Sequence 6, Appl	C 669	9	50.0	24	9	US-09-940-185-263	Sequence 263, App
C 597	9.2	51.1	20	10	US-09-734-847A-48	Sequence 48, Appl	C 670	9	50.0	24	9	US-09-940-185-263	Sequence 263, App
C 598	9.2	51.1	20	10	US-09-734-847A-61	Sequence 61, Appl	C 671	9	50.0	24	9	US-09-978-187B-486	Sequence 486, App
C 599	9.2	51.1	20	10	US-09-734-847A-62	Sequence 62, Appl	C 672	9	50.0	24	10	US-09-784-443-105	Sequence 105, Appl
C 600	9.2	51.1	20	10	US-09-734-847A-63	Sequence 63, Appl	C 673	9	50.0	24	10	US-09-949-145-24	Sequence 24, Appl
C 601	9.2	51.1	20	10	US-09-734-847A-64	Sequence 64, Appl	C 674	9	50.0	25	7	US-09-859-854-8	Sequence 8, Appl
C 602	9.2	51.1	20	10	US-09-734-847A-65	Sequence 65, Appl	C 675	9	50.0	25	10	US-08-722-570-16	Sequence 16, Appl
C 603	9.2	51.1	20	10	US-09-855-722-26	Sequence 26, Appl	C 676	9	50.0	25	9	US-10-040-497-11	Sequence 11, Appl

677	9	50.0	25	9	US-10-151-668-4	Sequence 4, Appl1	750	8.8	48.9	17	9	US-09-930-423-383	Sequence 383, App
678	9	50.0	25	9	US-09-750-110-25	Sequence 25, Appl	751	8.8	48.9	17	9	US-09-930-423-385	Sequence 385, App
679	9	50.0	25	9	US-10-215-112-2619	Sequence 2619, Ap	752	8.8	48.9	17	9	US-09-930-423-1350	Sequence 1350, App
680	9	50.0	25	9	US-10-215-112-5553	Sequence 5553, Ap	753	8.8	48.9	17	9	US-09-930-423-1458	Sequence 1458, App
C 681	9	50.0	25	9	US-10-215-112-6419	Sequence 6419, Ap	754	8.8	48.9	17	9	US-09-930-423-1459	Sequence 1459, App
C 682	9	50.0	25	9	US-10-215-112-7210	Sequence 7210, Ap	755	8.8	48.9	17	9	US-09-930-423-1478	Sequence 1478, App
C 683	9	50.0	25	9	US-10-215-112-7332	Sequence 7332, Ap	756	8.8	48.9	17	10	US-09-832-382-4	Sequence 4, App
C 684	9	50.0	25	9	US-10-215-112-8793	Sequence 8793, Ap	757	8.8	48.9	17	10	US-09-866-108-647	Sequence 647, App
C 685	9	50.0	25	9	US-10-215-112-8919	Sequence 8919, Ap	758	8.8	48.9	17	10	US-09-866-108-648	Sequence 648, App
C 686	9	50.0	25	9	US-10-215-112-9159	Sequence 9159, Ap	759	8.8	48.9	17	10	US-09-866-108-2585	Sequence 2585, App
C 687	9	50.0	25	9	US-10-215-112-9905	Sequence 9905, Ap	760	8.8	48.9	17	10	US-09-866-108-6393	Sequence 6393, App
C 688	9	50.0	25	9	US-10-215-112-10017	Sequence 10017, A	761	8.8	48.9	17	10	US-09-866-108-10349	Sequence 10349, App
C 689	9	50.0	25	9	US-10-215-112-11145	Sequence 11145, A	762	8.8	48.9	17	10	US-09-866-108-10346	Sequence 10346, App
C 690	9	50.0	25	9	US-09-940-185-4092	Sequence 4092, Ap	763	8.8	48.9	17	10	US-09-866-108-10347	Sequence 10347, App
C 691	9	50.0	25	9	US-09-940-185-4244	Sequence 4244, Ap	764	8.8	48.9	17	10	US-09-866-108-10350	Sequence 10350, App
C 692	9	50.0	25	9	US-10-161-025-2	Sequence 2, Appl1	765	8.8	48.9	17	10	US-09-811-737-25	Sequence 10351, App
C 693	9	50.0	25	10	US-09-866-108-3590	Sequence 3590, Ap	766	8.8	48.9	17	10	US-09-263-955-47	Sequence 25, App
C 694	9	50.0	25	10	US-09-866-108-5378	Sequence 5378, Ap	767	8.8	48.9	17	10	US-09-866-108-10351	Sequence 47, App
C 695	9	50.0	25	10	US-09-866-108-5379	Sequence 5379, Ap	768	8.8	48.9	17	10	US-09-866-108-10350	Sequence 201, App
C 696	9	50.0	25	10	US-09-866-108-5380	Sequence 5380, Ap	769	8.8	48.9	17	10	US-09-866-108-10351	Sequence 201, App
C 697	9	50.0	25	10	US-09-866-108-5381	Sequence 5381, Ap	770	8.8	48.9	17	10	US-09-866-108-10351	Sequence 201, App
C 698	9	50.0	25	10	US-09-866-108-5382	Sequence 5382, Ap	771	8.8	48.9	18	9	US-09-866-108-10347	Sequence 201, App
C 699	9	50.0	25	10	US-09-866-108-5383	Sequence 5383, Ap	772	8.8	48.9	18	9	US-09-866-108-10347	Sequence 201, App
C 700	9	50.0	25	10	US-09-866-108-5384	Sequence 5384, Ap	773	8.8	48.9	18	9	US-09-866-108-10347	Sequence 201, App
C 701	9	50.0	25	10	US-09-866-108-5385	Sequence 5385, Ap	774	8.8	48.9	18	9	US-09-866-108-10347	Sequence 201, App
C 702	9	50.0	25	10	US-09-866-108-5386	Sequence 5386, Ap	775	8.8	48.9	18	9	US-09-866-108-10347	Sequence 201, App
C 703	9	50.0	25	10	US-09-866-108-14861	Sequence 14861, A	776	8.8	48.9	18	9	US-09-878-403A-201	Sequence 201, App
C 704	9	50.0	25	10	US-09-866-108-14862	Sequence 14862, A	777	8.8	48.9	18	9	US-09-878-403A-201	Sequence 201, App
C 705	9	50.0	25	10	US-09-866-108-14863	Sequence 14863, A	778	8.8	48.9	18	9	US-09-878-403A-201	Sequence 201, App
C 706	9	50.0	25	10	US-09-866-108-14864	Sequence 14864, A	779	8.8	48.9	18	9	US-09-878-403A-201	Sequence 201, App
C 707	9	50.0	25	10	US-09-866-108-14865	Sequence 14865, A	780	8.8	48.9	18	9	US-09-878-403A-201	Sequence 201, App
C 708	9	50.0	25	10	US-09-866-108-14866	Sequence 14866, A	781	8.8	48.9	18	9	US-09-878-403A-201	Sequence 201, App
C 709	9	50.0	25	10	US-09-866-108-14867	Sequence 14867, A	782	8.8	48.9	18	9	US-09-878-403A-201	Sequence 201, App
C 710	9	50.0	25	10	US-09-866-108-14868	Sequence 14868, A	783	8.8	48.9	18	9	US-09-878-403A-201	Sequence 201, App
C 711	9	50.0	25	10	US-09-866-108-14869	Sequence 14869, A	784	8.8	48.9	18	9	US-09-878-403A-201	Sequence 201, App
C 712	8.8	48.9	15	9	US-09-880-313A-271	Sequence 271, App	785	8.8	48.9	18	9	US-09-881-915A-201	Sequence 201, App
C 713	8.8	48.9	15	9	US-09-979-593-65	Sequence 65, Appl	786	8.8	48.9	18	9	US-09-959-833A-201	Sequence 201, App
C 714	8.8	48.9	15	9	US-10-423-074-51	Sequence 51, Appl	787	8.8	48.9	18	9	US-10-167-749-201	Sequence 201, App
C 715	8.8	48.9	15	10	US-09-504-231A-651	Sequence 651, App	788	8.8	48.9	18	9	US-09-918-858A-201	Sequence 201, App
C 716	8.8	48.9	15	10	US-09-274-553D-651	Sequence 651, App	789	8.8	48.9	18	9	US-09-978-423A-201	Sequence 201, App
C 717	8.8	48.9	16	9	US-09-853-526-140	Sequence 140, App	790	8.8	48.9	18	9	US-10-013-921A-201	Sequence 201, App
C 718	8.8	48.9	16	9	US-10-387-919-1306	Sequence 1306, Ap	791	8.8	48.9	18	9	US-09-978-193A-201	Sequence 201, App
C 719	8.8	48.9	16	9	US-10-387-919-1307	Sequence 1307, Ap	792	8.8	48.9	18	9	US-10-013-929A-201	Sequence 201, App
C 720	8.8	48.9	16	9	US-10-287-919-1314	Sequence 1314, Ap	793	8.8	48.9	18	9	US-10-016-177A-201	Sequence 201, App
C 721	8.8	48.9	16	9	US-10-287-919-1314	Sequence 140, App	794	8.8	48.9	18	9	US-09-959-830A-201	Sequence 201, App
C 722	8.8	48.9	17	9	US-09-901-484A-140	Sequence 666, App	795	8.8	48.9	18	9	US-09-978-757A-201	Sequence 201, App
C 723	8.8	48.9	17	9	US-09-864-785-666	Sequence 431, App	796	8.8	48.9	18	10	US-09-878-187B-201	Sequence 2, Appl
C 724	8.8	48.9	17	9	US-09-825-805-431	Sequence 566, App	797	8.8	48.9	18	10	US-09-832-382-2	Sequence 9, Appl
C 725	8.8	48.9	17	9	US-09-825-805-566	Sequence 569, App	798	8.8	48.9	18	10	US-09-832-382-9	Sequence 27, Appl
C 726	8.8	48.9	17	9	US-09-825-805-739	Sequence 739, App	799	8.8	48.9	19	10	US-09-853-526-178	Sequence 178, App
C 727	8.8	48.9	17	9	US-09-825-805-830	Sequence 80, Appl	800	8.8	48.9	19	9	US-09-974-97A-13	Sequence 13, Appl
C 728	8.8	48.9	17	9	US-10-060-830-81	Sequence 81, Appl	801	8.8	48.9	19	9	US-09-880-311A-61	Sequence 61, Appl
C 729	8.8	48.9	17	9	US-10-060-830-82	Sequence 83, Appl	802	8.8	48.9	19	10	US-09-947-258-3	Sequence 3, Appl
C 730	8.8	48.9	17	9	US-10-060-830-83	Sequence 84, Appl	803	8.8	48.9	19	10	US-09-925-548-56	Sequence 56, Appl
C 731	8.8	48.9	17	9	US-10-060-830-84	Sequence 85, Appl	804	8.8	48.9	19	10	US-09-901-484A-178	Sequence 178, App
C 732	8.8	48.9	17	9	US-10-060-830-85	Sequence 1535, Ap	805	8.8	48.9	19	10	US-09-263-959-1172	Sequence 1172, App
C 733	8.8	48.9	17	9	US-09-818-875-1536	Sequence 477, App	806	8.8	48.9	20	9	US-09-905-291A-327	Sequence 327, App
C 734	8.8	48.9	17	9	US-09-818-875-1536	Sequence 1203, Ap	807	8.8	48.9	20	9	US-09-961-700A-13	Sequence 13, Appl
C 735	8.8	48.9	17	9	US-09-877-478-477	Sequence 1204, Ap	808	8.8	48.9	20	9	US-09-902-853-327	Sequence 327, App
C 736	8.8	48.9	17	9	US-09-877-478-1203	Sequence 1204, Ap	809	8.8	48.9	20	9	US-09-907-824-327	Sequence 327, App
C 737	8.8	48.9	17	9	US-09-877-478-1204	Sequence 1771, Ap	810	8.8	48.9	20	9	US-09-907-824-327	Sequence 327, App
C 738	8.8	48.9	17	9	US-09-877-478-1204	Sequence 2062, Ap	811	8.8	48.9	20	9	US-09-774-809-23	Sequence 23, Appl
C 739	8.8	48.9	17	9	US-09-877-478-1204	Sequence 1216, Ap	812	8.8	48.9	20	9	US-09-904-001-327	Sequence 327, App
C 740	8.8	48.9	17	9	US-09-848-754A-1116	Sequence 1217, Ap	813	8.8	48.9	20	9	US-09-961-077-1260	Sequence 1260, App
C 741	8.8	48.9	17	9	US-09-848-754A-1117	Sequence 3313, Ap	814	8.8	48.9	20	9	US-09-906-744-327	Sequence 327, App
C 742	8.8	48.9	17	9	US-09-848-754A-3113	Sequence 3314, Ap	815	8.8	48.9	20	9	US-10-219-246-26	Sequence 26, Appl
C 743	8.8	48.9	17	9	US-09-848-754A-3114	Sequence 8, Appl1	816	8.8	48.9	20	9	US-09-906-838-337	Sequence 337, App
C 744	8.8	48.9	17	9	US-09-930-423-8	Sequence 302, App	817	8.8	48.9	20	9	US-09-907-613-337	Sequence 337, App
C 745	8.8	48.9	17	9	US-09-930-423-302	Sequence 302, App	818	8.8	48.9	20	9	US-09-907-947-327	Sequence 327, App
C 746	8.8	48.9	17	9	US-09-930-423-303	Sequence 356, App	819	8.8	48.9	20	9	US-10-219-247-26	Sequence 26, Appl
C 747	8.8	48.9	17	9	US-09-930-423-356	Sequence 357, App	820	8.8	48.9	20	9	US-09-904-820-337	Sequence 327, App
C 748	8.8	48.9	17	9	US-09-930-423-357	Sequence 357, App	821	8.8	48.9	20	9	US-09-904-859-337	Sequence 327, App
C 749	8.8	48.9	17	9	US-09-930-423-383	Sequence 383, App	822	8.8	48.9	20	9	US-09-909-204-337	Sequence 327, App


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C 971 8.8 48.9 24 9 US-09-902-759-242 Sequence 242, App
C 972 8.8 48.9 24 9 US-09-905-075-242 Sequence 242, App
C 973 8.8 48.9 24 9 US-09-902-634-242 Sequence 242, App
C 974 8.8 48.9 24 9 US-09-902-713-242 Sequence 242, App
C 975 8.8 48.9 24 9 US-09-907-979-242 Sequence 242, App
C 976 8.8 48.9 24 9 US-09-902-615-242 Sequence 242, App
C 977 8.8 48.9 24 9 US-10-046-433-36 Sequence 36, Appl
C 978 8.8 48.9 24 9 US-09-903-923-242 Sequence 242, App
C 979 8.8 48.9 24 9 US-09-906-760A-242 Sequence 34, Appl
C 980 8.8 48.9 24 9 US-09-940-185-1500 Sequence 1500, Ap
C 981 8.8 48.9 24 9 US-09-940-185-1585 Sequence 1514, Ap
C 982 8.8 48.9 24 9 US-09-940-185-1585 Sequence 1597, Ap
C 983 8.8 48.9 24 9 US-09-940-185-1585 Sequence 1907, Ap
C 984 8.8 48.9 24 9 US-09-940-185-2408 Sequence 2408, Ap
C 985 8.8 48.9 24 9 US-09-940-185-2635 Sequence 2635, Ap
C 986 8.8 48.9 24 9 US-09-940-185-2835 Sequence 2835, Ap
C 987 8.8 48.9 24 9 US-09-940-185-2892 Sequence 2892, Ap
C 988 8.8 48.9 24 10 US-09-122-383-17 Sequence 17, Appl
C 989 8.8 48.9 24 10 US-09-785-632A-81 Sequence 81, Appl
C 990 8.8 48.9 24 10 US-09-909-330-242 Sequence 242, App
C 991 8.8 48.9 24 10 US-09-859-854-7 Sequence 7, Appl
C 992 8.8 48.9 24 10 US-09-859-854-7 Sequence 7, Appl
C 993 8.8 48.9 24 10 US-09-895-382-6 Sequence 6, Appl
C 994 8.8 48.9 24 10 US-09-909-088B-242 Sequence 242, App
C 995 8.8 48.9 25 9 US-09-745-317-4 Sequence 4, Appl
C 996 8.8 48.9 25 9 US-09-879-461-36 Sequence 36, Appl
C 997 8.8 48.9 25 9 US-09-964-261-119 Sequence 119, Appl
C 998 8.8 48.9 25 9 US-10-228-070-11 Sequence 11, Appl
C 999 8.8 48.9 25 9 US-10-060-830-356 Sequence 356, App
C1000 8.8 48.9 25 9 US-10-060-830-357 Sequence 357, App
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ALIGNMENTS

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RESULT 1
US-10-080-959A-5
; Sequence 5, Application US/10080959A
; Publication No. US20030054369A1
; GENERAL INFORMATION:
; APPLICANT: Cruz-Perez, Patricia
; APPLICANT: Butner, Mark P
; TITLE OF INVENTION: Method for Detection of Stachybotrys chartarum in Pure Culture an
; FILE REFERENCE: 0001-00001
; CURRENT FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: US 60/280,712
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 5
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Stachybotrys chartarum
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION:
US-10-080-959A-5
Query Match 100.0%; Score 18; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2
US-09-911-176B-28/c
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; Sequence 28, Application US/09911176B
; Patent No. US20020156243A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: ANTIBODIES THAT BIND AN
; FILE REFERENCE: 97-30D1
; CURRENT APPLICATION NUMBER: US/09/911,176B
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: 09/118,408
; PRIOR FILING DATE: 1998-07-17
; PRIOR APPLICATION NUMBER: 60/053,154
; PRIOR FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC15035
US-09-911-176B-28
Query Match 67.8%; Score 12.2; DB 9; Length 24;
Best Local Similarity 82.4%; Pred. No. 8e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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RESULT 3
US-10-180-762-28/c
; Sequence 28, Application US/10180762
; Publication No. US20030022838A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Laesser, Gerald W.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND IMMUNE FUNCTION
; FILE REFERENCE: 99-12C3
; CURRENT APPLICATION NUMBER: US/10/180,762
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: 09/253,604
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/444,794
; PRIOR FILING DATE: 1999-11-22
; PRIOR APPLICATION NUMBER: 09/506,855
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC15035
US-10-180-762-28
Query Match 67.8%; Score 12.2; DB 9; Length 24;
Best Local Similarity 82.4%; Pred. No. 8e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 1 CTGCGCCCGATCCAGC 17
1 CTGCGCCCGATCCAGC 17
20 CCGAGCCCGATCCAGC 4
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RESULT 4
US-10-241-258-28/c
; Sequence 28, Application US/10241258
; Publication No. US20030078206A1
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/ GENERAL INFORMATION:
/ APPLICANT: Shepard, Paul O.
/ APPLICANT: Laeber, Gerald W.
/ APPLICANT: Bishop, Paul D.
/ TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND
/ TITLE OF INVENTION: IMMUNE FUNCTION
/ FILE REFERENCE: 99-12
/ CURRENT APPLICATION NUMBER: US/10/241,258
/ CURRENT FILING DATE: 2002-09-10
/ NUMBER OF SEQ ID NOS: 50
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 28
/ LENGTH: 24
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Oligonucleotide ZC15035
US-10-241-258-28
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Query Match          67.8%; Score 12.2; DB 9; Length 24;
Best Local Similarity 82.4%; Pred.No.8e+03; 3; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 20 CCGACCCGATCCATG 4
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RESULT 5
US-09-997-664-54/c
/ Sequence 54, Application US/09997664
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/ GENERAL INFORMATION:
/ APPLICANT: Ben-Bassat, Arle
/ APPLICANT: Catermole, Monica
/ APPLICANT: Gatenby, Anthony A.
/ APPLICANT: Gibson, Katherine J.
/ APPLICANT: Ramos-Gonzalez, Isabel
/ APPLICANT: Ramos, Juan
/ APPLICANT: Sariastani, Sima
/ TITLE OF INVENTION: Method for the Production of p-Hydroxybenzoate in Species of
/ TITLE OF INVENTION: Pseudomonas and Agrobacterium
/ FILE REFERENCE: BC1018 US CIP
/ CURRENT APPLICATION NUMBER: US/09/997,664
/ CURRENT FILING DATE: 2001-11-28
/ PRIOR APPLICATION NUMBER: 09/585,174
/ PRIOR FILING DATE: 2000-06-01
/ NUMBER OF SEQ ID NOS: 112
/ SOFTWARE: Microsoft Office 97
/ SEQ ID NO 54
/ LENGTH: 19
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: primer
/ OTHER INFORMATION: primer used for sequencing pcu
US-09-997-664-54
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Query Match          64.4%; Score 11.6; DB 10; Length 19;
Best Local Similarity 77.8%; Pred.No.1.6e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Qy 1 CTGCGCCCGATCCAGG 18
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Db 18 CAGCACCCGTATCAAGGC 1
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RESULT 6
US-09-423-800-34/c
/ Sequence 34, Application US/09423800
/ Patent No. US20020165363A1
/ GENERAL INFORMATION:
/ APPLICANT: SATO, KOH
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/ APPLICANT: TSUNENARI, TOSHIAKI
/ APPLICANT: ISHII, KIMIE
/ TITLE OF INVENTION: CACHEXIA REMEDY
/ FILE REFERENCE: 04853-0036
/ CURRENT APPLICATION NUMBER: US/09/423,800
/ CURRENT FILING DATE: 1999-11-12
/ PRIOR APPLICATION NUMBER: PCT/JP98/02116
/ PRIOR FILING DATE: 1998-05-13
/ PRIOR APPLICATION NUMBER: JP 125505/1997
/ PRIOR FILING DATE: 1997-05-15
/ PRIOR APPLICATION NUMBER: JP 194445/1997
/ PRIOR FILING DATE: 1997-07-18
/ NUMBER OF SEQ ID NOS: 87
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 34
/ LENGTH: 19
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-423-800-34
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Query Match          63.3%; Score 11.4; DB 9; Length 19;
Best Local Similarity 92.3%; Pred.No.2e+04; 1; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 13 GCCCGATCCAGG 1
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RESULT 7
US-10-182-018-34/c
/ Sequence 34, Application US/10182018
/ Publication No. US20030049211A1
/ GENERAL INFORMATION:
/ APPLICANT: CHUGAI SEIYAKU KABUSHIKI KAISHA
/ TITLE OF INVENTION: THERAPEUTIC AND PREVENTIVE AGENTS FOR DENTAL DISEASES
/ FILE REFERENCE: PH-1092-PCT
/ CURRENT APPLICATION NUMBER: US/10/182,018
/ CURRENT FILING DATE: 2002-07-24
/ PRIOR APPLICATION NUMBER: JP 2000-83034
/ PRIOR FILING DATE: 2000-01-25
/ NUMBER OF SEQ ID NOS: 75
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 34
/ LENGTH: 19
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic DNA
US-10-182-018-34
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```
Query Match          63.3%; Score 11.4; DB 9; Length 19;
Best Local Similarity 92.3%; Pred.No.2e+04; 1; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 5 GCCCGATCCAGG 17
    |||||
Db 13 GCCCGATCCAGG 1
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RESULT 8
US-10-085-906-496/c
/ Sequence 496, Application US/10085906
/ Publication No. US20030054371A1
/ GENERAL INFORMATION:
/ APPLICANT: YING, Vincent
/ APPLICANT: Wu, Paul
/ APPLICANT: Gray, Gary S.
/ TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
/ TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
/ FILE REFERENCE: GNN-5343CP2
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CURRENT APPLICATION NUMBER: US/10/085,906
CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: US 60/126,215
PRIOR FILING DATE: 1999-03-25
PRIOR APPLICATION NUMBER: US 09/534,061
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: PCT/US00/07938
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 545
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 496
LENGTH: 21
TYPE: DNA
ORGANISM: Homo sapiens
US-10-085-906-496

Query Match 63.3%; Score 11.4; DB 9; Length 21;
Best Local Similarity 92.3%; Pred. No. 2e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTGCGCCCGATC 13
Db 19 CTGCGCCCGATC 7

RESULT 9
US-09-990-385-20/c
Sequence 20, Application US/09990385
Publication No. US20020192771A1
GENERAL INFORMATION:
APPLICANT: KOJI YANAI et al.
TITLE OF INVENTION: BETA-FRUCTOFURANOSIDASE AND ITS GENE, METHOD OF
ISOLATING BETA-FRUCTOFURANOSIDASE GENE, SYSTEM FOR PRODUCT
BETA-FRUCTOFURANOSIDASE, AND BETA-FRUCTOFURANOSIDASE VARI

NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESS: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/990,385
FILING DATE: 10-Sep-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/142,623
FILING DATE: September 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 2001-1611
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: Nucleic acid
STRANDEDNESS: No. US20020192771A1 relevant
TOPOLOGY: linear
MOLECULE TYPE: Synthetic DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-990-385-20

Query Match 63.3%; Score 11.4; DB 9; Length 22;
Best Local Similarity 92.3%; Pred. No. 2e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCCCGATCCAG 17
Db 16 GCCCGATCCAG 4

RESULT 10
US-09-961-077-531
Sequence 531, Application US/09961077
Publication No. US20030014775A1
GENERAL INFORMATION:
APPLICANT: Zwick, Michael G.
Edington, Brent E.
McSwigen, James A.
Merlo, Patricia Ann Owens
Guo, Lining
Skokut, Thomas A.
Young, Scott A.
Folkerts, Otto
Merlo, Donald J.

TITLE OF INVENTION: COMPOSITION AND METHODS FOR
MODULATION OF GENE EXPRESSION
IN PLANTS

NUMBER OF SEQUENCES: 1263
CORRESPONDENCE ADDRESS:
ADDRESS: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/961,077
FILING DATE: 21-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/679,645
FILING DATE: July 12, 1996
APPLICATION NUMBER: 60/001,135
FILING DATE: July 13, 1995
APPLICATION NUMBER: 08/300,726
FILING DATE: September 2, 1994

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 219/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 531:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 531:
US-09-961-077-531

Query Match 62.2%; Score 11.2; DB 9; Length 16;
Best Local Similarity 68.8%; Pred. No. 2.6e+04;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTGCGCCCGATCCAG 16
Db 1 CTGCGCCCGATCCAG 16

PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 651
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-651

Query Match 62.2%; Score 11.2; DB 10; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.6e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CTGCGCCCGATCCAG 16
DB 17 CTGAGTCCGGGTCAG 2
RESULT 16
US-09-866-108-652/C
Sequence 652, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yizhong
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 652
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-652

Query Match 62.2%; Score 11.2; DB 10; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.6e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CTGCGCCCGATCCAG 16
DB 16 CTGAGTCCGGGTCAG 1

RESULT 17
US-09-961-077-621
Sequence 621, Application US/09961077
Publication No. US20030014775A1
GENERAL INFORMATION:
APPLICANT: Zwick, Michael G.
Edington, Brent E.
McSwiggan, James A.
Merlo, Patricia Ann Owens
Guo, Lining
Skokut, Thomas A.
Young, Scott A.
Folkerts, Otto
Merlo, Donald J.
TITLE OF INVENTION: COMPOSITION AND METHODS FOR
MODULATION OF GENE EXPRESSION
IN PLANTS
NUMBER OF SEQUENCES: 1263
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/961,077
FILING DATE: 21-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

```

/ APPLICATION NUMBER: 08/679,645
/ FILING DATE: July 12, 1996
/ APPLICATION NUMBER: 60/001,135
/ FILING DATE: July 13, 1995
/ APPLICATION NUMBER: 08/300,726
/ FILING DATE: September 2, 1994
/ ATTORNEY/AGENT INFORMATION:
/   NAME: Warburg, Richard J.
/   REGISTRATION NUMBER: 32,327
/   REFERENCE/DOCKET NUMBER: 219/247
/ TELECOMMUNICATION INFORMATION:
/   TELEPHONE: (213) 489-1600
/   TELEFAX: (213) 955-0440
/
/ INFORMATION FOR SEQ ID NO: 621:
/ SEQUENCE CHARACTERISTICS:
/   LENGTH: 18 base pairs
/   TYPE: nucleic acid
/   STRANDEDNESS: single
/   TOPOLOGY: linear
/
/ SEQUENCE DESCRIPTION: SEQ ID NO: 621:
US-09-961-077-621

Query Match      62.2% Score 11.2; DB 9; Length 18;
Best Local Similarity 68.8% Pred. No. 2.5e+04;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Cy 1 CTCGGCCCGATCCAG 16
Db 3 CUGCGCCCAUCCAG 18

RESULT 18
US-09-734-188-37/c
/ Sequence 37, Application US/09734188
/ Patent No. US2002010645A1
/ GENERAL INFORMATION:
/   APPLICANT: Richardson Ph.D., Mary Ann
/   APPLICANT: Goldman, Assistant Counsel, Robin A.
/   APPLICANT: New York State Office of Mental Health
/   APPLICANT: Nathan S. Kline Institute for Psychiatric Research
/ TITLE OF INVENTION: PAH
/ FILE REFERENCE: Kline Inst.
/ CURRENT APPLICATION NUMBER: US/09/734,188
/ PRIOR FILING DATE: 2000-12-12
/ PRIOR APPLICATION NUMBER: 09/253,025
/ PRIOR FILING DATE: 2001-05-03
/ NUMBER OF SEQ ID NOS: 62
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO: 37
/ LENGTH: 21
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-734-188-37

Query Match      62.2% Score 11.2; DB 10; Length 21;
Best Local Similarity 81.2% Pred. No. 2.5e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy 2 TGGCCCGGATCCAG 17
Db 17 TGGGCTCGGATCCAG 2

RESULT 19
US-10-118-100-2/c
/ Sequence 2, Application US/10118100
/ Publication No. US2003007613A1
/ GENERAL INFORMATION:
/   APPLICANT: Bioinvent International AB
/   APPLICANT: Soderlind, Ulf
/   APPLICANT: Borrebaeck, Carl
/ TITLE OF INVENTION: A Method For In Vitro Molecular
```

```

/ TITLE OF INVENTION: Evolution of Protein Function
/ FILE REFERENCE: Newburn 341711
/ CURRENT APPLICATION NUMBER: US/10/118,100
/ PRIOR FILING DATE: 2002-04-08
/ PRIOR APPLICATION NUMBER: US/09/341,711
/ PRIOR FILING DATE: 1999-09-21
/ PRIOR APPLICATION NUMBER: PCT/GB98/00219
/ PRIOR FILING DATE: 1998-01-26
/ PRIOR APPLICATION NUMBER: GB9701425.2
/ PRIOR FILING DATE: 1997-01-24
/ NUMBER OF SEQ ID NOS: 54
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO: 2
/ LENGTH: 22
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ OTHER INFORMATION: Primer
US-10-118-100-2

Query Match      62.2% Score 11.2; DB 9; Length 22;
Best Local Similarity 81.2% Pred. No. 2.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy 2 TGGCCCGGATCCAG 17
Db 18 TCGCCAGGCTCCAG 3

RESULT 20
US-09-813-289-3/c
/ Sequence 3, Application US/09813289
/ Patent No. US20020061571A1
/ GENERAL INFORMATION:
/   APPLICANT: Mahadevan, M.S.
/   APPLICANT: Tiscornia, G.
/ TITLE OF INVENTION: No. US20020061571A1 isoform of myotonic dysreophy associated pr
/ FILE REFERENCE: 800.027US1
/ CURRENT APPLICATION NUMBER: US/09/813,289
/ PRIOR FILING DATE: 2001-03-20
/ PRIOR APPLICATION NUMBER: US 60/190,590
/ PRIOR FILING DATE: 2000-03-20
/ NUMBER OF SEQ ID NOS: 22
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 3
/ LENGTH: 22
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-813-289-3

Query Match      62.2% Score 11.2; DB 10; Length 22;
Best Local Similarity 81.2% Pred. No. 2.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy 1 CTCGGCCCGATCCAG 16
Db 17 CTCGGCCAGCTCCAG 2

RESULT 21
US-10-118-100-36/c
/ Sequence 36, Application US/10118100
/ Publication No. US2003007613A1
/ GENERAL INFORMATION:
/   APPLICANT: Bioinvent International AB
/   APPLICANT: Soderlind, Ulf
/   APPLICANT: Borrebaeck, Carl
/ TITLE OF INVENTION: A Method For In Vitro Molecular
/ FILE REFERENCE: Newburn 341711
/ CURRENT APPLICATION NUMBER: US/10/118,100
/ CURRENT FILING DATE: 2002-04-08
```

```

; PRIOR APPLICATION NUMBER: US/09/341,711
; PRIOR FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: PCT/GB98/00219
; PRIOR FILING DATE: 1998-01-26
; PRIOR APPLICATION NUMBER: GB9701425.2
; PRIOR FILING DATE: 1997-01-24
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
; US-10-118-100-36

Query Match      62.2%; Score 11.2; DB 9; Length 23;
Best Local Similarity 81.2%; Pred. No. 2.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 TCGGCCCCGATCCAG 17
        |||||
DB      19 TCGCCAGGCTCCAG 4.

RESULT 22
US-10-199-550-17/c
; Sequence 17, Application US/10199550
; Publication No. US20030099615A1
; GENERAL INFORMATION:
; APPLICANT: TIKOO, Suresh K.
; TITLE OF INVENTION: PORCINE ADENOVIRUS E1 AND E4 REGIONS
; FILE REFERENCE: 29310203220
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 09/963,038
; PRIOR FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Porcine Adenovirus Type 3
; US-10-199-550-17

Query Match      62.2%; Score 11.2; DB 9; Length 24;
Best Local Similarity 81.2%; Pred. No. 2.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 CTGGCCCCGATCCAG 16
        |||||
DB      16 CAGCGCCGATCCCG 1

RESULT 23
US-09-866-108-3580/c
; Sequence 3580, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
```

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; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 3580
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108-3580

Query Match      62.2%; Score 11.2; DB 10; Length 25;
Best Local Similarity 81.2%; Pred. No. 2.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 CTGGCCCCGATCCAG 16
        |||||
DB      25 CTGAGTCCGGTCCAG 10

RESULT 24
US-09-866-108-3581/c
; Sequence 3581, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
```

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/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00662
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00661
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00670
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: US 60/234,687
/ PRIOR FILING DATE: 2000-09-21
/ PRIOR APPLICATION NUMBER: US 60/266,860
/ PRIOR FILING DATE: 2001-02-05
/ NUMBER OF SEQ ID NOS: 15752
/ SOFTWARE: Aecomica Sequence Listing Engine
/ SEQ ID NO: 3581
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-09-866-108-3581
```

```
Query Match      62.2% Score 11.2; DB 10; Length 25;
Best Local Similarity 81.2% Pred. No. 2.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy      1 CTGCGCCCGGATCCAG 16
        ||| ||| ||| ||| |||
Db      24 CTGAGTCCGGGTCAG 9
```

```
RESULT 25
US-09-866-108-3582/c
/ Sequence 3582, Application US/09866108
/ Patent No. US20020048800A1
/ GENERAL INFORMATION:
/ APPLICANT: GU, Yizhong
/ APPLICANT: JI, Yonggang
/ APPLICANT: PENN, Sharon G.
/ APPLICANT: HANZEL, David K.
/ APPLICANT: RANK, David R.
/ APPLICANT: CHEN, Wensheng
/ APPLICANT: SHANNON, Mark
/ TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
/ FILE REFERENCE: AECOMICA-7
/ CURRENT APPLICATION NUMBER: US/09/866,108
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00662
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00661
```

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/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00670
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: US 60/234,687
/ PRIOR FILING DATE: 2000-09-21
/ PRIOR APPLICATION NUMBER: US 60/266,860
/ PRIOR FILING DATE: 2001-02-05
/ NUMBER OF SEQ ID NOS: 15752
/ SOFTWARE: Aecomica Sequence Listing Engine
/ SEQ ID NO: 3582
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-09-866-108-3582
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```
Query Match      62.2% Score 11.2; DB 10; Length 25;
Best Local Similarity 81.2% Pred. No. 2.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy      1 CTGCGCCCGGATCCAG 16
        ||| ||| ||| ||| |||
Db      23 CTGAGTCCGGGTCAG 8
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```
RESULT 26
US-09-866-108-3583/c
/ Sequence 3583, Application US/09866108
/ Patent No. US20020048800A1
/ GENERAL INFORMATION:
/ APPLICANT: GU, Yizhong
/ APPLICANT: JI, Yonggang
/ APPLICANT: PENN, Sharon G.
/ APPLICANT: HANZEL, David K.
/ APPLICANT: RANK, David R.
/ APPLICANT: CHEN, Wensheng
/ APPLICANT: SHANNON, Mark
/ TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
/ FILE REFERENCE: AECOMICA-7
/ CURRENT APPLICATION NUMBER: US/09/866,108
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
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/ PRIOR APPLICATION NUMBER: PCT/US01/00661
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00670
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2000-09-21
/ PRIOR APPLICATION NUMBER: US 60/234,687
/ PRIOR FILING DATE: 2000-09-21
/ PRIOR APPLICATION NUMBER: US 60/266,860
/ PRIOR FILING DATE: 2001-02-05
/ NUMBER OF SEQ ID NOS: 15752
/ SOFTWARE: Aecomica Sequence Listing Engine
/ SEQ ID NO: 3583
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LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-3583

Query Match 62.2%; Score 11.2; DB 10; Length 25;
Best Local Similarity 81.2%; Pred. No. 2.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCGCCCGATCCAG 16
DB 22 CTGAGTCCGGGTCCAG 7

RESULT 27
US-09-866-108-3584/C
Sequence 3584, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOmica-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: AeoMica Sequence Listing Engine
SEQ ID NO 3584
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-3584

Query Match 62.2%; Score 11.2; DB 10; Length 25;
Best Local Similarity 81.2%; Pred. No. 2.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCGCCCGATCCAG 16

DB 21 CTGAGTCCGGGTCCAG 6

RESULT 28
US-09-866-108-3585/C
Sequence 3585, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOmica-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: AeoMica Sequence Listing Engine
SEQ ID NO 3585
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-3585

Query Match 62.2%; Score 11.2; DB 10; Length 25;
Best Local Similarity 81.2%; Pred. No. 2.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCGCCCGATCCAG 16
DB 20 CTGAGTCCGGGTCCAG 5

RESULT 29
US-09-866-108-3586/C
Sequence 3586, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong

APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO: 3586
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-3586

Query Match 62.2%; Score 11.2; DB 10; Length 25;
Best Local Similarity 81.2%; Pred. No. 2.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCGCCGGATCCAG 16
DB 19 CTGAGTCCGGATCCAG 4

RESULT 30
US-09-866-108-3587/c
Sequence 3587, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO: 3587
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-3587

Query Match 62.2%; Score 11.2; DB 10; Length 25;
Best Local Similarity 81.2%; Pred. No. 2.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCGCCGGATCCAG 16
DB 18 CTGAGTCCGGATCCAG 3

RESULT 31
US-09-866-108-3588/c
Sequence 3588, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
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PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aecomica Sequence Listing Engine
SEQ ID NO 3588
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-3588

Query Match 62.2%; Score 11.2; DB 10; Length 25;
Best Local Similarity 81.2%; Pred. No. 2.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCGCCCGATCCAG 16
DB 17 CTGAGTCCGGGTCAG 2

RESULT 32
US-09-866-108-3589/c
Sequence 3589, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AECOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aecomica Sequence Listing Engine
SEQ ID NO 3589
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-3589

Query Match 62.2%; Score 11.2; DB 10; Length 25;
Best Local Similarity 81.2%; Pred. No. 2.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCGCCCGATCCAG 16
DB 16 CTGAGTCCGGGTCAG 1

RESULT 33
US-10-080-959A-5/c
Sequence 5, Application US/10080959A
Publication No. US20030054369A1
GENERAL INFORMATION:
APPLICANT: Cruz-Perex, Patricia
APPLICANT: Butner, Mark P.
TITLE OF INVENTION: Method for Detection of Stachybotrys chartarum in Pure Culture an
FILE REFERENCE: 0001-00001
CURRENT APPLICATION NUMBER: US/10/080,959A
CURRENT FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: US 60/280,712
PRIOR FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 5
SEQ ID NO 5
LENGTH: 18
TYPE: DNA
ORGANISM: Stachybotrys chartarum
FEATURE:
NAME/KEY:
LOCATION:
OTHER INFORMATION:
US-10-080-959A-5

Query Match 60.0%; Score 10.8; DB 9; Length 18;
Best Local Similarity 85.7%; Pred. No. 3.9e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GCCCGATCCAGGC 18
DB 18 GCGTGAATCCGGGC 5

RESULT 34
US-10-251-482-17
Sequence 17, Application US/10251482
Publication No. US20030099631A1
GENERAL INFORMATION:
APPLICANT: Koji, Yoshimura
APPLICANT: Yuichi, Hikichi
APPLICANT: Atsushi, Nishimura
TITLE OF INVENTION: NOVEL PROTEINS, THEIR PRODUCTION AND USE
FILE REFERENCE: 48712/342
CURRENT APPLICATION NUMBER: US/10/251,482
CURRENT FILING DATE: 2002-09-19

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/ PRIOR APPLICATION NUMBER: US/09/171,545
/ PRIOR FILING DATE: 1999-07-26
/ NUMBER OF SEQ ID NOS: 23
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 17
/ LENGTH: 19
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
/ OTHER INFORMATION: primer
US-10-251-482-17

Query Match      60.0%; Score 10.8; DB 9; Length 19;
Best Local Similarity 85.7%; Pred. No. 3.9e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 GCGCCGATCCAGC 18
DB      2 GCGCCGATCCAGC 15

RESULT 35
US-10-057-550-82/c
/ Sequence 82, Application US/10057550
/ Publication No. US20030032607A1
/ GENERAL INFORMATION:
/ APPLICANT: Monla, Brett P.
/ TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/057,550
/ CURRENT FILING DATE: 2002-01-25
/ PRIOR APPLICATION NUMBER: 09/506,073
/ PRIOR FILING DATE: 2000-02-18
/ PRIOR APPLICATION NUMBER: US 09/143,214
/ PRIOR FILING DATE: 1998-08-28
/ PRIOR APPLICATION NUMBER: PCT/US98/13961
/ PRIOR FILING DATE: 1998-07-06
/ PRIOR APPLICATION NUMBER: US 08/888,982
/ PRIOR FILING DATE: 1997-07-07
/ PRIOR APPLICATION NUMBER: US 08/756,806
/ PRIOR FILING DATE: 1996-11-26
/ PRIOR APPLICATION NUMBER: PCT/US95/07111
/ PRIOR FILING DATE: 1995-05-31
/ PRIOR APPLICATION NUMBER: US 08/250,856
/ PRIOR FILING DATE: 1994-05-31
/ NUMBER OF SEQ ID NOS: 130
/ SEQ ID NO 82
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: artificial sequence
/ FEATURE:
/ OTHER INFORMATION: antisense sequence
US-10-057-550-82

Query Match      60.0%; Score 10.8; DB 9; Length 20;
Best Local Similarity 85.7%; Pred. No. 3.8e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 GCGCCGATCCAG 16
DB      14 GCGCCGATCCAG 1

RESULT 36
US-10-122-434-7
/ Sequence 7, Application US/10122434
/ Publication No. US20030078402A1
/ GENERAL INFORMATION:
/ APPLICANT: Leon G.J. FRENKEN
/ APPLICANT: Cornelis P.E. VAN DER LOGT
/ TITLE OF INVENTION: METHOD FOR PRODUCING ANTIBODY FRAGMENTS
/ FILE REFERENCE: 60113/266062 - 13076(C)
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/ CURRENT APPLICATION NUMBER: US/10/122,434
/ CURRENT FILING DATE: 2002-04-16
/ PRIOR APPLICATION NUMBER: 09/487,253
/ PRIOR FILING DATE: 2000-01-19
/ NUMBER OF SEQ ID NOS: 39
/ SOFTWARE: MS word
/ SEQ ID NO 7
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: PRIMER
US-10-122-434-7

Query Match      60.0%; Score 10.8; DB 9; Length 20;
Best Local Similarity 85.7%; Pred. No. 3.8e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 GCGCCGATCCAG 17
DB      7 GCGCCGATCCAG 20

RESULT 37
US-09-733-151-8/c
/ Sequence 8, Application US/09733151
/ Patent No. US20010029620A1
/ GENERAL INFORMATION:
/ APPLICANT: De Boch, et al.
/ TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
/ FILE REFERENCE: 514412-2019
/ CURRENT APPLICATION NUMBER: US/09/733,151
/ CURRENT FILING DATE: 2000-12-08
/ PRIOR APPLICATION NUMBER: 09/457,037
/ PRIOR FILING DATE: 1999-12-08
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 8
/ LENGTH: 21
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1)..(21)
/ OTHER INFORMATION: primer 254
US-09-733-151-8

Query Match      60.0%; Score 10.8; DB 10; Length 21;
Best Local Similarity 85.7%; Pred. No. 3.8e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 GCGCCGATCCAGC 18
DB      18 GCGCCGATCCAGC 5

RESULT 38
US-09-940-185-964/c
/ Sequence 964, Application US/09940185
/ Publication No. US20030096239A1
/ GENERAL INFORMATION:
/ APPLICANT: Gunderson, Kevin
/ APPLICANT: Chee, Mark
/ TITLE OF INVENTION: Probes and Decoder Oligonucleotides
/ FILE REFERENCE: A-69605-1
/ CURRENT APPLICATION NUMBER: US/09/940,185
/ CURRENT FILING DATE: 2001-08-27
/ PRIOR APPLICATION NUMBER: US 60/227,948
/ PRIOR FILING DATE: 2000-08-25
/ PRIOR APPLICATION NUMBER: US 60/228,854
/ PRIOR FILING DATE: 2000-08-29
/ NUMBER OF SEQ ID NOS: 4768
/ SOFTWARE: PatentIn version 3.1
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/ SEQ ID NO 964
/ LENGTH: 24
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-964

Query Match
Best Local Similarity 60.0%; Score 10.8; DB 9; Length 24;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCGCCGATCCAG 16
DB 21 GCGCTCGATCCAG 8

RESULT 39
US-10-076-157-21/c
/ Sequence 21, Application US/10076157
/ Publication No. US20030027309A1
/ GENERAL INFORMATION:
/ APPLICANT: Pompejus, Markus
/ APPLICANT: Snelberger, Harald
/ APPLICANT: Joefken, Hans Wolfgang
/ APPLICANT: Doval, Jose Luis Revuelta
/ APPLICANT: Jimenez, Alberto;
/ APPLICANT: Garcia, Maria Angeles Santos
/ TITLE OF INVENTION: Genes of purine biosynthesis from Ashbya Gossypii and the use the
/ TITLE OF INVENTION: in
/ FILE REFERENCE: 48684DIY
/ CURRENT APPLICATION NUMBER: US/10/076,157
/ PRIOR APPLICATION NUMBER: 2002-02-15
/ PRIOR FILING DATE: 1998-12-16
/ NUMBER OF SEQ ID NOS: 21
/ SOFTWARE: WordPerfect v. 6.1
/ SEQ ID NO 21
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: PCR primer
US-10-076-157-21

Query Match
Best Local Similarity 60.0%; Score 10.8; DB 9; Length 25;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GCGCCGATCCAGC 18
DB 15 GCCAGATCCAGC 2

RESULT 40
US-09-864-785-1566
/ Sequence 1566, Application US/09864785
/ Patent No. US20020177568A1
/ GENERAL INFORMATION:
/ APPLICANT: Ribozyme Pharmaceuticals, Inc.
/ APPLICANT: Stinchcomb, Dan
/ APPLICANT: Draper, Ken
/ APPLICANT: McSwiggen, Jim
/ TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
/ FILE REFERENCE: 400/022 (MBH00-812-D)
/ CURRENT APPLICATION NUMBER: US/09/864,785
/ NUMBER OF SEQ ID NOS: 2001-05-23
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 1566
/ LENGTH: 17
```

```
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-1566

Query Match
Best Local Similarity 58.9%; Score 10.6; DB 9; Length 17;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 TCGCCGATCCAGC 18
DB 1 UGCCCCAGGCTCCAGC 17

Search completed: June 7, 2003, 11:39:16
Job time : 76.7273 secs
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OM nucleic - nucleic search, using sw model

Run on: June 7, 2003, 08:19:34 ; Search time 37.9636 Seconds
(without alignments)
145,407 Million cell updates/sec

Title: US-10-080-959A-5

Perfect score: 18

Sequence: 1 ctgcgcgcgcgcgcgcgcgc 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 364038

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Issued_Patents_NA.*
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2: /cgn2_6/pdata/2/ina/5B.COMB.seq:*
3: /cgn2_6/pdata/2/ina/6A.COMB.seq:*
4: /cgn2_6/pdata/2/ina/6B.COMB.seq:*
5: /cgn2_6/pdata/2/ina/PCTUS.COMB.seq:*
6: /cgn2_6/pdata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	13	72.2	21	4	US-09-318-191-2
3	12.8	71.1	17	4	US-09-593-012-106
4	12.4	68.9	22	1	US-08-284-566A-2
5	12.2	67.8	24	4	US-09-118-408-28
6	12.2	67.8	24	4	US-09-506-855-28
7	12	66.7	25	3	US-08-840-316-88
8	12	66.7	25	3	US-08-809-523-88
9	12	66.7	25	4	US-08-471-971-88
10	12	66.7	25	4	US-09-402-776-88
11	12	66.7	25	5	PCT-US93-08849A-88
12	12	66.7	25	5	PCT-US93-08849-88
13	11.8	65.6	18	1	US-08-474-140-3
14	11.8	65.6	18	1	US-08-477-630-3
15	11.8	65.6	18	1	US-08-472-293-3
16	11.8	65.6	18	1	US-08-474-545-3
17	11.8	65.6	18	1	US-08-478-341-3
18	11.8	65.6	18	3	US-08-996-733-3
19	11.8	65.6	18	3	US-08-275-526C-17
20	11.8	65.6	18	4	US-09-076-677-17
21	11.8	65.6	18	4	US-09-073-055-17
22	11.8	65.6	24	1	US-08-425-299A-13
23	11.8	65.6	24	3	US-08-480-173A-25
24	11.8	65.6	24	3	US-08-480-173A-26
25	11.8	65.6	24	3	US-08-484-408A-25
26	11.8	65.6	24	3	US-08-484-408A-26
27	11.8	65.6	25	2	US-08-318-837-43

28	11.6	64.4	21	1	US-08-602-036A-23	Sequence 23, Appl
29	11.6	64.4	21	2	US-08-642-407A-23	Sequence 23, Appl
30	11.6	64.4	22	1	US-08-602-036A-3	Sequence 3, Appl
31	11.6	64.4	22	1	US-08-602-036A-4	Sequence 4, Appl
32	11.6	64.4	22	2	US-08-502-374A-3	Sequence 3, Appl
33	11.6	64.4	22	2	US-08-502-374A-4	Sequence 4, Appl
34	11.6	64.4	22	2	US-08-642-407A-3	Sequence 3, Appl
35	11.6	64.4	22	2	US-08-642-407A-4	Sequence 4, Appl
36	11.4	63.3	20	1	US-08-428-583-17	Sequence 17, Appl
37	11.4	63.3	22	4	US-08-585-595-35	Sequence 35, Appl
38	11.4	63.3	22	4	US-09-142-623-20	Sequence 20, Appl
39	11.4	63.3	24	2	US-08-244-122-25	Sequence 25, Appl
40	11.2	62.2	16	4	US-08-679-645-531	Sequence 531, App
41	11.2	62.2	18	4	US-08-679-645-531	Sequence 621, App
42	11.2	62.2	19	4	US-09-593-012-94	Sequence 94, Appl
43	11.2	62.2	21	4	US-09-253-025-37	Sequence 37, Appl
44	11.2	62.2	23	4	US-09-393-554-20	Sequence 20, Appl
45	11.2	62.2	24	2	US-07-808-457-11	Sequence 31, Appl
46	11.2	62.2	24	5	PCT-US92-10178-31	Sequence 31, Appl
47	11.1	61.1	25	2	US-08-588-983-25	Sequence 25, Appl
48	11.1	61.1	25	2	US-08-588-976-35	Sequence 25, Appl
49	11.1	61.1	25	3	US-08-589-028-27	Sequence 27, Appl
50	11.1	61.1	25	3	US-08-784-582-27	Sequence 27, Appl
51	11.1	61.1	25	3	US-08-785-271-27	Sequence 27, Appl
52	10.8	60.0	18	4	US-09-593-012-188	Sequence 188, App
53	10.8	60.0	20	3	US-09-428-584-14	Sequence 14, Appl
54	10.8	60.0	20	3	US-09-487-253A-7	Sequence 7, Appl
55	10.8	60.0	20	4	US-09-270-331-12	Sequence 12, Appl
56	10.8	60.0	20	4	US-09-506-073-82	Sequence 82, Appl
57	10.8	60.0	24	1	US-08-178-606-12	Sequence 12, Appl
58	10.8	60.0	24	1	US-08-050-073-56	Sequence 56, Appl
59	10.8	60.0	24	3	US-09-010-641-41	Sequence 41, Appl
60	10.8	60.0	24	3	US-09-356-281-41	Sequence 41, Appl
61	10.8	60.0	24	4	US-08-475-470A-18	Sequence 18, Appl
62	10.8	60.0	24	4	US-09-270-331-11	Sequence 11, Appl
63	10.8	60.0	25	3	US-08-737-607-21	Sequence 21, Appl
64	10.8	60.0	25	4	US-08-686-993A-24	Sequence 24, Appl
65	10.8	60.0	25	4	US-09-212-247C-21	Sequence 21, Appl
66	10.6	58.9	20	3	US-09-366-257-18	Sequence 18, Appl
67	10.6	58.9	20	3	US-09-418-641-33	Sequence 33, Appl
68	10.6	58.9	20	4	US-09-126-109-13	Sequence 13, Appl
69	10.6	58.9	23	3	US-09-165-042-19	Sequence 19, Appl
70	10.6	58.9	24	1	US-08-423-383-27	Sequence 27, Appl
71	10.6	58.9	24	1	US-08-423-383-76	Sequence 76, Appl
72	10.6	58.9	24	1	US-08-620-467A-43	Sequence 43, Appl
73	10.6	58.9	24	1	US-08-348-572-44	Sequence 44, Appl
74	10.6	58.9	24	2	US-08-437-353A-27	Sequence 27, Appl
75	10.6	58.9	24	2	US-08-437-353A-76	Sequence 76, Appl
76	10.6	58.9	24	2	US-08-761-704-4	Sequence 4, Appl
77	10.6	58.9	24	3	US-08-555-205-47	Sequence 47, Appl
78	10.6	58.9	24	3	US-09-041-090B-44	Sequence 44, Appl
79	10.6	58.9	24	4	US-09-095-332-34	Sequence 34, Appl
80	10.6	58.9	25	2	US-08-483-636-34	Sequence 34, Appl
81	10.6	58.9	25	2	US-08-483-636-34	Sequence 34, Appl
82	10.4	57.8	12	1	US-08-261-206A-78	Sequence 78, Appl
83	10.4	57.8	12	1	US-08-261-206A-78	Sequence 78, Appl
84	10.4	57.8	18	2	US-08-543-020-2	Sequence 2, Appl
85	10.4	57.8	18	2	US-08-735-692-4	Sequence 4, Appl
86	10.4	57.8	18	3	US-08-542-051-26	Sequence 26, Appl
87	10.4	57.8	19	1	US-08-376-362A-6	Sequence 6, Appl
88	10.4	57.8	19	1	US-08-484-129-18	Sequence 18, Appl
89	10.4	57.8	20	4	US-07-952-817-4	Sequence 4, Appl
90	10.4	57.8	20	4	US-09-318-799A-9	Sequence 9, Appl
91	10.4	57.8	20	4	US-09-506-073-82	Sequence 82, Appl
92	10.4	57.8	23	1	US-07-931-473B-36	Sequence 36, Appl
93	10.4	57.8	23	1	US-07-931-473B-36	Sequence 36, Appl
94	10.4	57.8	23	1	US-07-714-131C-36	Sequence 36, Appl
95	10.4	57.8	23	1	US-07-714-131C-36	Sequence 36, Appl
96	10.4	57.8	23	1	US-08-412-110-36	Sequence 36, Appl
97	10.4	57.8	23	1	US-08-412-110-36	Sequence 36, Appl
98	10.4	57.8	23	1	US-08-409-442A-36	Sequence 36, Appl
99	10.4	57.8	23	1	US-08-409-442A-36	Sequence 36, Appl
100	10.4	57.8	23	2	US-08-469-603A-36	Sequence 36, Appl

C 101	10.4	57.8	23	2	US-08-469-609A-36	Sequence 36, Appl
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C 103	10.4	57.8	23	3	US-09-143-190-36	Sequence 36, Appl
C 104	10.4	57.8	23	4	US-09-503-344-36	Sequence 36, Appl
C 105	10.4	57.8	23	4	US-09-503-344-36	Sequence 36, Appl
C 106	10.4	57.8	24	1	US-08-178-606-12	Sequence 12, Appl
C 107	10.4	57.8	24	1	US-08-199-507B-56	Sequence 56, Appl
C 108	10.4	57.8	24	1	US-08-199-507B-56	Sequence 56, Appl
C 109	10.4	57.8	24	1	US-08-243-870-3	Sequence 3, Appl
C 110	10.4	57.8	24	1	US-08-243-870-3	Sequence 3, Appl
C 111	10.4	57.8	24	1	US-08-442-572-59	Sequence 59, Appl
C 112	10.4	57.8	24	1	US-08-442-572-59	Sequence 59, Appl
C 113	10.4	57.8	24	1	US-08-399-412A-3	Sequence 3, Appl
C 114	10.4	57.8	24	1	US-08-399-412A-3	Sequence 3, Appl
C 115	10.4	57.8	24	1	US-08-477-530-3	Sequence 3, Appl
C 116	10.4	57.8	24	1	US-08-477-530-3	Sequence 3, Appl
C 117	10.4	57.8	24	1	US-08-477-530-3	Sequence 3, Appl
C 118	10.4	57.8	24	1	US-08-409-439A-3	Sequence 3, Appl
C 119	10.4	57.8	24	1	US-08-409-439A-3	Sequence 3, Appl
C 120	10.4	57.8	24	1	US-08-441-591-3	Sequence 3, Appl
C 121	10.4	57.8	24	1	US-08-441-591-3	Sequence 3, Appl
C 122	10.4	57.8	24	1	US-08-384-708A-3	Sequence 3, Appl
C 123	10.4	57.8	24	1	US-08-384-708A-3	Sequence 3, Appl
C 124	10.4	57.8	24	1	US-08-384-708A-3	Sequence 3, Appl
C 125	10.4	57.8	24	1	US-08-303-362A-3	Sequence 3, Appl
C 126	10.4	57.8	24	1	US-08-303-362A-3	Sequence 3, Appl
C 127	10.4	57.8	24	1	US-08-477-830-3	Sequence 3, Appl
C 128	10.4	57.8	24	1	US-08-477-830-3	Sequence 3, Appl
C 129	10.4	57.8	24	1	US-08-441-828-56	Sequence 56, Appl
C 130	10.4	57.8	24	1	US-08-441-828-56	Sequence 56, Appl
C 131	10.4	57.8	24	1	US-08-361-795-59	Sequence 59, Appl
C 132	10.4	57.8	24	1	US-08-361-795-59	Sequence 59, Appl
C 133	10.4	57.8	24	1	US-08-447-169A-3	Sequence 3, Appl
C 134	10.4	57.8	24	1	US-08-447-169A-3	Sequence 3, Appl
C 135	10.4	57.8	24	2	US-08-233-012C-3	Sequence 3, Appl
C 136	10.4	57.8	24	2	US-08-233-012C-3	Sequence 3, Appl
C 137	10.4	57.8	24	2	US-08-477-527A-207	Sequence 207, App
C 138	10.4	57.8	24	2	US-08-477-527A-207	Sequence 207, App
C 139	10.4	57.8	24	3	US-08-481-710-207	Sequence 207, App
C 140	10.4	57.8	24	3	US-08-481-710-207	Sequence 207, App
C 141	10.4	57.8	24	4	US-08-687-421-3	Sequence 3, Appl
C 142	10.4	57.8	24	4	US-08-687-421-3	Sequence 3, Appl
C 143	10.4	57.8	24	5	PCT-US95-05600-20	Sequence 20, Appl
C 144	10.4	57.8	24	5	PCT-US95-05600-20	Sequence 20, Appl
C 145	10.4	57.8	24	5	PCT-US95-05600-142	Sequence 142, App
C 146	10.4	57.8	24	5	PCT-US95-05600-142	Sequence 142, App
C 147	10.4	57.8	24	5	PCT-US96-09537-207	Sequence 207, App
C 148	10.4	57.8	24	5	PCT-US96-09537-207	Sequence 207, App
C 149	10.4	57.8	25	2	US-08-633-879C-20	Sequence 20, Appl
C 150	10.4	57.8	25	2	US-08-633-879C-20	Sequence 20, Appl
C 151	10.4	57.8	25	3	US-08-384-106A-12	Sequence 12, Appl
C 152	10.4	57.8	25	3	US-09-197-649-24	Sequence 24, Appl
C 153	10.4	57.8	25	5	PCT-US96-01643-12	Sequence 12, Appl
C 154	10.2	56.7	16	4	US-09-142-320-1	Sequence 1, Appl
C 155	10.2	56.7	17	4	US-09-216-909-4	Sequence 4, Appl
C 156	10.2	56.7	17	4	US-09-703-843-4	Sequence 4, Appl
C 157	10.2	56.7	17	4	US-09-702-847-4	Sequence 173, App
C 158	10.2	56.7	17	4	US-08-679-645-13	Sequence 106, App
C 159	10.2	56.7	17	4	US-09-593-012-106	Sequence 10, Appl
C 160	10.2	56.7	19	1	US-08-559-303B-10	Sequence 1, Appl
C 161	10.2	56.7	19	3	US-08-894-483-1	Sequence 1, Appl
C 162	10.2	56.7	19	3	US-09-252-806-1	Sequence 2, Appl
C 163	10.2	56.7	19	4	US-09-342-579-2	Sequence 10, Appl
C 164	10.2	56.7	19	4	US-09-175-828-10	Sequence 28, Appl
C 165	10.2	56.7	19	4	US-09-504-358-28	Sequence 2, Appl
C 166	10.2	56.7	19	4	US-09-617-854A-2	Sequence 28, Appl
C 167	10.2	56.7	19	4	US-09-954-314-28	Sequence 28, Appl
C 168	10.2	56.7	20	1	US-08-170-688-3	Sequence 3, Appl
C 169	10.2	56.7	20	1	US-08-263-072A-3	Sequence 3, Appl
C 170	10.2	56.7	20	1	US-08-665-565B-3	Sequence 1, Appl
C 171	10.2	56.7	20	1	US-08-665-565B-3	Sequence 1, Appl
C 172	10.2	56.7	20	1	US-08-757-653-151	Sequence 151, App
C 173	10.2	56.7	20	2	US-09-108-051-13	Sequence 13, Appl
C 174	10.2	56.7	20	3	US-09-034-724-1	Sequence 1, Appl
C 175	10.2	56.7	20	3	US-09-034-724-1	Sequence 3, Appl
C 176	10.2	56.7	20	3	US-08-782-798-3	Sequence 3, Appl
C 177	10.2	56.7	20	3	US-08-782-798-3	Sequence 9, Appl
C 178	10.2	56.7	20	3	US-09-191-099-9	Sequence 62, Appl
C 179	10.2	56.7	20	4	US-09-193-377B-62	Sequence 96, Appl
C 180	10.2	56.7	20	4	US-09-487-445-96	Sequence 122, Appl
C 181	10.2	56.7	20	4	US-09-593-711A-122	Sequence 3, Appl
C 182	10.2	56.7	20	4	US-08-943-571-3	Sequence 3, Appl
C 183	10.2	56.7	20	4	US-08-520-946-151	Sequence 151, App
C 184	10.2	56.7	20	4	US-09-549-953-5	Sequence 5, Appl
C 185	10.2	56.7	20	4	US-09-920-663-13	Sequence 13, Appl
C 186	10.2	56.7	20	4	US-09-920-663-13	Sequence 14, Appl
C 187	10.2	56.7	20	4	US-09-920-663-13	Sequence 15, Appl
C 188	10.2	56.7	20	4	US-09-920-663-15	Sequence 1, Appl
C 189	10.2	56.7	20	4	US-09-437-905-1	Sequence 1, Appl
C 190	10.2	56.7	20	4	US-08-469-260A-142	Sequence 14, App
C 191	10.2	56.7	20	4	US-08-469-260A-142	Sequence 15, Appl
C 192	10.2	56.7	21	1	US-08-138-641-5	Sequence 5, Appl
C 193	10.2	56.7	21	1	US-08-138-641-5	Sequence 9, Appl
C 194	10.2	56.7	21	1	US-08-462-305-9	Sequence 9, Appl
C 195	10.2	56.7	21	2	US-08-613-417A-9	Sequence 9, Appl
C 196	10.2	56.7	21	2	US-08-594-452-9	Sequence 9, Appl
C 197	10.2	56.7	21	3	US-08-578-686C-8	Sequence 8, Appl
C 198	10.2	56.7	21	3	US-08-578-686C-8	Sequence 9, Appl
C 199	10.2	56.7	21	3	US-09-094-405-9	Sequence 9, Appl
C 200	10.2	56.7	21	3	US-09-258-408-9	Sequence 9, Appl
C 201	10.2	56.7	21	3	US-09-166-112-9	Sequence 9, Appl
C 202	10.2	56.7	21	3	US-09-144-112-8	Sequence 8, Appl
C 203	10.2	56.7	21	4	US-09-311-260-31	Sequence 29, Appl
C 204	10.2	56.7	21	4	US-09-311-260-31	Sequence 245, App
C 205	10.2	56.7	21	4	US-08-943-731-245	Sequence 9, Appl
C 206	10.2	56.7	21	4	US-08-895-981-9	Sequence 9, Appl
C 207	10.2	56.7	22	2	US-08-457-273B-20	Sequence 20, Appl
C 208	10.2	56.7	22	2	US-09-237-115-1	Sequence 1, Appl
C 209	10.2	56.7	22	3	US-08-594-455-57	Sequence 57, Appl
C 210	10.2	56.7	23	3	US-09-073-445-1	Sequence 1, Appl
C 211	10.2	56.7	23	3	US-09-258-408-57	Sequence 57, Appl
C 212	10.2	56.7	23	3	US-08-102-751-6	Sequence 6, Appl
C 213	10.2	56.7	24	1	US-08-467-607-9	Sequence 9, Appl
C 214	10.2	56.7	24	2	US-08-469-362-9	Sequence 9, Appl
C 215	10.2	56.7	24	2	US-08-850-392-9	Sequence 9, Appl
C 216	10.2	56.7	24	3	US-08-564-110C-15	Sequence 15, Appl
C 217	10.2	56.7	24	4	US-09-336-441A-97	Sequence 97, Appl
C 218	10.2	56.7	24	4	US-09-053-831-3	Sequence 14, Appl
C 219	10.2	56.7	25	2	US-08-671-975A-14	Sequence 88, Appl
C 220	10.2	56.7	25	2	US-08-840-316-88	Sequence 88, Appl
C 221	10.2	56.7	25	4	US-08-809-523-88	Sequence 125, App
C 222	10.2	56.7	25	4	US-09-018-584A-125	Sequence 88, Appl
C 223	10.2	56.7	25	4	US-08-471-971-88	Sequence 88, Appl
C 224	10.2	56.7	25	4	US-09-592-891A-10	Sequence 88, Appl
C 225	10.2	56.7	25	4	US-09-402-776-88	Sequence 88, Appl
C 226	10.2	56.7	25	5	PCT-US93-08849A-88	Sequence 88, Appl
C 227	10.2	56.7	25	5	PCT-US93-08849A-88	Sequence 17, Appl
C 228	10.2	56.7	25	5	PCT-US93-08849A-88	Sequence 17, Appl
C 229	10.2	56.7	11	1	US-08-292-081A-17	Sequence 17, Appl
C 230	10.2	56.7	11	1	US-08-752-495-17	Sequence 17, Appl
C 231	10.2	56.7	11	2	US-08-268-679B-14	Sequence 14, Appl
C 232	10.2	56.7	14	1	US-08-706-135-1	Sequence 1, Appl
C 233	10.2	56.7	14	5	PCT-US95-1690A-1	Sequence 1, Appl
C 234	10.2	56.7	17	1	US-08-282-081A-18	Sequence 18, Appl
C 235	10.2	56.7	17	1	US-08-282-081A-18	Sequence 19, Appl
C 236	10.2	56.7	17	1	US-08-282-081A-20	Sequence 18, Appl
C 237	10.2	56.7	17	2	US-08-752-495-18	Sequence 19, Appl
C 238	10.2	56.7	17	2	US-08-752-495-19	Sequence 20, Appl
C 239	10.2	56.7	17	2	US-08-752-495-20	Sequence 16, Appl
C 240	10.2	56.7	19	3	US-09-369-618-16	Sequence 16, Appl
C 241	10.2	56.7	19	3	US-09-369-617-16	Sequence 23, Appl
C 242	10.2	56.7	20	1	US-08-308-949A-23	Sequence 23, Appl
C 243	10.2	56.7	20	3	US-09-357-070-13	Sequence 43, Appl
C 244	10.2	56.7	20	4	US-09-490-692-160	Sequence 160, App
C 245	10.2	56.7	20	4	US-08-894-818B-37	Sequence 37, Appl
C 246	10.2	56.7	20	4	US-09-467-642-48	Sequence 48, Appl

C 247	10	55.6	20	4	US-09-445-472-18	Sequence 18, Appl	C 320	9.8	54.4	21	1	US-08-044-506B-2	Sequence 2, Appl1
C 248	10	55.6	21	4	US-09-535-008-6	Sequence 6, Appl1	C 321	9.8	54.4	21	2	US-08-696-944-13	Sequence 13, Appl1
C 249	10	55.6	22	4	US-08-244-122-4	Sequence 4, Appl1	C 322	9.8	54.4	21	4	US-08-776-927-7	Sequence 7, Appl1
C 250	10	55.6	22	2	US-08-244-122-6	Sequence 6, Appl1	C 323	9.8	54.4	21	4	US-09-453-562A-7	Sequence 7, Appl1
C 251	10	55.6	22	4	US-09-117-927-12	Sequence 12, Appl1	C 324	9.8	54.4	22	2	US-08-766-982-8	Sequence 8, Appl1
C 252	10	55.6	22	4	US-09-117-927-14	Sequence 14, Appl1	C 325	9.8	54.4	22	4	US-08-766-982-8	Sequence 8, Appl1
C 253	10	55.6	22	4	US-09-560-639-32	Sequence 32, Appl1	C 326	9.8	54.4	22	4	US-08-766-982-8	Sequence 8, Appl1
C 254	10	55.6	22	4	US-09-308-090-3	Sequence 3, Appl1	C 327	9.8	54.4	22	4	US-08-766-982-8	Sequence 8, Appl1
C 255	10	55.6	24	2	US-08-547-979-2	Sequence 2, Appl1	C 328	9.8	54.4	22	4	US-08-766-982-8	Sequence 8, Appl1
C 256	10	55.6	24	2	US-08-708-958-4	Sequence 4, Appl1	C 329	9.8	54.4	22	4	US-09-256-219-8	Sequence 9, Appl1
C 257	10	55.6	25	1	US-08-605-541B-5	Sequence 5, Appl1	C 330	9.8	54.4	22	4	US-09-142-623-20	Sequence 20, Appl1
C 258	10	55.6	25	3	US-08-737-607-31	Sequence 31, Appl1	C 331	9.8	54.4	22	4	US-09-343-634-6	Sequence 6, Appl1
C 259	10	55.6	25	4	US-09-305-681-32	Sequence 32, Appl1	C 332	9.8	54.4	23	2	US-08-850-293-1	Sequence 1, Appl1
C 260	9.8	54.4	15	1	US-08-311-760A-13	Sequence 13, Appl1	C 333	9.8	54.4	23	3	US-08-746-397-3	Sequence 3, Appl1
C 261	9.8	54.4	15	1	US-08-311-760A-14	Sequence 14, Appl1	C 334	9.8	54.4	23	3	US-09-415-784-76	Sequence 76, Appl1
C 262	9.8	54.4	15	1	US-08-311-760A-44	Sequence 44, Appl1	C 335	9.8	54.4	23	4	US-09-415-785A-76	Sequence 76, Appl1
C 263	9.8	54.4	15	1	US-08-311-760A-64	Sequence 64, Appl1	C 336	9.8	54.4	23	4	US-08-944-465-76	Sequence 76, Appl1
C 264	9.8	54.4	15	1	US-08-311-760A-168	Sequence 168, Appl1	C 337	9.8	54.4	23	4	US-09-415-900-76	Sequence 76, Appl1
C 265	9.8	54.4	15	1	US-08-393-219-9	Sequence 9, Appl1	C 338	9.8	54.4	23	4	US-09-415-900-76	Sequence 76, Appl1
C 266	9.8	54.4	15	2	US-08-774-310-13	Sequence 13, Appl1	C 339	9.8	54.4	24	1	US-08-090-523-17	Sequence 17, Appl1
C 267	9.8	54.4	15	2	US-08-774-310-14	Sequence 14, Appl1	C 340	9.8	54.4	24	1	US-08-398-627-17	Sequence 17, Appl1
C 268	9.8	54.4	15	2	US-08-774-310-44	Sequence 44, Appl1	C 341	9.8	54.4	24	1	US-08-406-858-17	Sequence 17, Appl1
C 269	9.8	54.4	15	2	US-08-774-310-64	Sequence 64, Appl1	C 342	9.8	54.4	24	3	US-08-981-462-48	Sequence 48, Appl1
C 270	9.8	54.4	15	2	US-08-774-310-168	Sequence 168, Appl1	C 343	9.8	54.4	24	4	US-09-385-028-2	Sequence 2, Appl1
C 271	9.8	54.4	16	1	US-08-778-702-16	Sequence 16, Appl1	C 344	9.8	54.4	24	4	US-09-385-028-25	Sequence 25, Appl1
C 272	9.8	54.4	16	4	US-09-338-907-139	Sequence 139, Appl1	C 345	9.8	54.4	24	4	US-08-809-802-14	Sequence 14, Appl1
C 273	9.8	54.4	16	4	US-09-218-207-139	Sequence 139, Appl1	C 346	9.8	54.4	24	5	PCT-US91-04036-17	Sequence 17, Appl1
C 274	9.8	54.4	17	1	US-07-767-135-12	Sequence 12, Appl1	C 347	9.8	54.4	24	5	PCT-US94-05275-17	Sequence 17, Appl1
C 275	9.8	54.4	17	1	US-07-861-652-16	Sequence 16, Appl1	C 348	9.8	54.4	25	1	US-08-317-432A-45	Sequence 45, Appl1
C 276	9.8	54.4	17	4	US-08-584-040-7437	Sequence 7437, Appl1	C 349	9.8	54.4	25	3	US-09-081-180-26	Sequence 26, Appl1
C 277	9.8	54.4	18	1	US-07-977-284A-44	Sequence 44, Appl1	C 350	9.8	54.4	25	3	US-09-081-180-26	Sequence 26, Appl1
C 278	9.8	54.4	18	1	US-08-175-155-12	Sequence 12, Appl1	C 351	9.8	54.4	25	3	US-09-040-786-26	Sequence 26, Appl1
C 279	9.8	54.4	18	1	US-08-366-577-5	Sequence 5, Appl1	C 352	9.8	54.4	25	3	US-09-040-786-26	Sequence 26, Appl1
C 280	9.8	54.4	18	1	US-08-477-509B-46	Sequence 46, Appl1	C 353	9.8	54.4	25	3	US-09-415-784-78	Sequence 78, Appl1
C 281	9.8	54.4	18	2	US-08-707-237A-18	Sequence 18, Appl1	C 354	9.8	54.4	25	4	US-09-402-515A-11	Sequence 11, Appl1
C 282	9.8	54.4	18	2	US-08-533-306A-13	Sequence 13, Appl1	C 355	9.8	54.4	25	4	US-09-415-785A-78	Sequence 78, Appl1
C 283	9.8	54.4	18	2	US-08-543-020-2	Sequence 2, Appl1	C 356	9.8	54.4	25	4	US-08-944-465-78	Sequence 78, Appl1
C 284	9.8	54.4	18	2	US-08-742-923A-13	Sequence 13, Appl1	C 357	9.8	54.4	25	4	US-09-415-868-78	Sequence 78, Appl1
C 285	9.8	54.4	18	2	US-08-468-551-3	Sequence 3, Appl1	C 358	9.8	54.4	25	4	US-09-415-900-78	Sequence 78, Appl1
C 286	9.8	54.4	18	2	US-08-256-426B-44	Sequence 44, Appl1	C 359	9.8	53.3	16	2	US-08-527-060-11	Sequence 11, Appl1
C 287	9.8	54.4	18	2	US-08-735-692-4	Sequence 4, Appl1	C 360	9.8	53.3	17	2	US-08-626-023-1	Sequence 1, Appl1
C 288	9.8	54.4	18	3	US-08-542-051-26	Sequence 26, Appl1	C 361	9.8	53.3	17	2	US-08-626-023-1	Sequence 1, Appl1
C 289	9.8	54.4	18	3	US-08-482-085B-46	Sequence 46, Appl1	C 362	9.8	53.3	17	3	US-08-985-162-104	Sequence 104, Appl1
C 290	9.8	54.4	18	3	US-08-482-304-44	Sequence 44, Appl1	C 363	9.8	53.3	17	3	US-08-679-645-80	Sequence 80, Appl1
C 291	9.8	54.4	18	3	US-08-483-474-44	Sequence 44, Appl1	C 364	9.8	53.3	17	4	US-08-679-645-82	Sequence 82, Appl1
C 292	9.8	54.4	18	3	US-09-213-719-11	Sequence 11, Appl1	C 365	9.8	53.3	18	2	US-09-212-771-8	Sequence 8, Appl1
C 293	9.8	54.4	18	3	US-09-487-444-40	Sequence 40, Appl1	C 366	9.8	53.3	18	3	US-09-008-481A-19	Sequence 19, Appl1
C 294	9.8	54.4	18	4	US-09-423-439-6	Sequence 6, Appl1	C 367	9.8	53.3	18	4	US-08-718-388A-14	Sequence 14, Appl1
C 295	9.8	54.4	18	4	US-08-679-645-1179	Sequence 1179, Appl1	C 368	9.8	53.3	18	4	US-09-309-592-19	Sequence 19, Appl1
C 296	9.8	54.4	18	4	US-09-444-791A-46	Sequence 46, Appl1	C 369	9.8	53.3	18	4	US-08-584-040-6210	Sequence 6210, Appl1
C 297	9.8	54.4	18	5	PCT-US96-00005-5	Sequence 5, Appl1	C 370	9.8	53.3	20	2	US-08-466-337A-12	Sequence 12, Appl1
C 298	9.8	54.4	19	3	US-08-846-020A-40	Sequence 40, Appl1	C 371	9.8	53.3	20	2	US-08-465-359-12	Sequence 12, Appl1
C 299	9.8	54.4	19	3	US-09-125-324-2	Sequence 2, Appl1	C 372	9.8	53.3	20	3	US-08-465-887A-12	Sequence 12, Appl1
C 300	9.8	54.4	19	4	US-09-617-871-40	Sequence 40, Appl1	C 373	9.8	53.3	20	3	US-09-280-789-172	Sequence 172, Appl1
C 301	9.8	54.4	20	2	US-08-733-816-1	Sequence 1, Appl1	C 374	9.8	53.3	20	4	US-09-277-020-63	Sequence 63, Appl1
C 302	9.8	54.4	20	2	US-08-837-201C-15	Sequence 15, Appl1	C 375	9.8	53.3	20	4	US-09-277-020-64	Sequence 64, Appl1
C 303	9.8	54.4	20	3	US-08-995-960-17	Sequence 17, Appl1	C 376	9.8	53.3	20	4	US-09-180-437-226	Sequence 226, Appl1
C 304	9.8	54.4	20	3	US-08-981-462-3	Sequence 3, Appl1	C 377	9.8	53.3	20	4	US-09-732-199A-21	Sequence 21, Appl1
C 305	9.8	54.4	20	3	US-08-981-462-8	Sequence 8, Appl1	C 378	9.8	53.3	20	4	US-09-487-253A-9	Sequence 9, Appl1
C 306	9.8	54.4	20	3	US-08-892-540-1	Sequence 1, Appl1	C 379	9.8	53.3	20	4	US-09-853-768-65	Sequence 65, Appl1
C 307	9.8	54.4	20	3	US-08-953-171-21	Sequence 21, Appl1	C 380	9.8	53.3	20	4	US-09-853-768-65	Sequence 65, Appl1
C 308	9.8	54.4	20	3	US-08-953-171-23	Sequence 23, Appl1	C 381	9.8	53.3	21	4	US-09-780-173A-24	Sequence 24, Appl1
C 309	9.8	54.4	20	3	US-09-428-584-14	Sequence 14, Appl1	C 382	9.8	53.3	21	4	US-09-382-616A-39	Sequence 39, Appl1
C 310	9.8	54.4	20	3	US-09-428-584-15	Sequence 15, Appl1	C 383	9.8	53.3	22	4	US-09-439-362-2	Sequence 2, Appl1
C 311	9.8	54.4	20	4	US-09-557-246-3	Sequence 3, Appl1	C 384	9.8	53.3	22	1	US-08-943-731-554	Sequence 554, Appl1
C 312	9.8	54.4	20	4	US-09-364-415-45	Sequence 45, Appl1	C 385	9.8	53.3	23	1	US-08-181-556-5	Sequence 5, Appl1
C 313	9.8	54.4	20	4	US-09-270-542-15	Sequence 15, Appl1	C 386	9.8	53.3	23	1	US-08-181-556-11	Sequence 11, Appl1
C 314	9.8	54.4	20	4	US-09-556-031-17	Sequence 17, Appl1	C 387	9.8	53.3	24	2	US-08-928-992-2	Sequence 2, Appl1
C 315	9.8	54.4	20	4	US-09-506-073-78	Sequence 78, Appl1	C 388	9.8	53.3	24	3	US-08-871-267B-33	Sequence 33, Appl1
C 316	9.8	54.4	20	4	US-09-657-452A-142	Sequence 142, Appl1	C 389	9.8	53.3	24	3	US-09-010-641-29	Sequence 29, Appl1
C 317	9.8	54.4	20	4	US-09-657-452A-143	Sequence 143, Appl1	C 390	9.8	53.3	24	4	US-09-356-281-29	Sequence 29, Appl1
C 318	9.8	54.4	20	4	US-09-920-663-12	Sequence 12, Appl1	C 391	9.8	53.3	24	4	US-09-618-419-33	Sequence 33, Appl1
C 319	9.8	54.4	20	4	US-09-657-453A-30	Sequence 30, Appl1	C 392	9.8	53.3	24	4	US-09-339-972-2	Sequence 2, Appl1

C 393	9.6	53.3	24	4	US-09-171-710-14	Sequence 14, Appl	466	9.4	52.2	20	4	US-08-851-896-49	Sequence 49, Appl
C 394	9.6	53.3	24	4	US-09-117-847E-6	Sequence 6, Appl	467	9.4	52.2	20	4	US-09-167-109-51	Sequence 51, Appl
C 395	9.6	53.3	24	4	US-09-117-847E-12	Sequence 12, Appl	468	9.4	52.2	20	4	US-09-851-896-71	Sequence 71, Appl
C 396	9.6	53.3	24	6	5457089	Patent No. 5457089	C 469	9.4	52.2	20	4	US-09-506-073-78	Sequence 78, Appl
C 397	9.6	53.3	25	1	US-08-140-349-11	Sequence 11, Appl	C 470	9.4	52.2	20	4	US-09-657-452A-144	Sequence 144, Appl
C 398	9.6	53.3	25	1	US-08-175-236-11	Sequence 11, Appl	C 471	9.4	52.2	20	4	US-09-517-467B-85	Sequence 85, Appl
C 399	9.6	53.3	25	1	US-08-683-877-5	Sequence 5, Appl	C 472	9.4	52.2	20	5	PCT-US94-09881-75	Sequence 75, Appl
C 400	9.6	53.3	25	4	US-08-679-645-1250	Sequence 1250, Ap	C 473	9.4	52.2	21	1	US-07-661-378A-8	Sequence 8, Appl
C 401	9.6	53.3	25	5	PCT-US93-07051-11	Sequence 11, Appl	C 474	9.4	52.2	21	1	US-08-454-097-40	Sequence 40, Appl
C 402	9.6	53.3	25	6	5428147-6	Patent No. 5428147	C 475	9.4	52.2	21	2	US-08-637-899-14	Sequence 14, Appl
C 403	9.4	52.2	12	1	US-08-086-410-4	Sequence 4, Appl	C 476	9.4	52.2	21	2	US-08-522-841-2	Sequence 2, Appl
C 404	9.4	52.2	12	1	US-07-939-501A-17	Sequence 17, Appl	C 477	9.4	52.2	21	3	US-08-185-359-40	Sequence 40, Appl
C 405	9.4	52.2	14	3	US-08-923-558-5	Sequence 5, Appl	C 478	9.4	52.2	21	3	US-07-974-429C-355	Sequence 355, App
C 406	9.4	52.2	14	4	US-09-486-553-5	Sequence 5, Appl	C 479	9.4	52.2	22	1	US-08-367-227-4	Sequence 4, Appl
C 407	9.4	52.2	15	4	US-09-535-262-7	Sequence 7, Appl	C 480	9.4	52.2	22	2	US-08-543-020-4	Sequence 4, Appl
C 408	9.4	52.2	16	1	US-08-229-279-1	Sequence 1, Appl	C 481	9.4	52.2	22	2	US-08-910-484-4	Sequence 4, Appl
C 409	9.4	52.2	16	1	US-08-701-269-1	Sequence 1, Appl	C 482	9.4	52.2	22	2	US-08-735-692-6	Sequence 6, Appl
C 410	9.4	52.2	16	1	US-08-498-849B-38	Sequence 38, Appl	C 483	9.4	52.2	22	3	US-08-542-051-28	Sequence 28, Appl
C 411	9.4	52.2	17	1	US-08-373-124A-418	Sequence 418, Ap	C 484	9.4	52.2	22	3	US-09-178-089-13	Sequence 13, Appl
C 412	9.4	52.2	17	1	US-08-147-696E-3	Sequence 3, Appl	C 485	9.4	52.2	22	3	US-08-589-028-49	Sequence 49, Appl
C 413	9.4	52.2	17	1	US-08-484-334-3	Sequence 3, Appl	C 486	9.4	52.2	22	3	US-08-784-582-49	Sequence 49, Appl
C 414	9.4	52.2	17	1	US-08-435-628-418	Sequence 418, Ap	C 487	9.4	52.2	22	4	US-08-785-271-49	Sequence 49, Appl
C 415	9.4	52.2	17	1	US-08-292-620A-1654	Sequence 1654, Ap	C 488	9.4	52.2	23	1	US-07-920-519-7	Sequence 7, Appl
C 416	9.4	52.2	17	2	US-08-292-620A-1957	Sequence 1957, Ap	C 489	9.4	52.2	23	1	US-07-621-091G-20	Sequence 20, Appl
C 417	9.4	52.2	17	3	US-09-013-092-3	Sequence 3, Appl	C 490	9.4	52.2	23	1	US-08-314-586-7	Sequence 7, Appl
C 418	9.4	52.2	17	3	US-08-375-151-4	Sequence 4, Appl	C 491	9.4	52.2	23	1	US-08-371-121-18	Sequence 18, Appl
C 419	9.4	52.2	17	3	US-09-071-845-1654	Sequence 1654, Ap	C 492	9.4	52.2	23	1	US-08-047-413-1	Sequence 1, Appl
C 420	9.4	52.2	17	3	US-09-071-845-1957	Sequence 1957, Ap	C 493	9.4	52.2	23	1	US-08-738-944-34	Sequence 34, Appl
C 421	9.4	52.2	17	3	US-09-280-999-3	Sequence 3, Appl	C 494	9.4	52.2	23	2	US-08-821-914-6	Sequence 6, Appl
C 422	9.4	52.2	17	4	US-09-425-072-4	Sequence 4, Appl	C 495	9.4	52.2	23	2	US-08-399-889-20	Sequence 20, Appl
C 423	9.4	52.2	18	1	US-08-019-870-13	Sequence 13, Appl	C 496	9.4	52.2	23	2	US-08-332-562A-95	Sequence 95, Appl
C 424	9.4	52.2	18	1	US-08-633-760-57	Sequence 57, Appl	C 497	9.4	52.2	23	2	US-07-927-391-19	Sequence 19, Appl
C 425	9.4	52.2	18	1	US-08-633-760-58	Sequence 58, Appl	C 498	9.4	52.2	23	3	US-09-167-364-20	Sequence 20, Appl
C 426	9.4	52.2	18	1	US-08-757-024-4	Sequence 4, Appl	C 499	9.4	52.2	23	3	US-08-858-876A-5	Sequence 5, Appl
C 427	9.4	52.2	18	3	US-08-472-527-4	Sequence 4, Appl	C 500	9.4	52.2	23	3	US-08-379-452-28	Sequence 28, Appl
C 428	9.4	52.2	18	3	US-09-280-409-11	Sequence 11, Appl	C 501	9.4	52.2	23	3	US-08-815-785A-76	Sequence 76, Appl
C 429	9.4	52.2	18	4	US-09-290-577-36	Sequence 36, Appl	C 502	9.4	52.2	23	3	US-08-229-050-1	Sequence 1, Appl
C 430	9.4	52.2	18	4	US-09-316-083-4	Sequence 4, Appl	C 503	9.4	52.2	23	3	US-08-589-028-47	Sequence 47, Appl
C 431	9.4	52.2	18	4	US-09-230-452-36	Sequence 36, Appl	C 504	9.4	52.2	23	3	US-08-801-563-1	Sequence 1, Appl
C 432	9.4	52.2	19	1	US-07-964-589-4	Sequence 36, Appl	C 505	9.4	52.2	23	3	US-08-784-582-47	Sequence 47, Appl
C 433	9.4	52.2	19	1	US-08-196-016A-34	Sequence 34, Appl	C 506	9.4	52.2	23	3	US-09-409-670-28	Sequence 28, Appl
C 434	9.4	52.2	19	1	US-08-481-658B-4	Sequence 4, Appl	C 507	9.4	52.2	23	4	US-08-785-271-49	Sequence 49, Appl
C 435	9.4	52.2	19	2	US-08-477-504A-4	Sequence 4, Appl	C 508	9.4	52.2	23	4	US-09-439-897-22	Sequence 22, Appl
C 436	9.4	52.2	19	2	US-08-486-756A-4	Sequence 4, Appl	C 509	9.4	52.2	23	4	US-09-415-784-76	Sequence 76, Appl
C 437	9.4	52.2	19	2	US-08-485-862B-4	Sequence 4, Appl	C 510	9.4	52.2	23	4	US-09-415-785A-76	Sequence 76, Appl
C 438	9.4	52.2	19	2	US-08-485-862B-4	Sequence 4, Appl	C 511	9.4	52.2	23	4	US-08-944-465-76	Sequence 76, Appl
C 439	9.4	52.2	19	3	US-08-787-739-4	Sequence 4, Appl	C 512	9.4	52.2	23	4	US-09-415-868-76	Sequence 76, Appl
C 440	9.4	52.2	19	3	US-08-487-077A-4	Sequence 4, Appl	C 513	9.4	52.2	23	4	US-09-415-868-76	Sequence 76, Appl
C 441	9.4	52.2	19	3	US-08-485-863A-4	Sequence 4, Appl	C 514	9.4	52.2	23	4	US-08-684-612-5	Sequence 5, Appl
C 442	9.4	52.2	19	3	US-08-485-863A-4	Sequence 4, Appl	C 515	9.4	52.2	23	4	US-08-337-607A-34	Sequence 34, Appl
C 443	9.4	52.2	19	4	US-09-110-517-11	Sequence 11, Appl	C 516	9.4	52.2	24	1	US-08-564-496C-27	Sequence 27, Appl
C 444	9.4	52.2	19	4	US-09-110-517-11	Sequence 11, Appl	C 517	9.4	52.2	24	2	US-08-981-462-33	Sequence 33, Appl
C 445	9.4	52.2	19	4	US-09-117-349-12	Sequence 12, Appl	C 518	9.4	52.2	24	3	US-08-981-462-33	Sequence 33, Appl
C 446	9.4	52.2	19	4	US-09-178-115-4	Sequence 4, Appl	C 519	9.4	52.2	24	3	US-08-981-462-33	Sequence 33, Appl
C 447	9.4	52.2	19	4	US-09-178-115-4	Sequence 4, Appl	C 520	9.4	52.2	24	3	PCT-US95-15428-27	Sequence 27, Appl
C 448	9.4	52.2	19	4	US-09-178-776-4	Sequence 4, Appl	C 521	9.4	52.2	24	3	US-08-244-122-15	Sequence 15, Appl
C 449	9.4	52.2	19	5	PCT-US93-02024-4	Sequence 4, Appl	C 522	9.4	52.2	25	2	US-08-461-030C-7	Sequence 7, Appl
C 450	9.4	52.2	20	1	US-07-780-973-7	Sequence 7, Appl	C 523	9.4	52.2	25	2	US-08-467-265-12	Sequence 12, Appl
C 451	9.4	52.2	20	1	US-07-906-393-3	Sequence 3, Appl	C 524	9.4	52.2	25	3	US-08-384-106A-10	Sequence 10, Appl
C 452	9.4	52.2	20	1	US-08-178-606-13	Sequence 13, Appl	C 525	9.4	52.2	25	3	US-09-391-562-8	Sequence 8, Appl
C 453	9.4	52.2	20	1	US-08-178-606-13	Sequence 13, Appl	C 526	9.4	52.2	25	3	US-09-398-193-101	Sequence 101, App
C 454	9.4	52.2	20	1	US-08-325-071-37	Sequence 37, Appl	C 527	9.4	52.2	25	4	US-08-467-265-12	Sequence 12, Appl
C 455	9.4	52.2	20	1	US-08-246-862-3	Sequence 3, Appl	C 528	9.4	52.2	25	4	US-09-407-891-12	Sequence 12, Appl
C 456	9.4	52.2	20	2	US-08-609-443B-49	Sequence 49, Appl	C 529	9.4	52.2	25	4	PCT-US95-07135-7	Sequence 7, Appl
C 457	9.4	52.2	20	2	US-08-474-450A-21	Sequence 21, Appl	C 530	9.4	52.2	25	5	PCT-US96-01643-10	Sequence 10, Appl
C 458	9.4	52.2	20	3	US-08-338-579A-75	Sequence 75, Appl	C 531	9.4	52.2	25	5	US-08-406-089A-1	Sequence 1, Appl
C 459	9.4	52.2	20	3	US-09-288-461-56	Sequence 56, Appl	C 532	9.2	51.1	14	1	US-08-406-089A-1	Sequence 1, Appl
C 460	9.4	52.2	20	3	US-08-983-466-52	Sequence 52, Appl	C 533	9.2	51.1	14	1	US-08-418-085-49	Sequence 49, Appl
C 461	9.4	52.2	20	4	US-08-461-004A-37	Sequence 37, Appl	C 534	9.2	51.1	15	2	US-09-099-011A-49	Sequence 23, Appl
C 462	9.4	52.2	20	4	US-09-110-517-35	Sequence 35, Appl	C 535	9.2	51.1	15	4	US-09-056-995-22	Sequence 22, Appl
C 463	9.4	52.2	20	4	US-09-487-136A-203	Sequence 203, App	C 536	9.2	51.1	15	4	US-09-056-995-22	Sequence 22, Appl
C 464	9.4	52.2	20	4	US-08-943-136-10	Sequence 10, Appl	C 537	9.2	51.1	15	4	US-09-753-562-14	Sequence 14, Appl
C 465	9.4	52.2	20	4	US-08-973-518-10	Sequence 10, Appl	C 538	9.2	51.1	15	4	US-09-753-562-14	Sequence 14, Appl

539	9.2	51.1	16	1	US-08-281-106-6	Sequence 6, Appl1	c 612	9.2	51.1	20	4	US-08-829-637A-118	Sequence 118, App
540	9.2	51.1	16	1	US-08-314-309A-9	Sequence 9, Appl1	c 613	9.2	51.1	20	4	US-09-702-246-66	Sequence 66, Appl
541	9.2	51.1	16	1	US-08-314-309A-9	Sequence 9, Appl1	c 614	9.2	51.1	20	4	US-09-798-096-21	Sequence 21, Appl
542	9.2	51.1	16	2	US-08-626-023-2	Sequence 2, Appl1	c 615	9.2	51.1	20	4	US-09-545-814-19	Sequence 19, Appl
543	9.2	51.1	16	2	US-08-626-023-2	Sequence 2, Appl1	c 616	9.2	51.1	20	4	US-09-689-291A-12	Sequence 12, Appl
544	9.2	51.1	16	4	US-09-142-320-2	Sequence 2, Appl1	c 617	9.2	51.1	20	4	US-09-702-327-21	Sequence 21, Appl
545	9.2	51.1	17	4	US-08-820-931-10	Sequence 10, Appl1	c 618	9.2	51.1	20	4	US-09-920-663-16	Sequence 16, Appl
546	9.2	51.1	17	4	US-08-820-931-15	Sequence 15, Appl1	c 619	9.2	51.1	20	4	US-09-661-753-33	Sequence 33, Appl
547	9.2	51.1	17	4	US-08-584-040-5329	Sequence 5329, App	c 620	9.2	51.1	20	4	US-09-907-843-50	Sequence 50, Appl
548	9.2	51.1	17	4	US-08-679-645-1251	Sequence 1251, App	c 621	9.2	51.1	20	4	US-09-517-678B-136	Sequence 136, App
549	9.2	51.1	17	4	US-08-679-645-1251	Sequence 1251, App	c 622	9.2	51.1	20	4	US-09-517-678B-221	Sequence 221, App
550	9.2	51.1	18	1	US-08-379-081B-222	Sequence 222, App	c 623	9.2	51.1	20	5	PCT-US94-07770-81	Sequence 81, Appl
551	9.2	51.1	18	1	US-08-379-078-232	Sequence 222, App	c 624	9.2	51.1	20	5	PCT-US95-11114-10	Sequence 10, Appl
552	9.2	51.1	18	1	US-08-361-479-32	Sequence 32, Appl1	c 625	9.2	51.1	21	1	US-07-969-931-22	Sequence 22, Appl
553	9.2	51.1	18	1	US-08-361-479-32	Sequence 32, Appl1	c 626	9.2	51.1	21	1	US-07-855-417A-22	Sequence 22, Appl
554	9.2	51.1	18	1	US-08-462-305-16	Sequence 32, Appl1	c 627	9.2	51.1	21	1	US-07-865-960A-39	Sequence 39, Appl
555	9.2	51.1	18	1	US-08-473-576-32	Sequence 32, Appl1	c 628	9.2	51.1	21	1	US-08-106-802-39	Sequence 39, Appl
556	9.2	51.1	18	1	US-08-473-576-32	Sequence 32, Appl1	c 629	9.2	51.1	21	2	US-08-703-136-39	Sequence 39, Appl
557	9.2	51.1	18	2	US-08-843-718-32	Sequence 32, Appl1	c 630	9.2	51.1	21	3	US-09-014-065-16	Sequence 16, Appl
558	9.2	51.1	18	2	US-08-843-718-33	Sequence 33, Appl1	c 631	9.2	51.1	21	3	US-08-732-240-13	Sequence 13, Appl
559	9.2	51.1	18	2	US-08-613-417A-16	Sequence 16, Appl1	c 632	9.2	51.1	21	3	US-08-538-666-7	Sequence 7, Appl1
560	9.2	51.1	18	2	US-08-845-161A-37	Sequence 37, Appl1	c 633	9.2	51.1	21	4	US-09-485-636-18	Sequence 18, Appl
561	9.2	51.1	18	3	US-08-594-452-16	Sequence 16, Appl1	c 634	9.2	51.1	21	4	US-09-485-636-19	Sequence 19, Appl
562	9.2	51.1	18	3	US-08-578-686C-15	Sequence 15, Appl1	c 635	9.2	51.1	21	4	US-09-386-642-27	Sequence 27, Appl
563	9.2	51.1	18	3	US-08-281-203-11	Sequence 11, Appl1	c 636	9.2	51.1	21	4	US-09-338-174A-105	Sequence 105, App
564	9.2	51.1	18	3	US-09-094-405-18	Sequence 18, Appl1	c 637	9.2	51.1	22	2	US-08-910-484-5	Sequence 5, Appl1
565	9.2	51.1	18	3	US-09-258-408-16	Sequence 16, Appl1	c 638	9.2	51.1	22	2	US-08-766-982-8	Sequence 8, Appl1
566	9.2	51.1	18	3	US-09-196-132-16	Sequence 16, Appl1	c 639	9.2	51.1	22	2	US-08-888-497-13	Sequence 13, Appl1
567	9.2	51.1	18	3	US-09-144-112-15	Sequence 15, Appl1	c 640	9.2	51.1	22	4	US-09-226-219-8	Sequence 8, Appl1
568	9.2	51.1	18	4	US-09-270-751-37	Sequence 37, Appl1	c 641	9.2	51.1	22	4	US-09-560-639-32	Sequence 32, Appl1
569	9.2	51.1	18	4	US-08-895-981-16	Sequence 16, Appl1	c 642	9.2	51.1	22	4	US-09-362-230-13	Sequence 13, Appl1
570	9.2	51.1	18	4	US-08-337-120A-18	Sequence 18, Appl1	c 643	9.2	51.1	22	5	PCT-US93-08106-6	Sequence 6, Appl1
571	9.2	51.1	18	4	US-09-325-554-1	Sequence 1, Appl1	c 644	9.2	51.1	22	5	PCT-US94-00089-8	Sequence 8, Appl1
572	9.2	51.1	18	4	US-09-325-554-3	Sequence 3, Appl1	c 645	9.2	51.1	22	5	PCT-US94-07928-13	Sequence 13, Appl1
573	9.2	51.1	18	4	US-09-387-341-211	Sequence 211, App	c 646	9.2	51.1	23	1	US-07-665-960A-14	Sequence 14, Appl
574	9.2	51.1	19	2	US-08-629-039-7	Sequence 7, Appl1	c 647	9.2	51.1	23	1	US-08-106-802-14	Sequence 14, Appl
575	9.2	51.1	19	3	US-08-594-452-73	Sequence 73, Appl1	c 648	9.2	51.1	23	1	US-08-458-477A-3	Sequence 3, Appl1
576	9.2	51.1	19	3	US-08-702-870A-4	Sequence 4, Appl1	c 649	9.2	51.1	23	2	US-09-033-153-3	Sequence 3, Appl1
577	9.2	51.1	19	3	US-09-258-408-73	Sequence 73, Appl1	c 650	9.2	51.1	23	2	US-08-703-136-14	Sequence 14, Appl
578	9.2	51.1	19	3	US-09-267-031-23	Sequence 23, Appl1	c 651	9.2	51.1	23	3	US-08-594-452-2	Sequence 2, Appl1
579	9.2	51.1	19	3	US-09-135-021-40	Sequence 40, Appl1	c 652	9.2	51.1	23	3	US-08-276-968A-28	Sequence 28, Appl
580	9.2	51.1	19	4	US-09-135-020-42	Sequence 42, Appl1	c 653	9.2	51.1	23	3	US-08-276-968A-28	Sequence 28, Appl
581	9.2	51.1	19	4	US-09-135-010A-42	Sequence 42, Appl1	c 654	9.2	51.1	23	3	US-09-258-408-74	Sequence 74, Appl
582	9.2	51.1	19	4	US-09-444-871-42	Sequence 42, Appl1	c 655	9.2	51.1	23	4	US-09-325-430B-3	Sequence 3, Appl1
583	9.2	51.1	19	4	US-09-612-964-12	Sequence 12, Appl1	c 656	9.2	51.1	24	1	US-08-102-757-6	Sequence 6, Appl1
584	9.2	51.1	19	4	US-09-597-735-42	Sequence 42, Appl1	c 657	9.2	51.1	24	1	US-08-064-271-1	Sequence 1, Appl1
585	9.2	51.1	19	4	US-09-444-295-42	Sequence 42, Appl1	c 658	9.2	51.1	24	1	US-08-180-209B-47	Sequence 47, Appl1
586	9.2	51.1	19	4	US-09-597-733-42	Sequence 42, Appl1	c 659	9.2	51.1	24	2	US-08-547-979-2	Sequence 2, Appl1
587	9.2	51.1	20	1	US-08-299-187-10	Sequence 10, Appl1	c 660	9.2	51.1	24	2	US-08-702-682-2	Sequence 2, Appl1
588	9.2	51.1	20	2	US-08-609-443B-37	Sequence 37, Appl1	c 661	9.2	51.1	24	3	US-08-594-452-75	Sequence 75, Appl1
589	9.2	51.1	20	2	US-08-609-443B-50	Sequence 50, Appl1	c 662	9.2	51.1	24	3	US-08-594-452-76	Sequence 76, Appl1
590	9.2	51.1	20	2	US-08-478-178A-118	Sequence 118, App	c 663	9.2	51.1	24	3	US-08-712-610-1	Sequence 1, Appl1
591	9.2	51.1	20	2	US-08-488-177-118	Sequence 118, App	c 664	9.2	51.1	24	3	US-08-930-569A-1	Sequence 1, Appl1
592	9.2	51.1	20	2	US-08-481-072A-118	Sequence 118, App	c 665	9.2	51.1	24	3	US-09-258-408-75	Sequence 75, Appl1
593	9.2	51.1	20	2	US-08-664-335-118	Sequence 118, App	c 666	9.2	51.1	24	3	US-09-258-408-76	Sequence 76, Appl1
594	9.2	51.1	20	2	US-08-910-443-2	Sequence 2, Appl1	c 667	9.2	51.1	24	4	US-08-474-853-47	Sequence 47, Appl1
595	9.2	51.1	20	2	US-08-910-443-10	Sequence 10, Appl1	c 668	9.2	51.1	24	4	US-09-309-423-1	Sequence 4, Appl1
596	9.2	51.1	20	2	US-08-481-066A-118	Sequence 118, App	c 669	9.2	51.1	24	4	US-09-053-831-9	Sequence 9, Appl1
597	9.2	51.1	20	3	US-08-578-615A-81	Sequence 81, Appl1	c 670	9.2	51.1	24	4	US-09-053-831-9	Sequence 9, Appl1
598	9.2	51.1	20	3	US-09-366-257-8	Sequence 8, Appl1	c 671	9.2	51.1	24	4	US-09-599-781-1	Sequence 1, Appl1
599	9.2	51.1	20	3	US-09-287-796-112	Sequence 112, App	c 672	9.2	51.1	24	4	US-09-166-205B-47	Sequence 47, Appl1
600	9.2	51.1	20	3	US-09-388-461-21	Sequence 21, Appl1	c 673	9.2	51.1	24	4	US-09-600-031-9	Sequence 9, Appl1
601	9.2	51.1	20	4	US-09-435-296-58	Sequence 58, Appl1	c 674	9.2	51.1	24	5	PCT-US94-02629-47	Sequence 47, Appl1
602	9.2	51.1	20	4	US-09-290-640-70	Sequence 70, Appl1	c 675	9.2	51.1	25	1	US-08-137-954-51	Sequence 51, Appl1
603	9.2	51.1	20	4	US-09-226-012-50	Sequence 50, Appl1	c 676	9.2	51.1	25	1	US-08-050-073-59	Sequence 59, Appl1
604	9.2	51.1	20	4	US-09-277-020-62	Sequence 62, Appl1	c 677	9.2	51.1	25	1	US-08-336-132-47	Sequence 27, Appl1
605	9.2	51.1	20	4	US-09-277-020-65	Sequence 65, Appl1	c 678	9.2	51.1	25	1	US-08-421-356-18	Sequence 18, Appl1
606	9.2	51.1	20	4	US-09-130-616-112	Sequence 112, App	c 679	9.2	51.1	25	1	US-08-811-492-128	Sequence 128, App
607	9.2	51.1	20	4	US-09-171-878-22	Sequence 22, Appl1	c 680	9.2	51.1	25	2	US-08-807-332B-17	Sequence 17, Appl1
608	9.2	51.1	20	4	US-09-593-711A-103	Sequence 103, App	c 681	9.2	51.1	25	2	US-08-743-637B-93	Sequence 93, Appl1
609	9.2	51.1	20	4	US-09-484-617-120	Sequence 120, App	c 682	9.2	51.1	25	3	US-08-526-840B-93	Sequence 93, Appl1
610	9.2	51.1	20	4	US-08-851-896-37	Sequence 37, Appl1	c 683	9.2	51.1	25	3	US-08-750-145A-15	Sequence 15, Appl1
611	9.2	51.1	20	4	US-08-851-896-50	Sequence 50, Appl1	c 684	9.2	51.1	25	3	US-08-975-698A-19	Sequence 19, Appl1

C 685	9.2	51.1	25	4	US-08-338-876-17	Sequence 17, Appl	C 758	9	50.0	20	4	US-09-364-416-34	Sequence 34, Appl
C 686	9.2	51.1	25	4	US-08-914-421-12	Sequence 12, Appl	C 759	9	50.0	20	4	US-09-657-042A-45	Sequence 45, Appl
C 687	9.2	51.1	25	4	US-09-917-090-19	Sequence 19, Appl	C 760	9	50.0	20	4	US-09-716-161A-86	Sequence 86, Appl
C 688	9.2	51.1	25	4	US-09-102-528-1	Sequence 1, Appl1	C 761	9	50.0	20	4	US-09-629-642A-98	Sequence 98, Appl
C 689	9.2	51.1	25	4	US-08-683-409-12	Sequence 12, Appl	C 762	9	50.0	20	4	US-09-396-642A-3	Sequence 3, Appl1
C 690	9.2	51.1	25	4	US-09-446-402A-6	Sequence 6, Appl1	C 763	9	50.0	20	4	US-09-472-367-3	Sequence 3, Appl1
C 691	9.2	51.1	25	4	US-09-446-402A-13	Sequence 13, Appl	C 764	9	50.0	20	4	US-09-659-791A-57	Sequence 57, Appl1
C 692	9.2	51.1	25	4	US-09-592-891A-10	Sequence 10, Appl	C 765	9	50.0	20	4	US-09-661-751-55	Sequence 55, Appl
C 693	9.2	51.1	25	4	US-08-579-645-1250	Sequence 1250, Ap	C 766	9	50.0	20	4	US-09-780-175-66	Sequence 66, Appl
C 694	9.2	51.1	25	4	US-09-727-578-19	Sequence 19, Appl	C 767	9	50.0	20	4	US-09-658-679A-25	Sequence 25, Appl
C 695	9.2	51.1	25	4	US-09-212-247C-21	Sequence 21, Appl	C 768	9	50.0	20	4	US-09-517-467B-240	Sequence 240, Appl
C 696	9.2	51.1	25	4	US-09-457-066-31	Sequence 31, Appl	C 769	9	50.0	20	4	US-09-844-525A-74	Sequence 74, Appl
C 697	9.2	51.1	25	4	US-09-046-783-18	Sequence 18, Appl	C 770	9	50.0	20	6	5210025-17	Patent No. 5210025
C 698	9	50.0	15	4	US-08-482-918-91	Sequence 91, Appl	C 771	9	50.0	21	1	US-08-105-483-224	Sequence 224, App
C 699	9	50.0	15	4	US-08-482-918-92	Sequence 92, Appl	C 772	9	50.0	21	1	US-08-434-201-3	Sequence 3, Appl1
C 700	9	50.0	15	4	US-09-224-681-91	Sequence 91, Appl	C 773	9	50.0	21	1	US-08-709-203-224	Sequence 224, App
C 701	9	50.0	15	4	US-09-224-681-92	Sequence 92, Appl	C 774	9	50.0	21	1	US-08-433-583-3	Sequence 3, Appl1
C 702	9	50.0	15	4	US-08-336-728A-91	Sequence 91, Appl	C 775	9	50.0	21	1	US-08-358-171-13	Sequence 13, Appl
C 703	9	50.0	15	4	US-08-336-728A-92	Sequence 92, Appl	C 776	9	50.0	21	1	US-08-458-101-224	Sequence 224, App
C 704	9	50.0	17	1	US-08-064-400B-6	Sequence 6, Appl1	C 777	9	50.0	21	1	US-08-434-423-3	Sequence 3, Appl1
C 705	9	50.0	17	1	US-08-064-400B-7	Sequence 7, Appl1	C 778	9	50.0	21	1	US-08-399-988B-20	Sequence 20, Appl
C 706	9	50.0	17	1	US-08-458-067-39	Sequence 39, Appl	C 779	9	50.0	21	1	US-08-493-754A-20	Sequence 20, Appl
C 707	9	50.0	17	4	US-08-981-256A-14	Sequence 14, Appl	C 780	9	50.0	21	2	US-08-437-667-3	Sequence 3, Appl1
C 708	9	50.0	17	4	US-08-584-040-1463	Sequence 1463, Ap	C 781	9	50.0	21	2	US-08-798-738-11	Sequence 11, Appl
C 709	9	50.0	17	4	US-08-584-040-7436	Sequence 7436, Ap	C 782	9	50.0	21	3	US-09-090-947-13	Sequence 13, Appl
C 710	9	50.0	17	5	PCT-US94-05617-7	Sequence 7, Appl1	C 783	9	50.0	21	3	US-08-906-955-3	Sequence 3, Appl1
C 711	9	50.0	17	5	PCT-US94-05617-8	Sequence 8, Appl1	C 784	9	50.0	21	4	US-08-943-731-506	Sequence 506, App
C 712	9	50.0	17	5	PCT-US96-07795-39	Sequence 39, Appl	C 785	9	50.0	21	4	US-09-245-041-89	Sequence 89, Appl
C 713	9	50.0	17	5	PCT-US96-07796-39	Sequence 39, Appl	C 786	9	50.0	21	4	US-09-522-21-16	Sequence 16, Appl
C 714	9	50.0	18	1	US-08-256-720-2	Sequence 2, Appl1	C 787	9	50.0	21	4	US-09-468-826-5	Sequence 5, Appl1
C 715	9	50.0	18	1	US-08-175-155-13	Sequence 13, Appl	C 788	9	50.0	21	5	PCT-US96-06060-3	Sequence 3, Appl1
C 716	9	50.0	18	1	US-08-477-509B-47	Sequence 47, Appl	C 789	9	50.0	22	1	US-08-285-440-30	Sequence 30, Appl
C 717	9	50.0	18	2	US-08-707-237A-19	Sequence 19, Appl	C 790	9	50.0	22	1	US-08-630-340-30	Sequence 30, Appl
C 718	9	50.0	18	2	US-08-633-289-2	Sequence 2, Appl1	C 791	9	50.0	22	2	US-08-569-150A-5	Sequence 5, Appl1
C 719	9	50.0	18	3	US-08-482-085B-47	Sequence 47, Appl	C 792	9	50.0	22	2	US-08-951-718-12	Sequence 12, Appl
C 720	9	50.0	18	3	US-09-150-805-3	Sequence 3, Appl1	C 793	9	50.0	22	3	US-08-480-640A-129	Sequence 129, App
C 721	9	50.0	18	3	US-09-150-805-13	Sequence 13, Appl	C 794	9	50.0	22	3	US-08-491-954-63	Sequence 63, Appl
C 722	9	50.0	18	4	US-09-034-205-57	Sequence 57, Appl	C 795	9	50.0	22	3	US-09-010-641-5	Sequence 5, Appl1
C 723	9	50.0	18	4	US-08-986-069A-3	Sequence 3, Appl1	C 796	9	50.0	22	3	US-08-295-801-5	Sequence 129, App
C 724	9	50.0	18	4	US-08-996-069A-13	Sequence 13, Appl	C 797	9	50.0	22	4	US-09-356-281-5	Sequence 5, Appl1
C 725	9	50.0	18	4	US-09-677-218B-57	Sequence 57, Appl	C 798	9	50.0	22	4	US-08-686-968C-78	Sequence 78, Appl
C 726	9	50.0	18	4	US-09-444-791A-47	Sequence 47, Appl	C 799	9	50.0	22	4	US-09-041-886-66	Sequence 66, Appl
C 727	9	50.0	18	4	US-09-677-192-57	Sequence 57, Appl	C 800	9	50.0	22	4	US-08-488-237A-129	Sequence 129, App
C 728	9	50.0	18	4	US-09-593-012-200	Sequence 200, App	C 801	9	50.0	22	4	US-08-943-731-435	Sequence 435, App
C 729	9	50.0	18	6	5166318-19	Patent No. 5166318	C 802	9	50.0	22	4	US-09-099-749-5	Sequence 5, Appl1
C 730	9	50.0	19	3	US-08-846-020A-40	Sequence 40, Appl	C 803	9	50.0	22	4	US-09-090-535-15	Sequence 15, Appl
C 731	9	50.0	19	4	US-09-438-016-26	Sequence 26, Appl	C 804	9	50.0	22	4	US-08-375-992A-129	Sequence 129, App
C 732	9	50.0	19	4	US-09-617-871-40	Sequence 40, Appl	C 805	9	50.0	23	1	US-08-776-088-22	Sequence 22, Appl
C 733	9	50.0	20	1	US-07-952-817-2	Sequence 2, Appl1	C 806	9	50.0	23	1	US-08-776-088-22	Sequence 22, Appl
C 734	9	50.0	20	1	US-07-906-393-2	Sequence 2, Appl1	C 807	9	50.0	23	3	US-08-943-336A-6	Sequence 6, Appl1
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ALIGNMENTS

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; Patent No. 6387652
; GENERAL INFORMATION:
; APPLICANT: HAUGLAND, Richard
; APPLICANT: VESPER, Stephen
; TITLE OF INVENTION: METHOD OF IDENTIFYING AND QUANTIFYING SPECIFIC FUNGI AND BACTERIA
; FILE REFERENCE: HAUGLAND-1A
; CURRENT APPLICATION NUMBER: US/09/593,012
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US 09/290,990
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 60/081,773
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 188
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; TYPE: DNA
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US-09-593-012-188
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; Patent No. 6291190
; GENERAL INFORMATION:
; APPLICANT: Marcel Behr
; APPLICANT: Peter Small
; APPLICANT: Gary Schoonik
; APPLICANT: Michael Wilson
; TITLE OF INVENTION: Molecular differences between species of
; FILE REFERENCE: SUN-102P
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; CURRENT APPLICATION NUMBER: US/09/318,191A
; CURRENT FILING DATE: 1999-05-25
; EARLIER APPLICATION NUMBER: 60/097,936
; EARLIER FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 34
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; Sequence 106, Application US/09593012
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; GENERAL INFORMATION:
; APPLICANT: HAUGLAND, Richard
; APPLICANT: VESPER, Stephen
; TITLE OF INVENTION: METHOD OF IDENTIFYING AND QUANTIFYING SPECIFIC FUNGI AND BACTERIA
; FILE REFERENCE: HAUGLAND-1A
; CURRENT APPLICATION NUMBER: US/09/593,012
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US 09/290,990
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; Patent No. 5681725
; GENERAL INFORMATION:
; APPLICANT: Jensen, Ejner Bech
; TITLE OF INVENTION: A PROCESS FOR PRODUCING HEME PROTEINS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5681725 No. 5681725disk of No. 5681725th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
```

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,566A
FILING DATE: 09-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 3679,204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-284-566A-2

Query Match 68.9%; Score 12.4; DB 1; Length 22;
Best Local Similarity 92.9%; Pred. No. 2.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTGCGCCCGGATCC 14
Db 16 CTGCGCCCGGATCC 3

RESULT 5
US-09-118-408-28/c
Sequence 28, Application US/09118408A
Patent No. 6265544
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: ADIPOCTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-30
CURRENT APPLICATION NUMBER: US/09/118,408A
CURRENT FILING DATE: 1998-07-17
EARLIER APPLICATION NUMBER: 60/053,154
EARLIER FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 28
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide ZC15035
US-09-118-408-28

Query Match 67.8%; Score 12.2; DB 4; Length 24;
Best Local Similarity 82.4%; Pred. No. 3.1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTGCGCCCGGATCCAGG 17
Db 20 CCGAGCCCGGATCCATG 4

RESULT 6
US-09-506-855-28/c
Sequence 28, Application US/09506855
Patent No. 6448221
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Laeser, Gerald W.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND

TITLE OF INVENTION: IMMUNE FUNCTION
FILE REFERENCE: 99-12
CURRENT APPLICATION NUMBER: US/09/506,855
CURRENT FILING DATE: 2000-02-17
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 28
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide ZC15035
US-09-506-855-28

Query Match 67.8%; Score 12.2; DB 4; Length 24;
Best Local Similarity 82.4%; Pred. No. 3.1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTGCGCCCGGATCCAGG 17
Db 20 CCGAGCCCGGATCCATG 4

RESULT 7
US-08-840-316-88/c
Sequence 88, Application US/08840316
Patent No. 6054567
GENERAL INFORMATION:
APPLICANT: Emerson, Suzanne U., Purcell, Robert H.,
APPLICANT: Tsarev, Sergei, A., and Robinson, Robin A.
TITLE OF INVENTION: Recombinant Proteins Of
TITLE OF INVENTION: A Pakistani Strain Of Hepatitis B And Their
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/840,316
FILING DATE: 11-APR-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
CLASSIFICATION: 424
NAME: Richard W. Bork
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4255
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-840-316-88

Query Match 66.7%; Score 12; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCGATCCAGGC 18
| | | | |
Db 20 CCGATCCAGGC 9

RESULT 8
US-08-809-523-88/c
; Sequence 88, Application US/08809523
; Patent No. 6207416
; GENERAL INFORMATION:
; APPLICANT: Tearev, Sergei. A., Emerson,
; APPLICANT: Suzanne U., Purcell, Robert H.
; TITLE OF INVENTION: Recombinant Proteins Of
; TITLE OF INVENTION: A Pakistani Strain Of Hepatitis B And Their
; TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,523
; FILING DATE: 28-MAY-1997
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/11102
; FILING DATE: 03-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US08/316,765
; FILING DATE: 03-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/947,263
; FILING DATE: 18-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard W. Bork
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4032US4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-809-523-88

Query Match 66.7%; Score 12; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCGATCCAGGC 18
| | | | |
Db 20 CCGATCCAGGC 9

RESULT 9
US-08-471-971-88/c
; Sequence 88, Application US/08471971
; Patent No. 6287759
; GENERAL INFORMATION:
; APPLICANT: Tearev, Sergei. A., Emerson,
; APPLICANT: Suzanne U., Purcell, Robert H.
; TITLE OF INVENTION: Recombinant Proteins Of
; TITLE OF INVENTION: A Pakistani Strain Of Hepatitis B And Their

; TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,971
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US08/316,765
; FILING DATE: 03-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US07/947,263
; FILING DATE: 18-SEP-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard W. Bork
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4032US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-471-971-88

Query Match 66.7%; Score 12; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCGATCCAGGC 18
| | | | |
Db 20 CCGATCCAGGC 9

RESULT 10
US-09-402-776-88/c
; Sequence 88, Application US/09402776
; Patent No. 6458562
; GENERAL INFORMATION:
; APPLICANT: Emerson, Suzanne U., Purcell, Robert H.,
; APPLICANT: Tearev, Sergei. A., and Robinson, Robin A.
; TITLE OF INVENTION: Recombinant Proteins Of
; TITLE OF INVENTION: A Pakistani Strain Of Hepatitis B And Their
; TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/402,776
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/840,316
;; FILING DATE: 11-APR-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Richard W. Bork
;; REGISTRATION NUMBER: 36,459
;; REFERENCE/DOCKET NUMBER: 2026-4255
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 758-4800
;; TELEFAX: (212) 751-6849
;; INFORMATION FOR SEQ ID NO: 88:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 25 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-09-402-776-88

Query Match 66.7%; Score 12; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCGGATCCAGGC 18
|||||
DB 20 CCGGATCCAGGC 9

RESULT 11
PCT-US93-08849A-88/C
Sequence 88, Application PC/TUS9308849A
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Recombinant Proteins Of
TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & PINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08849A
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US07/947,263
FILING DATE: 18-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: William S. Feller
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4032 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US93-08849A-88

Query Match 66.7%; Score 12; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCGGATCCAGGC 18
|||||
DB 20 CCGGATCCAGGC 9

RESULT 12
PCT-US93-08849-88/C
Sequence 88, Application PC/TUS9308849
GENERAL INFORMATION:
APPLICANT: Tsarev, Sergei A., Emerson,
APPLICANT: Suzanne U., Purcell, Robert H.
TITLE OF INVENTION: Recombinant Proteins Of
TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & PINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08849
FILING DATE: 17-SEP-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/947,263
FILING DATE: 18-SEP-1992
NAME:
ATTORNEY/AGENT INFORMATION:
NAME: Bork, Richard, W.
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US93-08849-88

Query Match 66.7%; Score 12; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCGGATCCAGGC 18
|||||
DB 20 CCGGATCCAGGC 9

RESULT 13
US-08-474-140-3/C
Sequence 3, Application US/08474140
Patent No. 5721127
GENERAL INFORMATION:
APPLICANT: DEMEER, PHILIPPE
APPLICANT: AMORY, ANTOINE
TITLE OF INVENTION: PULULANASE, MICROORGANISMS WHICH
TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREPARATION OF THIS
TITLE OF INVENTION: PULULANASE AND THE USES THEREOF

NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.
STREET: 2000 K Street, N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,140
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: William F. Gaddano, Esq.
REGISTRATION NUMBER: 37,136
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acid (other);
DESCRIPTION: synthetic DNA
US-08-474-140-3
Query Match 65.6%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 CTGCGCCCGGATCCA 15
Db 16 CTGCGCCGAGAGCA 2
RESULT 14
US-08-477-630-3/c
Sequence 3, Application US/08477630
Patent No. 5721128
GENERAL INFORMATION:
APPLICANT: DEMER, PHILIPPE
APPLICANT: AMORY, ANTOINE
TITLE OF INVENTION: PULULANASE, MICROORGANISMS WHICH
PRODUCE IT, PROCESSES FOR THE PREPARATION OF THIS
TITLE OF INVENTION: PULULANASE AND THE USES THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.
STREET: 2000 K Street, N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,630
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: William F. Gaddano, Esq.

REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-42
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acid (other);
DESCRIPTION: synthetic DNA
US-08-477-630-3
Query Match 65.6%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 CTGCGCCCGGATCCA 15
Db 16 CTGCGCCGAGAGCA 2
RESULT 15
US-08-472-293-3/c
Sequence 3, Application US/08472293
Patent No. 5731174
GENERAL INFORMATION:
APPLICANT: DEMER, PHILIPPE
APPLICANT: AMORY, ANTOINE
TITLE OF INVENTION: PULULANASE, MICROORGANISMS WHICH
PRODUCE IT, PROCESSES FOR THE PREPARATION OF THIS
TITLE OF INVENTION: PULULANASE AND THE USES THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.
STREET: 2000 K Street, N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,293
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: William F. Gaddano, Esq.
REGISTRATION NUMBER: 37,136
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acid (other);
DESCRIPTION: synthetic DNA
US-08-472-293-3
Query Match 65.6%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CTGCGCCCGGATCCA 15
DB 16 CTGCGCCGAGAGCCA 2

RESULT 16

US-08-474-545-3/C
Sequence 3, Application US/08474545
Patent No. 5736375
GENERAL INFORMATION:
APPLICANT: DEMEER, PHILIPPE
APPLICANT: AMORY, ANTOINE
TITLE OF INVENTION: PULULANASE, MICROORGANISMS WHICH
PRODUCE IT, PROCESSES FOR THE PREPARATION OF THIS
TITLE OF INVENTION: PULULANASE AND THE USES THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.
STREET: 2000 K Street, N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,545
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wilhem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-43
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ. ID NO. 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acid (other);
DESCRIPTION: synthetic DNA

Query Match 65.6%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CTGCGCCCGGATCCA 15
DB 16 CTGCGCCGAGAGCCA 2

RESULT 17
US-08-478-341-3/C
Sequence 3, Application US/08478341
Patent No. 5817498
GENERAL INFORMATION:
APPLICANT: DEMEER, PHILIPPE
APPLICANT: AMORY, ANTOINE
TITLE OF INVENTION: PULULANASE, MICROORGANISMS WHICH
PRODUCE IT, PROCESSES FOR THE PREPARATION OF THIS
TITLE OF INVENTION: PULULANASE AND THE USES THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.

STREET: 2000 K Street, N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,341
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wilhem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-45
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ. ID NO. 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acid (other);
DESCRIPTION: synthetic DNA

Query Match 65.6%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CTGCGCCCGGATCCA 15
DB 16 CTGCGCCGAGAGCCA 2

RESULT 18
US-08-996-733-3/C
Sequence 3, Application US/08996733
Patent No. 6074854
GENERAL INFORMATION:
APPLICANT: DEMEER, PHILIPPE
APPLICANT: AMORY, ANTOINE
TITLE OF INVENTION: PULULANASE, MICROORGANISMS WHICH
PRODUCE IT, PROCESSES FOR THE PREPARATION OF THIS
TITLE OF INVENTION: PULULANASE AND THE USES THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genecor International, Inc.
STREET: 925 Page Mill Road
CITY: Palo Alto,
STATE: CA
COUNTRY: U.S.A.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,733
FILING DATE: 23-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,293
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/174,893
FILING DATE: 28-DEC-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: BE 09301278
FILING DATE: 19-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BE 09300744
FILING DATE: 15-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BE 09201156
FILING DATE: 28-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Debra J. Gaiaster, Esq.
REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: GC446C1-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 846-7620
TELEFAX: (650) 845-6504
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acid (other);
DESCRIPTION: synthetic DNA
US-08-996-733-3

Query Match 65.6%; Score 11.8; DB 3; Length 18;
Best Local Similarity 86.7%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CTGCGCCCGGATCCA 15
Db 16 CTGCGCCGAGAGCCA 2.

RESULT 19
US-08-275-526C-17/c
Sequence 17, Application US/08275526C
Patent No. 6180382
GENERAL INFORMATION:
APPLICANT: DE BUYL, ERIC
APPLICANT: LAHAYE, ANDR E
APPLICANT: LEDOUX, PIERRE
APPLICANT: AMORY, ANTOINE
APPLICANT: DETROZ, REN
APPLICANT: ANDRE, CHRISTOPHE
APPLICANT: VETTER, ROMAN
TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
TITLE OF INVENTION: EXPRESSION VECTORS FOR SUCH XYLANASE AND
TITLE OF INVENTION: OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
TITLE OF INVENTION: USE THEREOF
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE, P.C.
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/275,526C
FILING DATE: 15-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gagliano, Wilhem F.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-49
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 429-0625
TELEFAX: (202) 293-0625
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acid (synthetic oligonucleotide)
US-08-275-526C-17

Query Match 65.6%; Score 11.8; DB 4; Length 18;
Best Local Similarity 86.7%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CTGCGCCCGGATCCA 15
Db 16 CTGCGCCGAGAGCCA 2

RESULT 20
US-09-076-677-17/c
Sequence 17, Application US/09076677
Patent No. 6423523
GENERAL INFORMATION:
APPLICANT: DE BUYL, ERIC
APPLICANT: LAHAYE, ANDR E
APPLICANT: LEDOUX, PIERRE
APPLICANT: AMORY, ANTOINE
APPLICANT: DETROZ, REN E
APPLICANT: ANDRE, CHRISTOPHE
APPLICANT: VETTER, ROMAN
TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
TITLE OF INVENTION: EXPRESSION VECTORS FOR SUCH XYLANASE AND
TITLE OF INVENTION: OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
TITLE OF INVENTION: USE THEREOF
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE, P.C.
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/076,677
FILING DATE: 12-May-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/275,526
FILING DATE: 15-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Gagliano, Wilhem F.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
TELEFAX: (202) 293-0625
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acid (synthetic oligonucleotide)
SEQUENCE DESCRIPTION: SEQ ID NO: 17;

US-09-076-677-17

Query Match 65.6%; Score 11.8; DB 4; Length 18;
Best Local Similarity 86.7%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGGCCCGGATCCA 15
DB 16 CTGGCCGAGAGCCA 2

RESULT 21

US-09-073-055-17/c

Sequence 17, Application US/09073055
Patent No. 6426211

GENERAL INFORMATION:

APPLICANT: DE BUYL, ERIC

LAHAYE, ANDR E

LEDOUX, PIERRE

AMORY, ANTOINE

DETROZ, REN

ANDRE, CHRISTOPHE

VETTER, ROMAN

TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
EXPRESSION VECTORS FOR SUCH XYLANASE AND
OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
USE THEREOF

NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/073,055

FILING DATE: 05-May-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/275,526

FILING DATE: 15-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: Gagliano, William F.

REGISTRATION NUMBER: 37,136

REFERENCE/DOCKET NUMBER: 4121-49

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 429-0625

TELEFAX: (202) 293-0625

TELEX: 650 383 5605

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: nucleic acid (synthetic oligonucleotide)

SEQUENCE DESCRIPTION: SEQ ID NO: 17:

US-09-073-055-17

Query Match 65.6%; Score 11.8; DB 4; Length 18;
Best Local Similarity 86.7%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGGCCCGGATCCA 15
DB 16 CTGGCCGAGAGCCA 2

RESULT 22

US-08-425-299A-13

Sequence 13, Application US/08425299A
Patent No. 5726025

GENERAL INFORMATION:

APPLICANT: Kirschner, Marc W.

APPLICANT: King, Randall W.

TITLE OF INVENTION: Assay and Reagents for Detecting Inhibitors
of Ubiquitin-Dependent Degradation of
Cell Cycle Regulatory Proteins

TITLE OF INVENTION: Cell Cycle Regulatory Proteins

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII(text)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/425,299A

FILING DATE: 20-APR-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Vincent, Matthew P.

REGISTRATION NUMBER: 36,709

REFERENCE/DOCKET NUMBER: HMI-014

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 24 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-08-425-299A-13

Query Match 65.6%; Score 11.8; DB 1; Length 24;
Best Local Similarity 86.7%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGGCCCGATCCAG 17
DB 1 GGGCCCGATCCAG 15

RESULT 23

US-08-480-173A-25/c

Sequence 25, Application US/08480173A
Patent No. 6072049

GENERAL INFORMATION:

APPLICANT: Thoma, Hans A

TITLE OF INVENTION: HEPATITIS B SURFACE ANTIGEN VACCINE

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSEE: Popovich & Willes, P.A.

STREET: 80 S. 8th Street, Suite 1902

CITY: Minneapolis

STATE: MN

COUNTRY: USA

ZIP: 55402

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,173A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Popovich, Thomas E
REGISTRATION NUMBER: 30,099
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-334-8994
TELEFAX: 612-334-8994
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..4
OTHER INFORMATION: /note= "Nucleotides 1-4 form a
OTHER INFORMATION: single-stranded "sticky end"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 5..24
OTHER INFORMATION: /note= "Adapter sequence results
OTHER INFORMATION: from oligonucleotide duplex formation with nucleotides 5-24 c
OTHER INFORMATION: SEQ ID NO: 26"
US-08-480-173A-25

Query Match 65.6%; Score 11.8; DB 3; Length 24;
Best Local Similarity 86.7%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGCGCCGCGATCCAG 16
Db 24 TGAGCTCGATCCAG 10

RESULT 24
US-08-480-173A-26
Sequence 26, Application US/08480173A
Patent No. 6072049
GENERAL INFORMATION:
APPLICANT: Thoma, Hans A.
TITLE OF INVENTION: HEPATITIS B SURFACE ANTIGEN VACCINE
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Popovich & Wiles, P.A.
STREET: 80 S. 8th Street, Suite 1902
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,173A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Popovich, Thomas E
REGISTRATION NUMBER: 30,099
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-334-8994
TELEFAX: 612-334-8994
INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..4
OTHER INFORMATION: /note= "Nucleotides 1-4 form a
OTHER INFORMATION: single-stranded "sticky end"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 5..24
OTHER INFORMATION: /note= "Adapter sequence results
OTHER INFORMATION: from oligonucleotide duplex formation with nucleotides 5-24
OTHER INFORMATION: SEQ ID NO: 25"
US-08-480-173A-26

Query Match 65.6%; Score 11.8; DB 3; Length 24;
Best Local Similarity 86.7%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGCGCCGCGATCCAG 16
Db 5 TGAGCTCGATCCAG 19

RESULT 25
US-08-484-408A-25/c
Sequence 25, Application US/08484408A
Patent No. 6117653
GENERAL INFORMATION:
APPLICANT: Thoma, Hans A.
TITLE OF INVENTION: HEPATITIS B SURFACE ANTIGEN VACCINE
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Popovich & Wiles, P.A.
STREET: 80 S. 8th Street, Suite 1902
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,408A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Popovich, Thomas E
REGISTRATION NUMBER: 30,099
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-334-8994
TELEFAX: 612-334-8994
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..4
OTHER INFORMATION: /note= "Nucleotides 1-4 form a
OTHER INFORMATION: single-stranded "sticky end"
FEATURE:
NAME/KEY: misc_feature

LOCATION: 5..24 /note="Adapter sequence results
OTHER INFORMATION: from oligonucleotide duplex formation with nucleotides 5-24 c
OTHER INFORMATION: SEQ ID NO: 26"
US-08-484-408A-25

Query Match 65.6%; Score 11.8; DB 3; Length 24;
Best Local Similarity 86.7%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGCCCGGATCCAG 16
DB 24 TGAGCTCGATCCAG 10

RESULT 26
US-08-484-408A-26
Sequence 26, Application US/08484408A
Patent No. 6117653
GENERAL INFORMATION:
APPLICANT: Thoma, Hans A
TITLE OF INVENTION: HEPATITIS B SURFACE ANTIGEN VACCINE
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Popovich & Miles, P.A.
STREET: 80 S. 8th Street, Suite 1902
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,408A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Popovich, Thomas E
REGISTRATION/DOCKET NUMBER: 30,099
REFERENCE/DOCKET NUMBER: MED1003USD4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-334-8991
TELEFAX: 612-334-8994
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
FEATURES:
NAME/KEY: misc feature
LOCATION: 1..4
OTHER INFORMATION: /note="Nucleotides 1-4 form a
OTHER INFORMATION: single-stranded "sticky end"
FEATURE:
NAME/KEY: misc feature
LOCATION: 5..24
OTHER INFORMATION: /note="Adapter sequence results
OTHER INFORMATION: from oligonucleotide duplex formation with nucleotides 5-24 c
OTHER INFORMATION: SEQ ID NO: 25"
US-08-484-408A-26

Query Match 65.6%; Score 11.8; DB 3; Length 24;
Best Local Similarity 86.7%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGCCCGGATCCAG 16
DB 5 TGAGCTCGATCCAG 19

RESULT 27
US-08-318-837-43/c
Sequence 43, Application US/08318837
Patent No. 5981277
GENERAL INFORMATION:
APPLICANT: FRANKEN, LUCIA; DEVOS, KATHLEEN; VAN DE VOORDE,
APPLICANT: ANDRE; VAN HEUVERSWYN, HUGO
TITLE OF INVENTION: NEW POLYPEPTIDES AND PEPTIDES, NUCLEIC ACID
TITLE OF INVENTION: CODING FOR THEM, AND THEIR USE IN THE FIELD OF TUMOR THERAPY O
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN AND MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,837
FILING DATE: 13-OCT-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP 93/01022
FILING DATE: 28-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 92,401,231.3
FILING DATE: 30-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION/DOCKET NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410,007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Human
CELL LINE: THP-1
US-08-318-837-43

Query Match 65.6%; Score 11.8; DB 2; Length 25;
Best Local Similarity 86.7%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CGCCCGATCCAGGC 18
DB 17 CGCCCTGCTCCAGGC 3

RESULT 28
US-08-602-036A-23/c
Sequence 23, Application US/08602036A
Patent No. 5789248
GENERAL INFORMATION:
APPLICANT: Oeystein, Fodestad
APPLICANT: Hovig, Bivind
APPLICANT: Engebretsen, Olav
APPLICANT: Maelandemo, Gunhild H.

APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND
METHODS OF INHIBITING METASTATIC CANCER
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,036A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HY2-039CIP
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-602-036A-23

Query Match 64.4%; Score 11.6; DB 1; Length 21;
Best Local Similarity 77.8%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 CTGCGCCGCGATCCAGGC 18
Db 18 CTGCTCCAGATCTGAC 1

RESULT 29
US-08-642-407A-23/c
Sequence 23, Application US/08642407A
Patent No. 5677308
GENERAL INFORMATION:
APPLICANT: Oeystein, Fodestad
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,036A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HY2-039CIP
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA

APPLICATION NUMBER: US/08/642,407A
FILING DATE: 03-May-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HY2-039CPDV
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-642-407A-23

Query Match 64.4%; Score 11.6; DB 2; Length 21;
Best Local Similarity 77.8%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 CTGCGCCGCGATCCAGGC 18
Db 18 CTGCTCCAGATCTGAC 1

RESULT 30
US-08-602-036A-3/c
Sequence 3, Application US/08602036A
Patent No. 5789248
GENERAL INFORMATION:
APPLICANT: Oeystein, Fodestad
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,036A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HY2-039CIP
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA

HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-602-036A-3

Query Match 64.4%; Score 11.6; DB 1; Length 22;
Best Local Similarity 77.8%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGGCGCCGATCCAGGC 18
DB 18 CTGCTCCAGATCTGAC 1

RESULT 31
US-08-602-036A-4/C

Sequence 4, Application US/08602036A
Patent No. 5789248
GENERAL INFORMATION:
APPLICANT: Oeystein, Podstad
APPLICANT: Hovig, Elvind
APPLICANT: Engebraaten, Olav
APPLICANT: Maelandmo, Gunhild H.
TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND
METHODS OF INHIBITING METASTATIC CANCER
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,036A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HY2-039CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-602-036A-4

Query Match 64.4%; Score 11.6; DB 1; Length 22;
Best Local Similarity 77.8%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGGCGCCGATCCAGGC 18
DB 18 CTGCTCCAGATCTGAC 1

RESULT 32
US-08-502-374A-3/C
Sequence 3, Application US/08502374A
Patent No. 5872007

GENERAL INFORMATION:
APPLICANT: Podstad, Oeystein
APPLICANT: Hovig, Elvind
APPLICANT: Engebraaten, Olav
APPLICANT: Maelandmo, Gunhild H.
TITLE OF INVENTION: CAPL-SPECIFIC OLIGONUCLEOTIDES AND
METHODS OF INHIBITING METASTATIC CANCER
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/502,374A
FILING DATE: 14-Jul-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HY2-039DV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-526-6000
TELEFAX: 617-526-5000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-502-374A-3

Query Match 64.4%; Score 11.6; DB 2; Length 22;
Best Local Similarity 77.8%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGGCGCCGATCCAGGC 18
DB 18 CTGCTCCAGATCTGAC 1

RESULT 33
US-08-502-374A-4/C

Sequence 4, Application US/08502374A
Patent No. 5872007
GENERAL INFORMATION:
APPLICANT: Podstad, Oeystein
APPLICANT: Hovig, Elvind
APPLICANT: Engebraaten, Olav
APPLICANT: Maelandmo, Gunhild H.
TITLE OF INVENTION: CAPL-SPECIFIC OLIGONUCLEOTIDES AND
METHODS OF INHIBITING METASTATIC CANCER
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/502,374A
CLASSIFICATION: 514
FILING DATE: 14-Jul-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-039DV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-526-6000
TELEFAX: 617-526-5000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-502-374A-4

Query Match 64.4%; Score 11.6; DB 2; Length 22;
Best Local Similarity 77.8%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGCGCCCGATCCAGC 18
DB 18 CTGCTCCAGATCTGAC 1

RESULT 34
US-08-642-407A-3/C
Sequence 3, Application US/08642407A
Patent No. 5877308
GENERAL INFORMATION:
APPLICANT: Oeystein, Fodstad
APPLICANT: Hovig, Elvind
APPLICANT: Engebraaten, Olav
APPLICANT: Maelandemo, Gunhild H.
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND
METHODS OF INHIBITING METASTATIC CANCER
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,407A
FILING DATE: 03-May-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-039CPDV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-642-407A-3

Query Match 64.4%; Score 11.6; DB 2; Length 22;
Best Local Similarity 77.8%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGCGCCCGATCCAGC 18
DB 18 CTGCTCCAGATCTGAC 1

RESULT 35
US-08-642-407A-4/C
Sequence 4, Application US/08642407A
Patent No. 5877308
GENERAL INFORMATION:
APPLICANT: Oeystein, Fodstad
APPLICANT: Hovig, Elvind
APPLICANT: Engebraaten, Olav
APPLICANT: Maelandemo, Gunhild H.
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND
METHODS OF INHIBITING METASTATIC CANCER
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,407A
FILING DATE: 03-May-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-039CPDV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-642-407A-4

Query Match 64.4%; Score 11.6; DB 2; Length 22;
Best Local Similarity 77.8%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGCGCCCGATCCAGC 18
DB 18 CTGCTCCAGATCTGAC 1

RESULT 36
US-09-428-583-17/C
; Sequence 17, Application US/09428583
; Patent No. 6271029
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowest
; TITLE OF INVENTION: ANTISENSE MODULATION OF CYTOSIN-2 EXPRESSION
; FILE REFERENCE: RTS-0096
; CURRENT APPLICATION NUMBER: US/09/428,583
; CURRENT FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-428-583-17

Query Match 63.3%; Score 11.4; DB 4; Length 20;
Best Local Similarity 92.3%; Pred. No. 7.2e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCGGATCCAGC 18
| | | | | | | | | | | | | | | | | | | | | |
Db 16 CCGGATCCAGC 4

RESULT 37
US-08-585-595-35/C
; Sequence 35, Application US/08585595
; Patent No. 5795761
; GENERAL INFORMATION:
; APPLICANT: POWERS, DAVID B.
; TITLE OF INVENTION: IMPROVED METHODS FOR PRODUCING VITAMIN C
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWREY & SIMON
; STREET: 1299 PENNSYLVANIA AVENUE, N.W.
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/585,595
; FILING DATE: 16-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/584,019
; FILING DATE: 11-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: AUERBACH, JEFFREY I.
; REGISTRATION NUMBER: 32680
; REFERENCE/DOCKET NUMBER: 6137-0014 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 383-7451
; TELEFAX: (202) 383-6610
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO

ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: CORINBACTERIUM SP
US-08-585-595-35

Query Match 63.3%; Score 11.4; DB 1; Length 22;
Best Local Similarity 92.3%; Pred. No. 7.1e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCGCCCGATC 13
| | | | | | | | | | | | | | | | | | | | | |
Db 13 CCGGCGCCCGATC 1

RESULT 38
US-09-142-623-20/C
; Sequence 20, Application US/09142623
; Patent No. 6337201
; GENERAL INFORMATION:
; APPLICANT: KOJI YANAI et al.
; TITLE OF INVENTION: -FRUCTOFURANOSIDASE AND ITS GENE, METHOD OF
; TITLE OF INVENTION: ISOLATING -FRUCTOFURANOSIDASE GENE, SYSTEM FOR PRODUCING
; TITLE OF INVENTION: -FRUCTOFURANOSIDASE, AND -FRUCTOFURANOSIDASE VARIANT
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Menderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., Suite 800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; OPERATING SYSTEM: IBM Compatible
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/142,623
; FILING DATE: September 10, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee Cheng
; REGISTRATION NUMBER: 40,949
; REFERENCE/DOCKET NUMBER: 98-0989*/LC(WMC)/144
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-721-8250
; TELEFAX: 202-721-8250
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: Nucleic acid
; STRANDEDNESS: No. 6337201 relevant
; TOPOLOGY: Linear
; MOLECULE TYPE: Synthetic DNA
US-09-142-623-20

Query Match 63.3%; Score 11.4; DB 4; Length 22;
Best Local Similarity 92.3%; Pred. No. 7.1e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCCCGATCCAG 17
| | | | | | | | | | | | | | | | | | | | | |
Db 16 GCCCGATCCAG 4

RESULT 39
US-08-244-122-25/C
; Sequence 25, Application US/08244122
; Patent No. 5665777
; GENERAL INFORMATION:
; APPLICANT: Sijmons, Peter J.

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APPLICANT: Goddijn, Oscar J.M.
APPLICANT: Van Den Elzen, Petrus J. M.
APPLICANT: Van Der Lee, Frederique M.
TITLE OF INVENTION: Method for Obtaining Plants with
NUMBER OF SEQUENCES: Reduced Susceptibility to Plant-Parasitic Nematodes
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ladas & Parry
STREET: 26 West 61st Street
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10023
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
COMPUTER: IBM PC/XT/AT or compatibles
OPERATING SYSTEM: DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,122
FILING DATE: 19-MAY-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP92/02559
FILING DATE: 02-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NL91203041
FILING DATE: 20-NOV-1991
APPLICATION NUMBER: NL9200046
FILING DATE: 10-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: MASS, CLIFFORD, J.
REGISTRATION NUMBER: 30086
REFERENCE/DOCKET NUMBER: U-9672-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 708-1800
TELEFAX: (212) 246-8959
TELEX: 233288
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA
HYPOTHETICAL: YES
US-08-244-122-25

Query Match 63.3%; Score 11.4; DB 2; Length 24;
Best Local Similarity 92.3%; Pred. No. 7.1e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 5 GCCCGATCCAG 17
Db 14 GTCCGATCCAG 2

RESULT 40
US-08-679-645-531
Sequence 531, Application US/08679645
Patent No. 6350934
GENERAL INFORMATION:
APPLICANT: Zwick, Michael G.
APPLICANT: Edington, Brent E.
APPLICANT: McSwigen, James A.
APPLICANT: Merlo, Patricia Ann Owens
APPLICANT: Guo, Lining
APPLICANT: Skokut, Thomas A.
APPLICANT: Young, Scott A.
APPLICANT: Folkerts, Otto
APPLICANT: Merlo, Donald J.
TITLE OF INVENTION: COMPOSITION AND METHODS FOR
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TITLE OF INVENTION: MODULATION OF GENE EXPRESSION
TITLE OF INVENTION: IN PLANTS
NUMBER OF SEQUENCES: 1263
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/679,645
FILING DATE: July 12, 1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/001,135
FILING DATE: July 13, 1995
APPLICATION NUMBER: 08/300,726
FILING DATE: September 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 219/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 531:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-679-645-531

Query Match 62.2%; Score 11.2; DB 4; Length 16;
Best Local Similarity 68.8%; Pred. No. 8.9e+03;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy 1 CTGGCGCCGATCCAG 16
Db 1 CUGGCGCCUCACUCCAG 16

Search completed: June 7, 2003, 09:45:39
Job time : 47.9636 secs
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